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OM nucleic - nucleic search, using sw model

Run on: October 6, 2004, 17:57:26 ; Search time 698 Seconds
(without alignments)
9282.101 Million cell updates/sec

Title: US-10-016-647-1

Perfect score: 1278

Sequence: 1 atgactctggcgagcggg.....ccactgaattcctgaattaa 1278

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 3340653 seqs, 2534793454 residues

Total number of hits satisfying chosen parameters: 6681306

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/prodata/2/pubna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/prodata/2/pubna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/prodata/2/pubna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/prodata/2/pubna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/prodata/2/pubna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/prodata/2/pubna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/prodata/2/pubna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/prodata/2/pubna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/prodata/2/pubna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/prodata/2/pubna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/prodata/2/pubna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/prodata/2/pubna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/prodata/2/pubna/US09_NEW_PUB.seq:*
- 14: /cgn2_6/prodata/2/pubna/US10_PUBCOMB.seq:*
- 15: /cgn2_6/prodata/2/pubna/US10_PUBCOMB.seq:*
- 16: /cgn2_6/prodata/2/pubna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/prodata/2/pubna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/prodata/2/pubna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/prodata/2/pubna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1278	100.0	1278	14	US-10-016-647-1
2	1278	100.0	1844	14	US-10-016-647-3
3	1276.4	99.9	3215	15	US-10-198-869-1
4	1178.4	92.2	2235	16	US-10-415-378-39
5	1099.4	86.0	1651	13	US-10-114-270-45
6	594	46.5	594	15	US-10-198-869-26
7	403.4	31.6	417	15	US-10-198-869-27
8	363	30.0	461	13	US-09-852-386-25
9	348.4	27.3	777	9	US-09-989-920-7
10	336.4	26.3	911	9	US-09-989-920-8
11	280	21.9	2370	10	US-09-971-392-139
12	277.4	21.7	2127	14	US-10-143-002-1
13	277.4	21.7	2127	15	US-10-325-891-1
14	260.6	20.4	3756	17	US-10-377-139-18

15	260.2	20.4	2565	13	US-10-435-935-10	Sequence 10, Appl
16	258.8	20.3	2022	17	US-10-738-455-18	Sequence 18, Appl
17	256	20.0	2499	15	US-10-101-510-628	Sequence 628, App
18	253.6	19.8	2882	17	US-10-377-139-19	Sequence 19, Appl
19	251	19.6	1518	17	US-10-738-455-2	Sequence 2, Appl
20	198.2	15.5	2483	14	US-10-143-002-3	Sequence 3, Appl
21	198.2	15.5	2483	15	US-10-325-891-3	Sequence 3, Appl
22	197.8	15.5	3102	15	US-10-121-746-17	Sequence 17, Appl
23	197.8	15.5	5027	15	US-10-101-510-439	Sequence 439, App
c	171	13.4	998	9	US-09-864-761-1804	Sequence 1804, Ap
25	171	13.4	1979	9	US-09-864-761-3784	Sequence 3784, Ap
26	166.2	13.0	1340	9	US-09-864-761-20550	Sequence 20550, A
27	157.4	12.3	3080	15	US-10-121-746-7	Sequence 7, Appl
28	151.8	11.9	1455	13	US-10-114-270-43	Sequence 43, Appl
29	151.6	11.9	1638	13	US-09-833-466-2	Sequence 2, Appl
30	151.6	11.9	2103	17	US-10-815-297-2	Sequence 2, Appl
31	151.6	11.9	2103	17	US-09-833-466-1	Sequence 1, Appl
32	151.6	11.9	2103	17	US-10-815-297-1	Sequence 1, Appl
33	151.2	11.8	1638	13	US-09-818-359-1	Sequence 1, Appl
34	151.2	11.8	2310	13	US-09-818-359-5	Sequence 5, Appl
35	150.4	11.8	2850	10	US-09-999-2203-1	Sequence 1, Appl
36	148.6	11.6	1871	10	US-09-999-2203-119	Sequence 119, App
37	148.6	11.6	2850	10	US-09-999-2203-115	Sequence 115, App
38	148.4	11.6	1871	10	US-09-999-2203-35	Sequence 35, Appl
39	146	11.4	1475	13	US-10-435-935-2	Sequence 2, Appl
40	146	11.4	2293	15	US-10-121-746-5	Sequence 5, Appl
41	146	11.4	2421	13	US-10-435-935-1	Sequence 1, Appl
42	145.4	11.4	1657	15	US-10-029-386-25090	Sequence 25090, A
c	143	11.2	763	15	US-10-029-386-24921	Sequence 24921, A
44	143	11.2	804	15	US-10-029-386-25062	Sequence 25062, A
45	141.6	11.1	2573	17	US-10-467-595-73	Sequence 73, Appl

ALIGNMENTS

RESULT 1

US-10-016-647-1
; Sequence 1, Application US/10016647
; Publication No. US0020160475A1
; GENERAL INFORMATION:
; APPLICANT: Hilbule, Carl Johan
; APPLICANT: Hilbule, Erin
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20020160475A1 Human Ion Channel Protein and Polynucleotide
; FILE REFERENCE: LEX-0284-USA
; CURRENT APPLICATION NUMBER: US/10/016,647
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/257,932
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1278
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-016-647-1

Query Match 100.0%; Score 1278; DB 14; Length 1278;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACCTTCGGGCGCAGCGGGCGGCTCGTGTGTGCTGAACGTGGCGCGCCCGGTAT 60

Db 1 ATGACCTTCGGGCGCAGCGGGCGGCTCGTGTGTGCTGAACGTGGCGCGCCCGGTAT 60

QY 61 TCGGTGTCCGGGAGCTGCTGAAGACTTCCGCTGCGCGCGCTGAGCCGCTCAGGC 120

Db 61 TCGGTGTCCGGGAGCTGCTGAAGACTTCCGCTGCGCGCGCTGAGCCGCTCAGGC 120

QY 121 TCGCGCTCCGAGCGCGAGCTGCTCGAGGTGTGCGACACTACGACCGCGAGCGAAG 180

Db 121 TCGCGCTCCGAGCGCGAGCTGCTCGAGGTGTGCGACACTACGACCGCGAGCGAAG 180

QY 181 TACTTCTTCGACCGGCACTCGAGGCTTCGGCTTCATCTGCTCTACGTCGCGCGCCAC 240
 Db 181 TACTTCTTCGACCGGCACTCGAGGCTTCGGCTTCATCTGCTCTACGTCGCGCGCCAC 240
 QY 241 GGCAAGCTGGGCTTCGGCGCGCGAGATGCGAGCTCTCTCTTACAAACGAGATGATCTAC 300
 Db 241 GGCAAGCTGGGCTTCGGCGCGCGAGATGCGAGCTCTCTCTTACAAACGAGATGATCTAC 300
 QY 301 TGGGGCTGGAGCGCGGCACTTCGAGTACTGTCGAGCGCGCTTCGAGCAGCCATG 360
 Db 301 TGGGGCTGGAGCGCGGCACTTCGAGTACTGTCGAGCGCGCTTCGAGCAGCCATG 360
 QY 361 TCCGACACCTACCTTCTACTCGCGCGAGCGCGGCTGTCGCGCGCGAGGCG 420
 Db 361 TCCGACACCTACCTTCTACTCGCGCGAGCGCGGCTGTCGCGCGCGAGGCG 420
 QY 421 CGCGCGCGCGCGCGGCTTCCTTCAGGGCTGGCTGGAGCGCATGCGCGGAC 480
 Db 421 CGCGCGCGCGCGCGGCTTCCTTCAGGGCTGGCTGGAGCGCATGCGCGGAC 480
 QY 481 TTCGAGAGCCACGTCGTCGCGCGCGAGATCTGCTAGCGTTCGCTGCTG 540
 Db 481 TTCGAGAGCCACGTCGTCGCGCGCGAGATCTGCTAGCGTTCGCTGCTG 540
 QY 541 GTGATCGTGTCCATGCTGTGTCGCGCGAGCACTGTCGCGCGAGCGCGAGCC 600
 Db 541 GTGATCGTGTCCATGCTGTGTCGCGCGAGCACTGTCGCGCGAGCGCGAGCC 600
 QY 601 GCCGACACCGCGCTGGATGACCGGAGCAGATATTCAGCTATCTCATAGTTG 660
 Db 601 GCCGACACCGCGCTGGATGACCGGAGCAGATATTCAGCTATCTCATAGTTG 660
 QY 661 TTACTGCGAGTGCATCGTAGGTTCAATGTTCTCCAAAACAAAGTGTGAGTTG 720
 Db 661 TTACTGCGAGTGCATCGTAGGTTCAATGTTCTCCAAAACAAAGTGTGAGTTG 720
 QY 721 AGACCCCTGACATCATGATTTACTGGCAATCAGCGCTATTACATCTGTTGATG 780
 Db 721 AGACCCCTGACATCATGATTTACTGGCAATCAGCGCTATTACATCTGTTGATG 780
 QY 781 ACAGTGTTCACGCGAGAACTCTCAACTCCAGAGGCTCGAGTCACTTTGAGGTA 840
 Db 781 ACAGTGTTCACGCGAGAACTCTCAACTCCAGAGGCTCGAGTCACTTTGAGGTA 840
 QY 841 AGAATGATGAGGATTTTGGTGATTAAGCTTCGCGCTCACTTCATGCTTCAGACA 900
 Db 841 AGAATGATGAGGATTTTGGTGATTAAGCTTCGCGCTCACTTCATGCTTCAGACA 900
 QY 901 CTCGGTTGACTCTCAACAGTTGCTACCGAGATGTTATGTTACTTGTCTTCA 960
 Db 901 CTCGGTTGACTCTCAACAGTTGCTACCGAGATGTTATGTTACTTGTCTTCA 960
 QY 961 GTTGCCATGGAATCTTTAGTGCACTTTCTCAGCTTCTTGAAATGCGCTGGAA 1020
 Db 961 GTTGCCATGGAATCTTTAGTGCACTTTCTCAGCTTCTTGAAATGCGCTGGAA 1020
 QY 1021 ACATCCACAGGACTTTACGACATTCCTGCTGCTGCTGGTGGTATCTCTATG 1080
 Db 1021 ACATCCACAGGACTTTACGACATTCCTGCTGCTGCTGGTGGTATCTCTATG 1080
 QY 1081 ACTACAGTGGCTATGGAGATATGATATCTATCAGTGTGCTGGAAGATTTTGAGGA 1140
 Db 1081 ACTACAGTGGCTATGGAGATATGATATCTATCAGTGTGCTGGAAGATTTTGAGGA 1140
 QY 1141 GTTTGCTGTTCAGTGAATGTTCTATGCGATTTACCTATCACTTTATCTACCATAG 1200
 Db 1141 GTTTGCTGTTCAGTGAATGTTCTATGCGATTTACCTATCACTTTATCTACCATAG 1200
 QY 1201 TTTGTGAGTGTATCATGAGCTCAAGTTTAGATCTGCTAGGTATAGTAGGACCTCTCC 1260
 Db 1201 TTTGTGAGTGTATCATGAGCTCAAGTTTAGATCTGCTAGGTATAGTAGGACCTCTCC 1260

QY 1261 ACTGAATTCCTGAATTA 1278
 Db 1261 ACTGAATTCCTGAATTA 1278
 RESULT 2
 US-10-016-647-3
 ; Sequence 3, Application US/10016647
 ; Publication No. US20020160475A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fiddle, Carl Johan
 ; APPLICANT: Hibun, Erin
 ; APPLICANT: Turner, C. Alexander Jr.
 ; TITLE OF INVENTION: NO. US20020160475A1 Human Ion Channel Protein and Polynucleotide
 ; FILE REFERENCE: LEX-0284-USA
 ; CURRENT APPLICATION NUMBER: US/10/016,647
 ; CURRENT FILING DATE: 2001-12-10
 ; PRIOR APPLICATION NUMBER: US 60/257,932
 ; PRIOR FILING DATE: 2000-12-20
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 1844
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 ; US-10-016-647-3
 Query Match 100.0%; Score 1278; DB 14; Length 1844;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGACCTTCGGCGCGAGCGCGCTCGTGTGCTGACGTCGCGCGCGCGCGGAT 60
 Db 457 ATGACCTTCGGCGCGAGCGCGCGCTCGTGTGCTGACGTCGCGCGCGCGCGGAT 515
 QY 61 TCGCTGTCCCGGAGCTGCTGAAGACTTCCCGCTGCGCGCGCTGAGCGCGCTG 120
 Db 517 TCGCTGTCCCGGAGCTGCTGAAGACTTCCCGCTGCGCGCGCTGAGCGCGCTG 576
 QY 121 TCGCGCTCGAGCGCGAGCTGCTGAGGTGCGAGCACTACGACCGCGCGCAAGAG 180
 Db 577 TCGCGCTCGAGCGCGAGCTGCTGAGGTGCGAGCACTACGACCGCGCGCAAGAG 636
 QY 181 TACTTCTTCGACCGGCACTCGAGGCTTCGCGCTTCATCTCTACGTCGCGCGCAC 240
 Db 637 TACTTCTTCGACCGGCACTCGAGGCTTCGCGCTTCATCTCTACGTCGCGCGCAC 696
 QY 241 GGCAAGCTGCGCTTCGCGCGCGGATGTCGAGCTCTCTCTTACAAACGAGATCTAC 300
 Db 697 GGCAAGCTGCGCTTCGCGCGCGGATGTCGAGCTCTCTCTTACAAACGAGATCTAC 756
 QY 301 TGGGCGCTGGAGGCGCGCACTCGAGTACTGCTGCGAGCGCGCTCGACCGCGCATG 360
 Db 757 TGGGCGCTGGAGGCGCGCACTCGAGTACTGCTGCGAGCGCGCTCGACCGCGCATG 816
 QY 361 TCCGACACCTACCTTCTACTCGCGCGAGCGAGCGCGCTGTCGCGCGCGAGCGCG 420
 Db 817 TCCGACACCTACCTTCTACTCGCGCGAGCGAGCGCGCTGTCGCGCGCGAGCGCG 876
 QY 421 CGCGCGCGCGCGCGGCTTCCTTCAGGCGCTGGCTGGAGCGCATGCGCGCGGAC 480
 Db 877 CGCGCGCGCGCGCGGCTTCCTTCAGGCGCTGGCTGGAGCGCATGCGCGCGGAC 936
 QY 481 TTCGAGAGCGCGCTGCTGCTGCGCGCGAGATCTCTGCTAGCGTGTGGTGTGTT 540
 Db 937 TTCGAGAGCGCGCTGCTGCTGCGCGCGAGATCTCTGCTAGCGTGTGGTGTGTT 996
 QY 541 GTGATCGTGTTCAGTGGTGTGCTGTCGCGCGAGCTGTCGCGCGCGCGCGCGG 600
 Db 997 GTGATCGTGTTCAGTGGTGTGCTGTCGCGCGAGCTGTCGCGCGCGCGCGG 1056
 QY 601 GCCGACACCGCGCTGATGACCGGAGCAGGATAATTGAAGCTATCTGATAGTTGG 660

Db 1057 GCGCAACACCGCAGCCCTGGATGACCGGAGCAGGATAATTGAAGCTATCTGCATAGTTGG 1116
QY 661 TTCACCTGCCAGTGCATCTGAGGTTCAATGCTCCAAACAAAGTGTGAGTTTCTCAAG 720
Db 1117 TTCACCTGCCAGTGCATCTGAGGTTCAATGCTCCAAACAAAGTGTGAGTTTCTCAAG 1176
QY 721 AGACCCCTGAACATCATATTGATTTACTGGCAATCACGCCGTATTACATCTCTGTGTGATG 780
Db 1177 AGACCCCTGAACATCATATTGATTTACTGGCAATCACGCCGTATTACATCTCTGTGTGATG 1236
QY 781 ACAGTGTTCACAGGCGAGACTCTCACTCCAGAGGGCTGGAGTCACTTGGAGTACTT 840
Db 1237 ACAGTGTTCACAGGCGAGACTCTCACTCCAGAGGGCTGGAGTCACTTGGAGTACTT 1296
QY 841 AGAATGATGAGGATTTTTTGGGTGATTAAGCTTTGCCCGTCACTTCATTGGTCTTCAGACA 900
Db 1297 AGAATGATGAGGATTTTTTGGGTGATTAAGCTTTGCCCGTCACTTCATTGGTCTTCAGACA 1356
QY 901 CTCGGTTTCACTCTCAAGCTTGTACCGAGAGATGGTTATGTTACTTGTCTTCAATTTGT 960
Db 1357 CTCGGTTTCACTCTCAAGCTTGTACCGAGAGATGGTTATGTTACTTGTCTTCAATTTGT 1416
QY 961 GTTGCCATGGCAATCTTTAGTGCACTTCTCAGCTTCTTGAACATGGGCTGGACCTGGAA 1020
Db 1417 GTTGCCATGGCAATCTTTAGTGCACTTCTCAGCTTCTTGAACATGGGCTGGACCTGGAA 1476
QY 1021 ACATCAACAAGGACTTTACCAAGCATTCCTGTGCTGCTGTGCTGTGCTGTGCTGTGCTGTG 1080
Db 1477 ACATCAACAAGGACTTTACCAAGCATTCCTGTGCTGCTGTGCTGTGCTGTGCTGTGCTGTG 1536
QY 1081 ACTACAGTTGGCTATGAGATATGATCTATCAGCTTCTTGAACATGGGCTGGAGAACTTCTGGAGGA 1140
Db 1537 ACTACAGTTGGCTATGAGATATGATCTATCAGCTTCTTGAACATGGGCTGGAGAACTTCTGGAGGA 1596
QY 1141 GTTGCTGTTGTCACTGGAAATTTCTTATGGCAATACCTATCACTTTTATCTACCATAGC 1200
Db 1597 GTTGCTGTTGTCACTGGAAATTTCTTATGGCAATACCTATCACTTTTATCTACCATAGC 1656
QY 1201 TTGTGCACTGTATCATGAGCTCAAGTTAGATCTGCTAGGTATAGTAGGAGCTCTCC 1260
Db 1657 TTGTGCACTGTATCATGAGCTCAAGTTAGATCTGCTAGGTATAGTAGGAGCTCTCC 1716
QY 1261 ACTGAATTCCTGAAATTA 1278
Db 1717 ACTGAATTCCTGAAATTA 1734

RESULT 3

US-10-199-869-1
; Sequence 1, Application US/10199869
; Publication No. US20030152953A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUB
; TITLE OF INVENTION: K-alpha2
; FILE REFERENCE: D0161 NP
; CURRENT APPLICATION NUMBER: US/10/199,869
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/306,577
; PRIOR FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 3215
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1275)
; OTHER INFORMATION:
US-10-199-869-1

Query Match

99.9%; Score 1276.4; DB 15; Length 3215;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 1277; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGACCTTCGGGCGCAGCGGGCGCTCGTGGTGTGAACGTGGCGCGCGCGCTAT 60
Db 1 ATGACCTTCGGGCGCAGCGGGCGCGCTCGTGGTGTGAACGTGGCGCGCGCGCTAT 60
QY 61 TCGCTGTCCCGGAGCTGTCTGAAGGACTTCCCGCTGCGCGCGCTGAGCCGGCTGACGGC 120
Db 61 TCGCTGTCCCGGAGCTGTCTGAAGGACTTCCCGCTGCGCGCGCTGAGCCGGCTGACGGC 120
QY 121 TCGCGCTCCAGAGCGCAGCTGCTCGAGGTGTGGAGCACTACGACCGGAGCGCAAGAG 180
Db 121 TCGCGCTCCAGAGCGCAGCTGCTCGAGGTGTGGAGCACTACGACCGGAGCGCAAGAG 180
QY 181 TACTTCTTCGACCGGCACTCGGAGGCTTCCGCTTCACTCTGCTCTACGTGCGCGGCGAC 240
Db 181 TACTTCTTCGACCGGCACTCGGAGGCTTCCGCTTCACTCTGCTCTACGTGCGCGGCGAC 240
QY 241 GCGAAGCTGCGCTTCGCGCGCGGATGTGCGAGCTCTCTTACACGAGATGATCTAC 300
Db 241 GCGAAGCTGCGCTTCGCGCGCGGATGTGCGAGCTCTCTTACACGAGATGATCTAC 300
QY 301 TGGGGCTTCGAGGCGCGCAGCTCGAGTACTGTGCCAGCGCGCTTCGAGCGCGCATG 360
Db 301 TGGGGCTTCGAGGCGCGCAGCTCGAGTACTGTGCCAGCGCGCTTCGAGCGCGCATG 360
QY 361 TCCGACACCTTACACCTTCTACTCGGCGCAGCGCGCGCTGCTGGCGCGCGAGCGG 420
Db 361 TCCGACACCTTACACCTTCTACTCGGCGCAGCGCGCGCTGCTGGCGCGCGAGCGG 420
QY 421 CGCCCGCGCGCGCGCGCGCTCCCTCCAGCGCTGGCTGGAGCGCATGCGCGCGAC 480
Db 421 CGCCCGCGCGCGCGCGCGCTCCCTCCAGCGCTGGCTGGAGCGCATGCGCGCGAC 480
QY 481 TTCAGAGAGCCACGCTCGCTGCGCGCGCAGATCTCGCTAGCGTGTGCGTGTTC 540
Db 481 TTCAGAGAGCCACGCTCGCTGCGCGCGCAGATCTCGCTAGCGTGTGCGTGTTC 540
QY 541 GTGATCGTGTCCATGCTGTGCGCGCAGCAGTGTGCCAGCTGCGCGCGCAAGCGAC 600
Db 541 GTGATCGTGTCCATGCTGTGCGCGCAGCAGTGTGCCAGCTGCGCGCGCAAGCGAC 600
QY 601 GCCGACAAACCGCAGCTGGATGACCGGAGCAGGATTAATGAAGCTATCTGCTAGGTGG 660
Db 601 GCCGACAAACCGCAGCTGGATGACCGGAGCAGGATTAATGAAGCTATCTGCTAGGTGG 660
QY 661 TTCACTGCGAGTGCATCTGAGGTTCAATGCTTCCAAAAACAAGTGTGAGTTTGTCAAG 720
Db 661 TTCACTGCGAGTGCATCTGAGGTTCAATGCTTCCAAAAACAAGTGTGAGTTTGTCAAG 720
QY 721 AGACCCCTGAACATCATTTGATTTACTGGCAATCACGCCGTATTACATCTCTGTTGATG 780
Db 721 AGACCCCTGAACATCATTTGATTTACTGGCAATCACGCCGTATTACATCTCTGTTGATG 780
QY 781 ACAGTGTTCACAGCGAGAACTCTCAACTCCAGAGGGCTGGAGTCACTTGGAGGTACTT 840
Db 781 ACAGTGTTCACAGCGAGAACTCTCAACTCCAGAGGGCTGGAGTCACTTGGAGGTACTT 840
QY 841 AGAATGATGAGGATTTTTTGGGTGATTAAGCTTTGCCCGTCACTTCATTGGTCTTCAGATA 900
Db 841 AGAATGATGAGGATTTTTTGGGTGATTAAGCTTTGCCCGTCACTTCATTGGTCTTCAGATA 900
QY 901 CTCGGTTTGACTCTCAACCGTTGTACCGAGAGATGGTTATGTTACTTGTCTTCAATTTGT 960
Db 901 CTCGGTTTGACTCTCAACCGTTGTACCGAGAGATGGTTATGTTACTTGTCTTCAATTTGT 960
QY 961 GTTGCCATGGCAATCTTTAGTGCACTTTCTCAGCTTCTTGAACATGGGCTGGACCTGGAA 1020
Db 961 GTTGCCATGGCAATCTTTAGTGCACTTTCTCAGCTTCTTGAACATGGGCTGGACCTGGAA 1020
QY 1021 ACATCAACAAGGACTTTACCAAGCATTCCTGTGCTGCTGTGCTGTGCTGTGCTGTG 1080

Db 1487 ACTACAGTGGCTATGAGATATGTATCTCATCACAGTGCCTGGAGAAATTTCTGGAGGA 1546
 QY 1141 GTTTGGTTGTAGTGGAAATTTGTTATTGGCAATACCTATACATTTTATCTACCATAGC 1200
 Db 1547 GTTTGGTTGTAGTGGAAATTTGTTATTGGCAATACCTATACATTTTATCTACCATAGC 1606
 QY 1201 TTTGTCAGTGTATCATGAGCTCAAGTTTAGATTCTGCTAGGTATAGTAG 1250
 Db 1607 TTTGTCAGTGTATCATGAGCTCAAGTTTAGATTCTGCTAGGTATAGTAG 1656

RESULT 5

US-10-114-270-45
 ; Sequence 45: Application US/10114270
 ; Publication No. US20040030110A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Miller, Charles E.
 ; APPLICANT: Malyankar, Uriel M.
 ; APPLICANT: Spytek, Kimberly A.
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Liu, Ziaohong
 ; APPLICANT: Gusev, Vladimir Y.
 ; APPLICANT: Li, Li
 ; APPLICANT: Vernst, Corine
 ; APPLICANT: Zerhusen, Bryan D.
 ; APPLICANT: Gorman, Linda
 ; APPLICANT: Shenoy, Suresh G.
 ; APPLICANT: Pena, Carol E.A.
 ; APPLICANT: Smithson, Glennda
 ; APPLICANT: Burgess, Catherine E.
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Shimkets, Richard A.
 ; APPLICANT: Gangolli, Esha A.
 ; APPLICANT: Taupier Jr., Raymond J.
 ; APPLICANT: Casman, Stacie J.
 ; APPLICANT: Ji, Weizhen
 ; APPLICANT: Anderson, David W.
 ; APPLICANT: Liette, Mario W.
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Edinger, Shlomit R.
 ; APPLICANT: Stone, David J.
 ; APPLICANT: MacDougall, John R.
 ; APPLICANT: Rothenberg, Mark E.
 ; TITLE OF INVENTION: No. US20040030110A1el Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 21402-322C
 ; CURRENT APPLICATION NUMBER: US/10/114,270
 ; PRIOR FILING DATE: 2002-11-27
 ; PRIOR APPLICATION NUMBER: 60/281,086
 ; PRIOR FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: 60/281,136
 ; PRIOR FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: 60/281,863
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/281,906
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/282,020
 ; PRIOR FILING DATE: 2001-04-06
 ; PRIOR APPLICATION NUMBER: 60/282,930
 ; PRIOR FILING DATE: 2001-04-10
 ; PRIOR APPLICATION NUMBER: 60/282,934
 ; PRIOR FILING DATE: 2001-04-10
 ; PRIOR APPLICATION NUMBER: 60/283,512
 ; PRIOR FILING DATE: 2001-04-12
 ; PRIOR APPLICATION NUMBER: 60/283,710
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/284,234
 ; PRIOR FILING DATE: 2001-04-17
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 470
 ; SEQ ID NO 45

; LENGTH: 1651
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1642)
 ; US-10-114-270-45
 Query Match 86.0%; Score 1099.4; DB 13; Length 1651;
 Best Local Similarity 91.4%; Pred. No. 1.6e-309;
 Matches 1231; Conservative 0; Mismatches 11; Indels 105; Gaps 2;
 QY 1 ATGACCTTCGGCGCAGCGGGCGCTCGTGTGTCTGAACGTGGCGGGCCCGGTAT 60
 Db 58 ATGACCTTCGGCGCAGCGGGCGCTCGTGTGTCTGAACGTGGCGGGCCCGGTAT 117
 QY 61 TCGCTGTCCCGGAGCTGCTGAAGGACTTCCCGTGGCGCGGTGAGCCCGGTGCAAGGC 120
 Db 118 TCGCTGTCCCGGAGCTGCTGAAGGACTTCCCGTGGCGCGGTGAGCCCGGTGCAAGGC 177
 QY 121 TCGCGCTCCGAGCGCGAGGTGCTCGAGGTGTGCGAGCTACGACCTACGCGCGGCAACGAG 180
 Db 178 TCGCGCTCCGAGCGCGAGGTGCTCGAGGTGTGCGAGCTACGACCTACGCGCGGCAACGAG 237
 QY 181 TACTTCTTCGACCGCGCACTCGAGGCGCTTCGGCTTCATCTCTCTACGTGCGGCGCAC 240
 Db 238 TACTTCTTCGACCGCGCACTCGAGGCGCTTCGGCTTCATCTCTCTACGTGCGGCGCAC 297
 QY 241 GCGAGCTGCGCTTCGCGCGCGCGATGTGCGAGCTCTCTCTTCTACAGAGATGATCTAC 300
 Db 298 GCGAGCTGCGCTTCGCGCGCGCGATGTGCGAGCTCTCTCTTCTACAGAGATGATCTAC 357
 QY 301 TGGGCGCTGGAGGGCGCGCACTCGAGTACTGCTGCCAGCGCGCGCTCGACGCGCATG 360
 Db 358 TGGGCGCTGGAGGGCGCGCACTCGAGTACTGCTGCCAGCGCGCGCTCGACGCGCATG 417
 QY 361 TCCGACACCTACACTTTTACTCGGCCGAGCGAGCGGCGGTGCTGGGCGCGCGAGGCG 420
 Db 418 TCCGACACCTACACTTTTACTCGGCCGAGCGAGCGGCGGTGCTGGGCGCGCGAGGCG 477
 QY 421 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 434
 Db 478 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 537
 QY 435 -----CGAGGGCGCGCTCCCTCCAGGCGCGCTGGTGGAGCGCATGCGGCGGACCTT 483
 Db 538 CGAGGAGCCACGCTCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTT 597
 QY 484 GAGGAGCCACGCTGCTGCGCGCGCGCGAGATCTGCGTAGCGGTGCGGTGCTGCTG 543
 Db 598 GAGGAGCCACGCTGCTGCGCGCGCGCGAGATCTGCGTAGCGGTGCGGTGCTGCTG 657
 QY 544 ATCGTGTCCATGGTGTGCTGCGCGCGCGAGCATGTCGCCGCTGGCGCAACGCGAGCCGCC 603
 Db 658 ATCGTGTCCATGGTGTGCTGCGCGCGCGAGCATGTCGCCGCTGGCGCAACGCGAGCCGCC 717
 QY 604 GACAAACGCGAGCGGTGATGACCGGAG----- 629
 Db 718 GACAAACGCGAGCGGTGATGACCGGAGCGAGGTACTCCGCGCGCGCTGGGAGGAGCGCTCC 777
 QY 630 -----CAGGATTAATGAGCTATCTGCATAGGTGCTTCACTCGCGAGTGC 675
 Db 778 GGGTGTTCCTTTGACAGGATTAATGAGCTATCTGCATAGGTGCTTCACTCGCGAGTGC 837
 QY 676 ATCGTGAGGTTCATGTCTCCAAAAACAAGTGTGAGTTGTCAAGAGACCCCTGAACATC 735
 Db 838 ATCGTGAGGTTCATGTCTCCAAAAACAAGTGTGAGTTGTCAAGAGACCCCTGAACATC 897
 QY 736 ATGATTTACTGGCAATCACGCCGTATTACATCTCTGTGTTGATGACAGTGTTCACAGC 795
 Db 898 ATGATTTACTGGCAATCACGCCGTATTACATCTCTGTGTTGATGACAGTGTTCACAGC 957
 QY 796 GAGAACTCTCAACTCCAGAGGGCTGGAGTCACTTGGAGGTACTTAGAATGATGAGGATT 855

Qy	391	GAGCGGGCTGTGGCGCGCGAGGGCGGCCCGCGGGCGAGCGGCTCCCTC	449
Db	361	GAGCGGGCTGTGGCGCGCGAGGGCGGCCCGCGGGCGGCGGCTCCCTC	417

RESULT 8

```

US-09-852-386-25
; Sequence 25, Application US/09852386
; Publication No. US2003064433A1
; GENERAL INFORMATION:
; APPLICANT: Roberts, Steven L.
; APPLICANT: Benjamin, Christopher
; APPLICANT: Karnovsky, Alla M.
; APPLICANT: Ruble, Cara L.
; TITLE OF INVENTION: Human Ion Channels
; FILE REFERENCE: 00133 US1
; CURRENT APPLICATION NUMBER: 09/852,386
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,305
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 60/207,092
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/206,526
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,033
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/207,093
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/216,893
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/237,873
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: 60/223,245
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn version 3.0

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; SEQ ID NO 25
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-852-386-25

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Query Match	30.0%	Score 383;	DB 13;	Length 461;
Best Local Similarity	99.7%	Pred. No. 5.7e-101;		
Matches 394:	Conservative	0;	Mismatches 0;	Indels 1;
				Gaps 1;

Qy	885	CATTGGTCTTTCAGACACCTCCGGTTTGA	CTCTCAACCGTTGCTACCCGAG-AGATGTTATG	943
Dp	1	CATTGGTCTTTCAGACACCTCCGGTTTGA	CTCTCAACCGTTGCTACCCGAGAGATGTTATG	60

944	TACTTGCTTTCAATTGTGTTGCCATGGCAATCTTTAGTGCACATTTCTCAGCTTCCTTGAACTTTGAAC	1003
D8	TACTTGCTCTCATTTGTGTTGCCATGGCAATCTTTAGTGCACATTTCTCAGCTTCCTTGAACTTTGAAC	120

Qy	1004	ATGGGCTGACCTGGAAACATCCAA	CAAGGACTTTTACCAAGCATTCCTGCTGCCTGCTGGT	1053
Dβ	121	ATGGGCTGACCTGGAAACATCCAA <th>CAAGGACTTTTACCAAGCATTCCTGCTGCCTGCTGGT</th> <td>180</td>	CAAGGACTTTTACCAAGCATTCCTGCTGCCTGCTGGT	180

Qy	1064	GGGTGATTCTCTATGACTACAGTTGGCTATGGAGATATGTATCTCTATCATCAGTCGCTG	1123
Db	181	GGGTGATTCTCTATGACTACAGTTGGCTATGGAGATATGTATCTCTATCATCAGTCGCTG	240

Accession	Gene	Accession	Gene
1124	GAAGAATCTTGGAGGAGTTTGTGTGTCAGTGGAAATGTTCTATTGGCAATTACCTATCA	1183	GAAGAATCTTGGAGGAGTTTGTGTGTCAGTGGAAATGTTCTATTGGCAATTACCTATCA
Qy			
241	GAAGAATCTTGGAGGAGTTTGTGTGTCAGTGGAAATGTTCTATTGGCAATTACCTATCA	300	GAAGAATCTTGGAGGAGTTTGTGTGTCAGTGGAAATGTTCTATTGGCAATTACCTATCA
Db			

Accession	Sequence	Length
Qy	CTTTTATCTACCACTAGCTTTGTGCAGTGTATCATGAGCTCAAGTTTAGATCTGCTAGGT	1184
Db	CTTTTATCTACCACTAGCTTTGTGCAGTGTATCATGAGCTCAAGTTTAGATCTGCTAGGT	301
	CTTTTATCTACCACTAGCTTTGTGCAGTGTATCATGAGCTCAAGTTTAGATCTGCTAGGT	360

1244 ATAGTAGGAGCCTCTCCACTGAATTCCCTGAATTAA 1278

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361 ATAGTAGGAGCCCTCTCCACTGAATTCCTGAATTAA 395

RESULT 9

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US-09-389-920-7/C
; Sequence 7, Application US/09099920
; Patent No. US20020172957A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Harve
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Liu, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions a
; FILE REFERENCE: DEX-0291
; CURRENT APPLICATION NUMBER: US/09/
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,5
; NUMBER OF SEQ ID NOS: 284
; PRIORITY FILING DATE: 2000-11-22
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 7
; LENGTH: 777
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-389-920-7

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Query Match 27.3%; Score 348.4; DB 9; Length 777;
Best Local Similarity 99.2%; Pred. NO. 9e-91;
Matches 371: Conservative 0; Mismatches 1; Indels 2

Qy	905	GTGTGACTCTCAAAACGTTGCTACCGAGAGATGTTTA	TGTTA	CTTGTCTTCATTGTGTG	964
Dp	703	GTGTGACTCTCAAAACG-TGCTACCGAGAGATGTTTA	TGTTAC-TGCTTCATATTGTGTG		646

Qy	965	CCATGGCAATCTTTTAGTGCATTTTCTAGCTTCTTGAACATGGGCTGGAACCTGGAAACAT	1024
pH	645	CCATGGCAATCTTTTAGTGCATTTTCTAGCTTCTTGAACATGGGCTGGAACCTGGAAACAT	586

Qy	1025	CCAAACAAGCATTTACAGCATTCTCGTGGGTGATTAATCTCTATGACTA	1084
Dh	585	CCAACAAGGACTTTACAGCACTTCCTGTCGCCTGGGTGATTAATCTCTATGACTA	526

Qy . 1085 CAGTTGGCTATGAGAGATATGTAATCTCTATCAACAGTGCCTGGAGAGAAATCTCTGGAGGAGTTT 1144

ph 525 CAGTTGGCTATGAGAGATATGTAATCTCTATCAACAGTGCCTGGAGAGAAATCTCTGGAGGAGTTT 466

Qy 1145 GGTGTGTCAGTGGAAATGCTTCATATTGGCAATTACCTATCACCTTTTATCTACCAATAGCTTTG 12045

QY 1205 TGCAGTGTATTCAATGAGCTCAAGTTTAGATCTGCTAGGTATAGTAGGAGCCTCTCCACATG 126

pb 405 TGCAGTGTATTCAATGAGCTCAAGTTTAGATCTGCTAGGTATAGTAGGAGCCTCTCCACATG 346

Qy	1265	AATTCCTGAATTAA	1278
Dh	345	AATTCCTGAATTAA	332

RESISTANCE

US-09-995-920-8
; Sequence 8, Application US/09989920
; Patent No. US20020172957A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Harve
; APPLICANT: Chen, Sei-yu
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions a
; FILE REFERENCE: DEX-0291
; CURRENT APPLICATION NUMBER: US/09/

Db 1712 CGACGGTGGGCTATGGGACATGGTCCCGAGAGACACCCCGGCGCAGGTAGTGGCCCTGA 1771
Qy 1142 TTGTGTTGTGTCAGTGAATTTGTTAATGGATTACCTATACATTTTATCTACCATAGCT 1201
Db 1772 GCAGCATCCTGAGCGGATCCTGCTCATGGCTTCCAGTCACCTCCATCTTCCACACT 1831
Qy 1202 TTGTGAGTGTATCATGAGCTCAAG 1227
Db 1832 TCTCCGGCTCTTACCTGGAGCTCAAG 1857

RESULT 12

US-10-143-002-1
; Sequence 1, Application US/10143002
; Publication No. US20020132775A1
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Potassium Channel Protein 1
; and 2

; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARBELL, BYRNE, BAIN, GILFILLAN,
; CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068

COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/143,002
; FILING DATE: 13-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/102,493
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/08/468,533
; FILING DATE: 6 JUNE 1995
; APPLICATION NUMBER: PCT/US94/08449
; FILING DATE: 28 JUL 1994

ATTORNEY/AGENT INFORMATION:

; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-310

TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 2127 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-143-002-1

Query Match 21.7%; Score 277.4; DB 14; Length 2127;
Best Local Similarity 55.2%; Pred. No. 7.4e-70;
Matches 676; Conservative 0; Mismatches 501; Indels 48; Gaps 5;

Qy 38 TGAAGTGGCGCGCGCGGATTCGGCTGTCGCGGAGCTGCTGAAGGACTTCCCGCTGC 97
Db 481 TCAACGTAGCGGCATCAAGTACTCGTCCCTGGACCACTGGACGAGTTCGCGCTGA 540
Qy 98 GCCCGGTAGCGGCTGCACGCGCTCCCGCTCGAGCGGACGCTGCTCGAGGTGTCGACG 157
Db 541 CGCGGCTGGCGCAGCTCAAGGCGCTGCACCACTTCGACGACATCTCAACGTGCGGATG 600

Qy 158 ACTACGACCGCGAGCGCAAGAGTACTTCTTCGACCGGCACCTCGGAGGCTTCGGCTTCA 217
Db 601 ACTACGACGTCACCTCAACGAGTCTTCTTCGACCGCAACCCGGGGGCTTCGGCACAT 660
Qy 218 TCCTGCTCTACGTGCGCGGCGACGCAAGCTGCGCTTCGCGCGCGGATGTGCGAGCTCT 277
Db 661 TCTGACCTTCTGCGG---CGGGCAAGCTGCGGCTGCTGCGCGAGATGTGCGCGCTGT 717
Qy 278 CTTTCTAACAGAGATGATCTACTGGGGCTTGAGGGCGGCGACCTCGAGTACTTGTGCC 337
Db 718 CTTTCCAGGAGGAGCTGCTGTACTGGGGCATCGCGAGGACACCTTGGAGCGGTGTGCA 777
Qy 338 AGCGCGCTCGACGACCGCATGTCCGACACCTTACTCGCGCGAGCGAGCGG 397
Db 778 AGCGCGCTTACTGCGAGAGATTGAGAGTTCCGCGAGATGGTGGAGCGGAGAGAGG 837
Qy 398 GCGTGTGGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 448
Db 838 ACGACGCTGGACAGCGAGGCGCGGACAGAGGCGCGCGCGCGCGCGCGCGCGCGCG 897
Qy 449 CCAGGCGCTGGAGCGCATCGCGGCGACCTTCGAGAGCGCCACGTCGTCCTGGCGG 508
Db 898 TGGGGCGCTCATGCGCGGACTCGCGGACATGGTGGAGAGCGCGGACTCGGGCTGCTG 957
Qy 509 CGCAGATCCTGGTAGCGTGTGCTGCTGATCGTGTCCATGGTGGTCTGTGCG 568
Db 958 GCAAGGTGTTGCGCTGCTTCTGCGCTGCTTCTGCGCGCTCACCGCGCTCAACCTCTCG 1017
Qy 569 CCAGCAGTTGCCGAGTGGCGCAAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 622
Db 1018 TCAGCACCTTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1077
Qy 623 ACCGAGCAGGATAATTGAAGCTATCTGCATAGTGTGGTTCAGTGGCGAGTGCATGCTGA 682
Db 1078 ACAAGCTTTCATCGTGGAGTCGCTGCGTGGCTGGTCTCCCTGGAGTCTCTCTGCG 1137
Qy 683 GGTTCATTGTCCTCAAAAACAAGTGTGAGTTGTCAAGAGACCCCTGAACATCAATTGAT 742
Db 1138 GGCTCATTCAGGCGCGCGCAGCAAGTTCGCTTCTCGGAGCGCGCTGACCTGATCGACC 1197
Qy 743 TACTGGCAATCACGCGGTATTACATCTCTGTGTTGATGACAGTGTTTACAGGCGAG--- 798
Db 1198 TGGTGGCAATCTGCGCTACTACATACGCTGCTGTGGAGCGCGCGCGCGCGCGCGCTC 1257
Qy 799 -----AACTCTCAACTCGAGGCGTGGAGTCACTTGGAGGTTACTTGA 841
Db 1258 GCAAGCGCGCGCGGCGCAACAGCTACTGGAACAAGGTGGGCTGGTGTGCTGCGGTGCTGC 1317
Qy 842 GAATGATGAGGATTTTGGTGTATTAAGCTTGGCGGTCACTTCAATGTTCTTCAGACAC 901
Db 1318 GGGCGCTGCGCATCCTGTAGTATGCGCTGGCGCGCACTCCCTGGGCTGCGACGCG 1377
Qy 902 TCGGTTTGAATCTCAAAACGTTGCTACCGAGAGATGGTTATGTTACTTGTCTTCATTGTG 961
Db 1378 TGGGGCTCACGGCGCGCGCTGCACCGGAGTTCGGGCTCCCTGCTGCTCTTCTCTGCG 1437
Qy 962 TTCCATGGCAATCTTTAGTGCACTTCTCAGCTTCTTGAACATGGCTGGAGCTGGAAA 1021
Db 1438 TGGCCATGCGCCCTCTTTCGCGCCCTGCTCTACGTCATCGAAGACGAGATGG----- 1488
Qy 1022 CATCCAAAGAGACTTTTACAGCATTCCTGCTGCCCTGCTGGTGGGTGATTATCTCTATGA 1081
Db 1489 CCAGACCCCGAGTTCAACAGCATCCCTGCTGCTACTTGGTGGTGTGTCATCACCATGA 1548
Qy 1082 CTACAGTTGGCTATGGAGATATATCTCTATACAGTGTCTGAAGATTCCTTGGAGGAG 1141
Db 1549 CGACGCTGAGCTATGGCGACATGGTCCCAAGAGACACCCCGGCGGAGTAGTGGCGCTGA 1508
Qy 1142 TTTGTGTTGTGAGTGAATTTGTTCTATTGGCATTTACTTCACTTTTATCTACATAGCT 1201
Db 1609 GCAGCATCTGAGCGGATCCTGCTATGGCTTCCAGTCCAGTCACTCACTTCCACACT 1668

APPLICANT: Mackinnon, Roderick
APPLICANT: Jiang, Youxing
APPLICANT: Lee MacKinnon, Alice
APPLICANT: Ruff, Vanessa
TITLE OF INVENTION: Voltage Sensor Domains of Voltage-Dependent Ion Channel Proteins
FILE REFERENCE: Seq. Nos. 1-21 for 1119-9
CURRENT APPLICATION NUMBER: US/10/377,139
CURRENT FILING DATE: 2003-03-01
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 3756
TYPE: DNA
ORGANISM: Homo sapiens
US-10-377-139-18

Query Match 20.4%; Score 260.6; DB 17; Length 3756;
Best Local Similarity 53.7%; Pred. No. 7,7e-65;
Matches 645; Conservative 0; Mismatches 529; Indels 27; Gaps 4;

30 GGTGGTGTGAACTGGCGGGCGCCGGTATTGCGTGTCCCGGAGCTGTGAAGGACTT 89
Db
260 GGTCCGCTCAAGCTCGGGGGCTGGCGACGAGTACTCTGGCGTACCTTGGACCGCC 319
QY 90 CCCGCTGGCGCGCTGAGCGGCTGACGGCTGCCGCTCCGAGCGCGAGTCTCGAGGT 149
Db 320 GCGCGCGAGCGGCTGGGGAAGCTCCGCGACTGCAACAGCGAGTCTGCTCGAGGT 379
QY 150 GTGCGACGACTACGACCGCGAGCGCAAGAGTACTTCTTCACCGGCACTCGAGGCGTT 209
Db 380 GTGCGATGACTACAGCTCGACGACACAGAGTACTTCTTGACCGCCACCCGGCGCCT 439
QY 210 CGGCTTCTCTGCTCTACAGCGAGTACTTCTGCGGCGCTGGAGGCGCGGCGGAGTGT 269
Db 440 CACCTCCATC---CTCAACTTCTACCGCACTGGCGAGTGCACATGATGGAGGAGTGT 496
QY 270 CGAGCTCTCTCTACAGCGAGTACTTCTGCGGCGCTGGAGGCGCGGCGGCGGAGTGT 329
Db 497 CCGCTCAGCTTCAGCGAGAGTCTGACTTGGGGCATCGACGAGATCTACCTGGAGTGT 556
QY 330 CTGCTGCCAGCGCGCTCGAGCGGATGTTCGACACCTTACCTTCTACTCGGCGCA 389
Db 557 CTGCTGCCAGCGCGCTACACCA-----GAAGAAGAGCAGATGAACGAGAGCT 607
QY 390 CGAGCGGCGGCTGCTGGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCC 449
Db 608 CAAGCTGAGCGCGAGACCTTACGGAGCGGGAAGCGGAGGATTCGATAACACGCTGT 667
QY 450 CAGGCGCTGCTGGAGCGCATGCGGCGGACCTTCGAGGAGCGCCACGCTGCTGCGCGCG 509
Db 668 CGCAGAGAGAGGAAAAAATCTGGGACCTTCTGGAGAGCGCCAAATCTCTGTGCTGT 727
QY 510 GCGATCTCGGTAGCGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 569
Db 728 CAAGATCTTGGCATTAATTCATATGCTATGCTGCTGCTGCTGCTGCTGCTGCTG 787
QY 570 CAGCAGTTGCGCGA---CTGGCGCAACGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 626
Db 788 CAACAGCTGCTGAGCTACAGAGCTCGATGAGTTCGCGCGAGTCCACAGACACCCCA 847
QY 627 GAGCAGGATAATGAAGCTATCGCATAGGTGCTGCTGCTGCTGCTGCTGCTGCTG 686
Db 848 GCTGGCGCGAGTGGAGCGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 907
QY 687 CATTTGCTCCAAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTGATT 746
Db 908 CCTCTCTGCGCCAGAGTGGAGTTCTCAAGGCGCCCACTCAATGCCATGACTTGT 967
QY 747 GCGAATCAGCGCGTATTACATCTCTGTGTGATGACAGTGTGTACAGGCGGAACTCTCA 806
Db 968 GGCATCTGCCATATCTATGTACCATTTTCTCACCAGTCTTCTCACCAGTCTCAAGCGGTGTCTCA 1027

RESULT 15
US-10-435-935-10
; Sequence 10, Application US/10435935
; Publication No. US2004003890A1
; GENERAL INFORMATION:
; APPLICANT: Aiyar, Jayashree
; Kang, Jiesheng
; TITLE OF INVENTION: HUMAN VOLTAGE-GATED POTASSIUM
; CHANNEL SUBUNIT
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZENECA Pharmaceuticals, Inc.
; STREET: 1800 Concord Pike
; CITY: Wilmington
; STATE: DE
; COUNTRY: USA
; ZIP: 19850-5437
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/435,935
; FILING DATE: 12-May-2003
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/074,878
; FILING DATE: 08-MAY-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Higgins, Patrick H
; REGISTRATION NUMBER: 39,709
; REFERENCE/DOCKET NUMBER: PHM.70310
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302.886.4889
; TELEFAX: 302.886.8221
; TELEX: <UNKNOWN>
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2565 base pairs

807 ACTCCAGAGGGCTGGAGTACCTTGAGGTACTTAGAATGATGAGGATTTTTTGGTGAT 866
Db 1028 ATTCCAGAAATGTCGCGCGGTGGTCCAGATCTTCGCAATCGGAAATCTCCGATCT 1087
QY 867 TAACTTTGCCCGTCACTTCATTGGTCTTCAGACACTTCGGTTTGAATCTCAAAAGTTGCTA 926
Db 1088 TAACTTTGCAAGCCACTCCACTGGCTCCAGTCTCTGGGCTTCACTTTGGGAGGAGCTA 1147
QY 927 CCGAGAGATGGTTATGTTACTTCTTCAATTTGTGTGTCATGGCAATCTTTAGTGCAT 986
Db 1148 CAATGAGTTGGGCTTGCTCATCTCTCTTCCATGGGCAATGATCTTCTCCAGCCT 1207
QY 987 TTCTCAGCTTCTTGAACATGGGCTGGACCTGGAACATCCAAACAGGACTTTACACGAT 1046
Db 1208 TGTCTTCTTGTGAGAAAGATGAGA-----CGACACCAAGTTCAAAAGCAT 1255
QY 1047 TCTGTGCTGCTGCTGGTGGTGAATATCTATGACTACAGTTGGCTATGGAGATGTA 1106
Db 1256 CCCAGAGCTCTCTCTGGGAAATTTGTGGGAGCTCTCTGCTGATTCGAGGATCTCTGGT 1315
QY 1107 TCTATCACAGTCCCTGGAGAAATTTCTGGAGAGTTTGTGTGTCAGTGGAAATTTGTTCT 1166
Db 1316 CCCAAGACTCTCTCTGGGAAATTTGTGGGAGCTCTCTGCTGATTCGAGGATCTCTGGT 1375
QY 1167 ATTGGCATTAACCTTACATTTTATCTACATAGCTTTGTGAGTGTATCATGAGCTCAA 1226
Db 1376 GATTGCTTCTCCATCCCATCCCATCTGTCATCAATCACTTCTCTGAGTCTCTATAAGGAGCAGAA 1435
QY 1227 G 1227
Db 1436 G 1436

TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
us-10-435-935-10

Query Match 20.4%; Score 260.2; DB 13; Length 2565;
Best Local Similarity 54.3%; Pred. No. 8.4e-65;
Matches 651; Conservative 0; Mismatches 523; Indels 27; Gaps 5;
QY 30 GTGTGCTGCTGAAAGTGGCGCGCCCGGTTATTCGTGTCGCCGGAGAGCTGCTGAAGACTT 89
DB 84 GGTCCGGCTCAACGTCGGGGGGGTGGCGCACGAGGTACTTGGCGTACCGCTGACCGCCT 143
QY 90 CCGCTGCGCGCGTGGAGCGGCTGACGCGCTGCCGCTCCGAGCGGAGCTGCTCGAGGT 149
DB 144 GCCCGCACGCGCTGGGCAAGCTCCGGACTGCCAACACGACGACTCGCTGCTCGAGGT 203
QY 150 GTGCGAGCTACGACCGGAGCGCAACGAGTACTTCTTGCACCGGACTCGGAGGCGCTT 209
DB 204 GTGCGATGACTACAGGCTTCGACGACAAACGAGTACTTCTTGCACCGGACTCGGAGGCGCTT 263
QY 210 CGGCTTCATCCTGCTGCTGCGCGCGGCGCACGCAAGCTGCGCTTCGCGCGCGGATGTG 269
DB 264 CACCTCCATC---CTCAACTTCTACCGCACTGGGCGACTGACATGATGGAGGAGATGTG 320
QY 270 CGAGCTCTCCTCTACAACGAGATGATCTACTGGGCGCTGGAGGCGCGCACTCGAGTA 329
DB 321 CGCGCTCAGCTTCAGCAAGAGCTCGACTACTTGGGSCATCGACGAGATCTACTGGAGTC 380
QY 330 CTGCTGGCAGCGCGCTCGACGACCGCATGTCCGACCTACACCTTCTACTCGGCGCA 389
DB 381 CTGCTGCCAGCGCGCTTACCAC--CAGAAGAAAGAGCAGATGAACGAGAGCTCAAGCGT 438
QY 390 CGAGCGCGGCGTCTGGGCGCGGACAGGCGCGCGCGCGCGCGCGCGCTCCCTC 449
DB 439 GAGCGCGAGACTTACGGGAGCGGGAAGGCGAG-----GAGTTCGATAACAGTGCTG 491
QY 450 CAGGCGCTGGTGGAGCGGACTGCGGCGGACCTTCGAGGAGCGCACGTCGTCGCTGGCGCG 509
DB 492 CGCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 551
QY 510 GCAGATCTGGCTAGCGTGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 569
DB 552 CAAGATCTTGCATTAATTTTCATCATGTTTCTCTCCCATTTGCCCTGTCCCT 611
QY 570 CAGCAGCTTGGCGCA---CTGGCGCAACGACGCGCGCGCAACCGCAGCCTGGATGACCG 626
DB 612 CAACACGCTGCTGAGCTACAGAGCTCGATGAGTTGGCGGAGTCCACAGACACCGCCCA 671
QY 627 GAGCAGGATTAATGAGCTATCTGATAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 686
DB 672 GCTGGCCACGTTGAGGCGGCTGTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 731
QY 687 CATTTGCTCAAAACAAGTGTGAGTTTGTCAAGAGAGCCCTGGAACATCAATTGATTACT 746
DB 732 CCTCTCTCGCCCAAGAGTGAAGTTCTTCAAGGGCGGCACTCAATGCCATTGACTTGT 791
QY 747 GGCATACGCGGTATTACATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 806
DB 792 GGCATTTGCGCATACTATGTACCATTTTCTCCGAAATCCAAACAGAGCGTGTGTGCA 851
QY 807 ACTCCAGAGGCTGGAGTCACTTGGAGTACTTAGAATGATGAGGATTTTGTGGTGTAT 866
DB 852 ATTCCAGATGTCGCGCGGTGTCCAGATCTTCGCAATCATGCGAATCTCCGATCCT 911
QY 867 TAAGCTTGCGCTGACTTCAATGCTTTCAGACACTCGGTTTGTACTCAAAAGTTGTCTA 926
DB 912 TAAGCTTGACGCCACTCCACTGGGCTCCAGTCTCTGGGCTTCACTTTGGGAGGAGCTA 971
QY 927 CCGAGAGATGGTTATGTTACTTGTCTTCAATTGTTGTGCGCATGGCAATCTTTAGTGCACT 986

DB 972 CAATGAGTTGGCTTGTCTCATCTCTTCTTGCCATGGGCATTATGATCTTCTCCAGCCT 1031
QY 987 TTCTCAGCTTCTTGAACATGGGCTGGACCTGGAAACATCCAAAGGACTTTACCAGCAT 1046
DB 1032 TGTCTTCTTGTCTGAGAAGGATGAGGA-----CGACACCAAGTTCAAAGCAT 1079
QY 1047 TCCTGCTGCTGCTGCTGGGTGATTATCTATGACTACAGTTGGCTATGGAGATATGTA 1106
DB 1080 CCCAGCCTCTTCTGCTGGGCCACCATCACCATGACTACTTGTGGGTATGGAGACATCTA 1139
QY 1107 TCCTATCAGAGTGCCTGGAAGAATCTTGGAGGAGTTTGTGTGTGTGTGTGTGTGTGTGT 1166
DB 1140 CCCAAGACTCTCTGGGGAATTTGTGGGGGACTCTGCTGCATTGCGAGGAGTCTCTGT 1199
QY 1167 ATTGGCATTACCTATCACTTTTATCTACCATAGCTTTGTGCAGTGTATCATGAGCTCAA 1226
DB 1200 GATTGCTCTTCCCATCCCATCATCTGCTCAATTAATCTCTCTGAGTTCTATTAAGGAGCGAA 1259
QY 1227 G 1227
DB 1260 G 1260

Search completed: October 6, 2004, 20:47:44
Job time : 707 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2004, 16:45:07 ; Search time 3656 Seconds
(without alignments)
10438.694 Million cell updates/sec

Title: US-10-016-647-1
Perfect score: 1278
Sequence: 1 atgaccttcggcgacgagg.....ccactgaattcctgaattaa 1278

Scoring table: OLIGO NUC
Gapop'60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 24

Total number of hits satisfying chosen parameters: 19

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: em_estba.*
2: em_estbhum.*
3: em_estin.*
4: em_estm.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_htc.*
9: gb_est1.*
10: gb_est2.*
11: gb_huc.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pin.*
20: em_gss_vrt.*
21: em_gss_fun.*
22: em_gss_mas.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rod.*
26: em_gss_phg.*
27: em_gss_vrl.*
28: gb_gss1.*
29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	152	11.9	500	28	AQ402619 HS 5066 A
2	115	9.0	385	28	AQ355274 CITBI-EL
3	115	9.0	474	28	AQ354648 CITBI-EI
C 4	104	8.1	301	29	CE495701 tigr-gss-

77 6.0 629 12 BM537928
70 5.5 298 9 A1137172
65 5.1 509 29 CG639652
50 3.9 166 29 CG513356
50 3.9 487 29 CG582101
49 3.8 484 29 CG662016
47 3.7 523 9 A1043703
43 3.4 314 10 BF552004
38 3.0 242 29 CG580684
38 3.0 499 28 AQ782780
34 2.7 262 29 CG661999
26 2.0 887 10 BF966122
25 2.0 772 13 BU274588
24 1.9 398 29 CG661991
24 1.9 487 29 CG604488

ALIGNMENTS

RESULT 1
AQ402619/c
LOCUS HS_5066_A2_E01_T7A RPCI-11 Human Male BAC Library Homo sapiens
DEFINITION Genomic clone Plate=642 Col=2 Row=1, genomic survey sequence.
ACCESSION AQ402619
VERSION AQ402619.1 GI:4413531
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 500)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
plate: 642 row: 1 column: 2
Seq primer: T7
Class: BAC ends
High quality sequence stop: 500.

FEATURES

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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=642 Col=2 Row=1"
/sex="male"
/clone_lib="RPCI-11 Human Male BAC Library"
/note="vector: PBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the PBACe3.6 vector at EcoRI sites"

ORIGIN

Query Match 11.9%; Score 152; DB 28; Length 500;
 Best Local Similarity 99.0%; Pred. No. 1.2e-65;
 Matches 302; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 878 GTCACTTCATTGGCTTCAGACACTCGGTTTGTACTCTCAAAAGCTTGCTACCGAGAGATGG 937
 Db 419 GTCACTTCATTGGCTTCAGACACTCGGTTTGTACTCTCAAAAGCTTGCTACCGAGAGATGG 360
 QY 938 TTATGTTACTTCTTCATTGTTGTCCTATGCAATCTTTAGTGCACTTCTTCAGCTTC 997
 Db 359 TTATGTTACTTCTTCATTGTTGTCCTATGCAATCTTTAGTGCACTTCTTCAGCTTC 300
 QY 998 TTGAACATGGGCTGGACCTGGAACATCCAAAGGAGCTTTACAGCATTCCTGCTGCT 1057
 Db 299 TTGAACATGGGCTGGACCTGGAACATCCAAAGGAGCTTTACAGCATTCCTGCTGCT 240
 QY 1058 GCTGTTGGGTGATATCTCTATGACTACAGTTGGCTATGGAGATATGATCTTATCACAG 1117
 Db 239 GCTGTTGGGTGATATCTCTATGACTACAGTTGGCTATGGAGATATGATCTTATCACAG 180
 QY 1118 TGCTGGAAGAAATCTTGGAGGAGTTTGTTGTCAGTGAATTTCTATTGGCAATAC 1177
 Db 179 TGCTGGAAGAAATCTTGGAGGAGTTTGTTGTCAGTGAATTTCTATTGGCAATAC 120
 QY 1178 CTATC 1182
 Db 119 CTATC 115

RESULT 2
 AQ355274
 LOCUS
 DEFINITION
 CITBI-E1-2533B23.TF CITBI-E1 Homo sapiens genomic clone 2533B23,
 genomic survey sequence.
 ACCESSION
 AQ355274
 VERSION
 AQ355274.1 GI:4182447
 KEYWORDS
 GSS.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 385)
 AUTHORS
 Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
 Venter,J.C.
 TITLE
 Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
 Map Building
 JOURNAL
 Unpublished (1997)
 COMMENT
 Other GSSs: CITBI-E1-2533B23.TR
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbeetigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
 http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
 Seq primer: M13-21
 Class: BAC ends.

FEATURES
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 /clone="2533B23"
 /sex="male"
 /cell_type="sperm"
 /clone_lib="CITBI-E1"
 /note="Vector: pBelOBAC11, Site_1: EcoRI; Site_2: EcoRI;
 CalTech Human BAC Library D"

ORIGIN

Query Match 9.0%; Score 115; DB 28; Length 385;
 Best Local Similarity 100.0%; Pred. No. 7.5e-47;
 Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1164 TCTATTGGCAATACCTATCACTTTTATCTACATAGCTTTTGTGAGTGTATCATGAGCT 1223
 Db 1 TCTATTGGCAATACCTATCACTTTTATCTACATAGCTTTTGTGAGTGTATCATGAGCT 60
 QY 1224 CAAGTTTAGATCTGCTAGGTATAGTAGGAGCTCTCCACTGAATTCCTGAATTA 1278
 Db 61 CAAGTTTAGATCTGCTAGGTATAGTAGGAGCTCTCCACTGAATTCCTGAATTA 115

RESULT 3
 AQ354648
 LOCUS
 DEFINITION
 CITBI-E1-2533A24.TF CITBI-E1 Homo sapiens genomic clone 2533A24,
 genomic survey sequence.
 ACCESSION
 AQ354648
 VERSION
 AQ354648.1 GI:4181821
 KEYWORDS
 GSS.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 474)
 AUTHORS
 Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
 Venter,J.C.
 TITLE
 Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
 Map Building
 JOURNAL
 Unpublished (1997)
 COMMENT
 Other GSSs: CITBI-E1-2533A24.TRB
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbeetigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
 http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
 Seq primer: M13-21
 Class: BAC ends.

FEATURES
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 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="2533A24"
 /sex="male"
 /cell_type="sperm"
 /clone_lib="CITBI-E1"
 /note="Vector: pBelOBAC11, Site_1: EcoRI; Site_2: EcoRI;
 CalTech Human BAC Library D"

Query Match 9.0%; Score 115; DB 28; Length 474;
 Best Local Similarity 100.0%; Pred. No. 7.9e-47;
 Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 TCTATTGGCAATACCTATCACTTTTATCTACATAGCTTTTGTGAGTGTATCATGAGCT 60
 QY 1224 CAAGTTTAGATCTGCTAGGTATAGTAGGAGCTCTCCACTGAATTCCTGAATTA 1278
 Db 61 CAAGTTTAGATCTGCTAGGTATAGTAGGAGCTCTCCACTGAATTCCTGAATTA 115

RESULT 4
 CE495701/c
 LOCUS
 CE495701 301 bp DNA linear GSS 28-SEP-2003

tigr-gss-dog-l7000373701868 Dog Library Canis familiaris genomic,
genomic survey sequence.
CE495701 GI:36812482
GSS.
Canis familiaris (dog)
Canis familiaris
Canis familiaris
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 301)
Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
22875432
14512627
Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
1..301
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"

Query Match 8.1%; Score 104; DB 29; Length 301;
Best Local Similarity 99.0%; Pred. No. 2.8e-41;
Matches 204; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACCTTCGGCGCAGCGCGCGCTCGGTGGTGTGAACGTGGCGCGCCCGGTAT 60
Db 218 ATGACCTTCGGCGCAGCGCGCGCTCGGTGGTGTGAACCTGGCGCGCCCGGTAC 159

QY 61 TCCTGTCCCGGAGCTGTGAAGACTTCCCGCTGCCCGGTGAGCCGCTCAGCGC 120
Db 158 TCCTGTTCCTCCCGGAGCTGTGAAGACTTCCCGCTGCCCGGTGAGCCGCTCAGCGC 99

QY 121 TGGCGCTCCGAGCGCGACGTGCTCGAGGTGTGCGACGACTACGACCGCGCGCAACGAG 180
Db 98 TGCGCTCGAGCGCGAGCTGTGAGGTGTGCGAGGTGTGCGACGACTACGACCGCGCGCAACGAG 39

QY 181 TACTTCTTCACCGGCACCTCGAGGC 206
Db 38 TACTTCTTCACCGGCACCTCGAGGC 13

RESULT 5
BM537928 629 bp mRNA linear EST 20-FEB-2002
LOCUS ha88c06.g1 Canis cDNAs from testes cells Canis familiaris cDNA
DEFINITION clone ha88c06 5', mRNA sequence.
ACCESSION BM537928
VERSION BM537928.1 GI:18818563
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 629)
O'Shaughnessy,A.L., McCombie,W.R., Baker,J.P., Balija,V.,
Cunniss,D., Dedhia,N.N., de la Bastide,M., Katzenberger,F.,
Kumar,V., Muller,S., Muller,S., Nascimben,C.L., U.
Muller,S.

/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match 3.9%; Score 50; DB 29; Length 166;
Best Local Similarity 100.0%; Pred. No. 7.1e-14;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 691 GTCTCCAAAACAAGTGTGAGTTTGTCAGAGACCCCTGACATCATTTGA 740
|||||
DB 41 GTCTCCAAAACAAGTGTGAGTTTGTCAGAGACCCCTGACATCATTTGA 90
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RESULT 9
CG582101 487 bp DNA linear GSS 02-OCT-2003
LOCUS OST222985 Mus musculus 129Sv/Ev Mus musculus genomic clone
DEFINITION OST222985, genomic survey sequence.

ACCESSION CG582101
VERSION CG582101.1 GI:37379484
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 487)

REFERENCE
AUTHORS Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Piggott, J., BeltrandeRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Spark, M.J., Van Slightenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Person, C. and Sands, A.T.

TITLE Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention

Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

CONTACT: Zambrowicz BP

COMMENT OmniBank

Lexicon Genetics Incorporated

4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

Class: Gene Trap.

Location/Qualifiers

1. .487
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST222985"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match 3.9%; Score 50; DB 29; Length 166;
Best Local Similarity 100.0%; Pred. No. 9.5e-14;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 691 GTCTCCAAAACAAGTGTGAGTTTGTCAGAGACCCCTGACATCATTTGA 740
|||||
DB 56 GTCTCCAAAACAAGTGTGAGTTTGTCAGAGACCCCTGACATCATTTGA 105
|||||

RESULT 10
CG662016 484 bp DNA linear GSS 02-OCT-2003
LOCUS OST444129 Mus musculus 129Sv/Ev Mus musculus genomic clone
DEFINITION OST444129, genomic survey sequence.

ACCESSION CG662016

VERSION CG662016.1 GI:37485865

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Piggott, J., BeltrandeRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Spark, M.J., Van Slightenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Person, C. and Sands, A.T.

TITLE Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention

JOURNAL

COMMENT

Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
CONTACT: Zambrowicz BP

OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as

described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

Class: Gene Trap.

Location/Qualifiers

1. .484
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST444129"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

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Query Match 3.8%; Score 49; DB 29; Length 166;
Best Local Similarity 100.0%; Pred. No. 3.1e-13;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 691 GTCTCCAAAACAAGTGTGAGTTTGTCAGAGACCCCTGACATCATTTG 739
|||||

DB 65 GTCTCCAAAACAAGTGTGAGTTTGTCAGAGACCCCTGACATCATTTG 113
|||||

RESULT 11

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

AI043703 523 bp mRNA linear EST 05-JUL-1999
UI-R-CO-J1-g-04-0-UI.s1 UI-R-CO Rattus norvegicus cDNA clone
UI-R-CO-J1-g-04-0-UI 3', mRNA sequence.
AI043703
AI043703.1 GI:3290438
EST.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

1 (bases 1 to 523)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548

CONTACT: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Oligo-dr track not found, Not 1 site shown in beginning of sequence

is likely internal to the message. cDNA Library Preparation: M.

Fatima Bonaldo, Ph.D. Clone distribution: clones will be available

through Research Genetics This clone is also available through the

I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE

Id=1793128

Seq primer: M13 Forward

FOIA=NO.

FEATURES

source
Location/Qualifiers
1. 523
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-C0-j1-g-04-0-UI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-C0"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco RI; The UI-R-C0
library is a subtracted library derived from the UI-R-Al
and UI-R-E1 libraries. The UI-R-Al library consisted of a
mixture of individually tagged normalized libraries
constructed from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, and muscle. The UI-R-E1
library consisted of a mixture of individually tagged
normalized libraries constructed from 8, 12 and 18-day
embryo. The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dt track which
allows identification of the library of origin of a clone
within the mixture. The subtracted library (UI-R-C0) was
constructed as follows: PCR amplified cDNA inserts from a
pool of UI-R-Al and UI-R-E1 clones from which 3' ESTs had
been derived was used as a driver in a hybridization with
the pooled UI-R-Al and UI-R-E1 library in the form of
single-stranded circles. The remaining single-stranded
circles (subtracted library) was purified by
hydroxyapatite column chromatography, converted to
double-stranded circles and electroporated into DH10B
bacteria (Life Technologies) to generate the UI-R-C0
library. This procedure has been previously described
(Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
1996)"

ORIGIN

Query Match 3.7%; Score 47; DB 9; Length 523;
Best Local Similarity 100.0%; Pred. No. 3.3e-12;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 691 GTCTCAAAACAAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCAT 737
Db 96 GTCTCAAAACAAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCAT 142

RESULT 12
BF552004
LOCUS
DEFINITION
UI-R-C2p-of-h-09-0-UI.r1 UI-R-C2p Rattus norvegicus cDNA clone
UI-R-C2p-of-h-09-0-UI 5', mRNA sequence.
BF552004
VERSION
BF552004.1 GI:11661734
EST.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

1 (bases 1 to 314)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

CDNA Library Preparation: M.B. Soares Lab Clone Distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (info@image.llnl.gov). IMAGE ID= 1793128 The following
repetitive elements were found in this cDNA sequence: 97-157,
>GC rich#Low complexity
Seq primer: M13 Forward.

FEATURES

source
Location/Qualifiers
1. 314
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-C2p-of-h-09-0-UI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-C2p"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco RI; The UI-R-C2p
library is a subtracted library derived from the UI-R-C1
library, which is a subtracted library derived from the
UI-R-C0 library. The UI-R-C0 library consisted of a
mixture of individually tagged normalized libraries
constructed from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day
embryo. The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dt track which allows
identification of the library of origin of a clone within
the mixture. The subtracted library (UI-R-C2p) was
constructed as follows: PCR amplified cDNA inserts from
UI-R-C1 clones from which 3' ESTs had been derived was
used as a driver in a hybridization with the UI-R-C1
library in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library) was
purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
into DH10B bacteria (Life Technologies) to generate the
UI-R-C2p library. This procedure has been previously
described (Bonaldo, Lennon and Soares, Genome Research 6:
791-806, 1996)"

ORIGIN

Query Match 3.4%; Score 43; DB 10; Length 314;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 17 GCAGGCGCGCTCGTGTGCTGAACTGGCGCGCGCCCGGTA 59
Db 147 GCAGGCGCGCTCGTGTGCTGAACTGGCGCGCGCCCGGTA 189

RESULT 13

CG580684
LOCUS
DEFINITION
Mus musculus 129Sv/Ev Mus musculus genomic clone
OST220291, genomic survey sequence.
CG580684
ACCESSION
VERSION
CG580684.1 GI:37376130
GSS.
Mus musculus (house mouse)

1 (bases 1 to 242)
Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
Key, B.W. Jr., Kipp, P., Kohlhaufl, B., Ma, Z.-Q., Markesich, D.,
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 242)
Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
Key, B.W. Jr., Kipp, P., Kohlhaufl, B., Ma, Z.-Q., Markesich, D.,
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,

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Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
Location/Qualifiers
1. .242
/organism="Mus musculus"
/mol_type="genomic DNA"
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/db_xref="taxon:10090"
/clone="OST220291"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129SV/Ev"

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Query Match 3.0%; Score 38; DB 29; Length 242;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 997 CTTGAACATGGCTGGACCTCGAACATCCACACAGGA 1034
DB 103 CTTGAACATGGCTGGACCTCGAACATCCACACAGGA 140

RESULT 14
A0782780 499 bp DNA linear GSS 02-AUG-1999
LOCUS HS 5301 AL E04 T7A RPT-11 Human Male BAC Library Homo sapiens
DEFINITION genomic_clone Plate=877 Col=7 Row=I, genomic survey sequence.
ACCESSION A0782780
VERSION A0782780.1 GI:5685740
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Carnivora; Hominidae; Homo.
1 (bases 1 to 499)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., and
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
10449764
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPT-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Research Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 877 row: I column: 7
Seq primer: T7
Class: BAC ends
High quality sequence stop: 499.
Location/Qualifiers
1. .499

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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=877 Col=7 Row=I"
/sex="male"
/clone_lib="RPT-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site1: EcoRI; Site2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"

ORIGIN
Query Match 3.0%; Score 38; DB 28; Length 499;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1162 GTTCTATTGGCATTACCTATCATTCTTTATCTACCATAG 1199
DB 54 GTTCTATTGGCATTACCTATCATTCTTTATCTACCATAG 91

RESULT 15
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LOCUS CST444070 Mus musculus 129SV/Ev Mus musculus genomic clone
DEFINITION CST444070, genomic survey sequence.
ACCESSION CG661999
VERSION CG661999.1 GI:37485848
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 262)
Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
Key,B.W., Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
Location/Qualifiers
1. .262
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129SV/Ev"
/db_xref="taxon:10090"
/clone="OST444070"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129SV/Ev"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 788 TTACAGCGGAGAACTCTCAACTCCAGAGGCTGG 821
DB 110 TTACAGCGGAGAACTCTCAACTCCAGAGGCTGG 143

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Thu Oct 7 10:52:17 2004

us-10-016-647-1.oligo.rst

Page 8

Search completed: April 19, 2004, 19:32:52
Job time : 3663 secs

; APPLICANT: HAFALIA, April J.A.; ELLIOTT, Vicki S.;
 ; APPLICANT: LU, Yan; CHAWIA, Narinder K.;
 ; APPLICANT: YAO, Monique G.; BAUGHN, Mariah R.;
 ; APPLICANT: GANDHI, Ameena R.; DING, Li;
 ; APPLICANT: SANJANKALA, Madhusudan M.; RAMKUNAR, Jayalaxmi;
 ; APPLICANT: ARVIZU, Chandra S.; GIETZEN, Kimberly J.;
 ; APPLICANT: LAU, Freeti G.; AZIMZAI, Yalda;
 ; APPLICANT: KHAN, Farrah A.; THANGAVELU, Kavitha;
 ; APPLICANT: THORNTON, Michael B.; LU, Dyung Aina M.;
 ; APPLICANT: TRIBOULEY, Catherine M.; WARREN, Bridget A.;
 ; APPLICANT: ISON, H. Craig; DAS, Debopriya;
 ; APPLICANT: RAUMANN, Brigitte E.; POLICKY, Jennifer L.;
 ; APPLICANT: KEARNEY, Liam
 ; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
 ; FILE REFERENCE: PI-0270 USN
 ; CURRENT APPLICATION NUMBER: US/10/415,378
 ; CURRENT FILING DATE: 2003-05-07
 ; PRIOR APPLICATION NUMBER: PCT/US01/46055
 ; PRIOR FILING DATE: 2001-10-27
 ; PRIOR APPLICATION NUMBER: US 60/250,790
 ; PRIOR FILING DATE: 2000-12-01
 ; PRIOR APPLICATION NUMBER: US 60/252,232
 ; PRIOR FILING DATE: 2000-11-20
 ; PRIOR APPLICATION NUMBER: US 60/249,661
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: US 60/247,673
 ; PRIOR FILING DATE: 2000-11-09
 ; PRIOR APPLICATION NUMBER: US 60/245,904
 ; PRIOR FILING DATE: 2000-11-03
 ; PRIOR APPLICATION NUMBER: US 60/243,989
 ; PRIOR FILING DATE: 2000-10-27
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 39
 ; LENGTH: 2235
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20040014945A1 7492060CB1
 ; US-10-415-378-39

Query Match 57.0%; Score 729; DB 16; Length 2235;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	514	ATCCTGGCTAGCTGCGGTGGTTCGTGATCGTGTCCATGCTGTGCTGTGCGCCAGC	573
DB	920	ATCCTGGCTAGCTGCGGTGGTTCGTGATCGTGTCCATGCTGTGCTGTGCGCCAGC	979
QY	574	ACGTTCCCGAGCTGGCGCAACGCGAGCGCGCGCAACCGGAGCTGTGATCGCGGAGCAGG	633
DB	980	ACGTTCCCGAGCTGGCGCAACGCGAGCGCGCGCAACCGGAGCTGTGATCGCGGAGCAGG	1039
QY	634	ATAATTGAAGCTATCTGCATAGTGTGGTTCACCTGCGAGTGCATGCTGATGTC	693
DB	1040	ATAATTGAAGCTATCTGCATAGTGTGGTTCACCTGCGAGTGCATGCTGATGTC	1099
QY	694	TCCAAAAACAAGTGTGAGTGTGTTGTCAGAGACCCCTGAACATCATTTACTTGGCAATC	753
DB	1100	TCCAAAAACAAGTGTGAGTGTGTTGTCAGAGACCCCTGAACATCATTTACTTGGCAATC	1159
QY	754	AGCCGCTATTACATCTCTGTGTTGATGACAGTGTGTACAGGCGAAGCTCTCAATCCAG	813
DB	1160	AGCCGCTATTACATCTCTGTGTTGATGACAGTGTGTACAGGCGAAGCTCTCAATCCAG	1219
QY	814	AGGCGTGGAGTCACTTGAAGGTGTTAGAAATGATGAGGATTTTGGTGTGTTAAGCTT	873
DB	1220	AGGCGTGGAGTCACTTGAAGGTGTTAGAAATGATGAGGATTTTGGTGTGTTAAGCTT	1279
QY	874	GCCCGTCACTTCAATGGTCTTCAGACACTCGGTTTGACTCTCAAAACGTTGCTACCGAG	933
DB	1280	GCCCGTCACTTCAATGGTCTTCAGACACTCGGTTTGACTCTCAAAACGTTGCTACCGAG	1339

RESULT 5

US-10-114-270-45
 ; Sequence 45, Application US/10114270
 ; Publication No. US20040030110A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Guo Xiaojia
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Miller, Charles E.
 ; APPLICANT: Malyankar, Uriel M.
 ; APPLICANT: Spytek, Kimberly A.
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Liu, Zhaozhong
 ; APPLICANT: Gusev, Vladimir Y.
 ; APPLICANT: Li, Li
 ; APPLICANT: Vernet, Corine
 ; APPLICANT: Zerhusen, Bryan D.
 ; APPLICANT: Gorman, Linda
 ; APPLICANT: Shenoy, Suresh G.
 ; APPLICANT: Pena, Carol E.A.
 ; APPLICANT: Smithson, Glenda
 ; APPLICANT: Burgess, Catherine E.
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Padigaru, Murallidhara
 ; APPLICANT: Shimkets, Richard A.
 ; APPLICANT: Gangolli, Esha A.
 ; APPLICANT: Taupier Jr., Raymond J.
 ; APPLICANT: Casman, Stacie J.
 ; APPLICANT: Ji, Weizhen
 ; APPLICANT: Anderson, David W.
 ; APPLICANT: Liote, Mario W.
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Edinger, Shlomit R.
 ; APPLICANT: Stone, David J.
 ; APPLICANT: MacDougall, John R.
 ; APPLICANT: Rothenberg, Mark E.
 ; TITLE OF INVENTION: No. US20040030110A1 Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 21402-322C
 ; CURRENT APPLICATION NUMBER: US/10/114,270
 ; CURRENT FILING DATE: 2002-11-27
 ; PRIOR APPLICATION NUMBER: 60/281,086
 ; PRIOR FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: 60/281,136
 ; PRIOR FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: 60/281,863
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/281,906
 ; PRIOR FILING DATE: 2001-04-05

QY	934	ATGTTATGTTACTTGTCTTCATTTGTTGCCATGGCAATCTTTAGTGCACTTTCTCAG	993
DB	1340	ATGTTATGTTACTTGTCTTCATTTGTTGCCATGGCAATCTTTAGTGCACTTTCTCAG	1399
QY	994	CTTCTTGAACATGGCTGGACCTGGAAACATCCAAAGAGACTTTACAGCAATTCCTGCT	1053
DB	1400	CTTCTTGAACATGGCTGGACCTGGAAACATCCAAAGAGACTTTACAGCAATTCCTGCT	1459
QY	1054	GCCTGCTGCTGGGTGATTATCTCTATGACTACAGTTGGCTATGGAGATATGATCTCTATC	1113
DB	1460	GCCTGCTGCTGGGTGATTATCTCTATGACTACAGTTGGCTATGGAGATATGATCTCTATC	1519
QY	1114	ACAGTGCCTGGAAGAAATCTTTGGAGGAGTTTGTCTTCAGTGGAAATTTCTATTGGCA	1173
DB	1520	ACAGTGCCTGGAAGAAATCTTTGGAGGAGTTTGTCTTCAGTGGAAATTTCTATTGGCA	1579
QY	1174	TTACTATCACTTTTATCTACCATAGCTTTGTGCAAGTGTATCATGAGCTCAAGTTTAGA	1233
DB	1580	TTACTATCACTTTTATCTACCATAGCTTTGTGCAAGTGTATCATGAGCTCAAGTTTAGA	1639
QY	1234	TCTGCTAGG	1242
DB	1640	TCTGCTAGG	1648

;; PRIOR APPLICATION NUMBER: 60/282,020
;; PRIOR FILING DATE: 2001-04-06
;; PRIOR APPLICATION NUMBER: 60/282,930
;; PRIOR FILING DATE: 2001-04-10
;; PRIOR APPLICATION NUMBER: 60/282,934
;; PRIOR FILING DATE: 2001-04-10
;; PRIOR APPLICATION NUMBER: 60/283,512
;; PRIOR FILING DATE: 2001-04-12
;; PRIOR APPLICATION NUMBER: 60/283,710
;; PRIOR FILING DATE: 2001-04-13
;; PRIOR APPLICATION NUMBER: 60/284,234
;; PRIOR FILING DATE: 2001-04-17
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 470
;; SEQ ID NO 45
;; LENGTH: 1651
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (1)..(1642)
US-10-114-270-45

Query Match 48.0%; Score 613; DB 13; Length 1651;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 613; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	630	CAGGATAATTGAAGCTATCTGCATAGTTTGGTTCACTGCCGAGTGCATCGTGAGTTTCAT	689
DB	792	CAGGATAATTGAAGCTATCTGCATAGTTTGGTTCACTGCCGAGTGCATCGTGAGTTTCAT	851
QY	690	TGTTCTCCAAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTTACTGGC	749
DB	852	TGTTCTCCAAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTTACTGGC	911
QY	750	AATCAGCCGCTATTACATCTCTGTGTGATGACAGTGTTCAGGCGGAACTCTCAACT	809
DB	912	AATCAGCCGCTATTACATCTCTGTGTGATGACAGTGTTCAGGCGGAACTCTCAACT	971
QY	810	CCAGAGGGCTGGAGTCACTTGGAGTACTTAGAATGATGAGATTTTGGGTGATTAA	869
DB	972	CCAGAGGGCTGGAGTCACTTGGAGTACTTAGAATGATGAGATTTTGGGTGATTAA	1031
QY	870	GCTTGCCTCTCACTTCACTTGGTCTTCAGACACTCGGTTTGAATCTCAAACTGCTACCG	929
DB	1032	GCTTGCCTCTCACTTCACTTGGTCTTCAGACACTCGGTTTGAATCTCAAACTGCTACCG	1091
QY	930	AGAGATGGTTTATGTTACTTCTTCACTTTTGTGTGCTATGGCAATCTTTAGTGCATTTTC	989
DB	1092	AGAGATGGTTTATGTTACTTCTTCACTTTTGTGTGCTATGGCAATCTTTAGTGCATTTTC	1151
QY	990	TCAGCTTCTTGAACATGGGCTGGACCTGGAAACATCCAAAGGACTTTTACCAGCAATTC	1049
DB	1152	TCAGCTTCTTGAACATGGGCTGGACCTGGAAACATCCAAAGGACTTTTACCAGCAATTC	1211
QY	1050	TGCTGCTGCTGGTGGTGAATATCTATGACTACAGTGGTGGTATGAGATATGATCC	1109
DB	1212	TGCTGCTGCTGGTGGTGAATATCTATGACTACAGTGGTGGTATGAGATATGATCC	1271
QY	1110	TATCAGAGTCCCTGGAAAGAAATCTTGGAGAGTTTGTGTGTGTCAGTGGAAATTTCTATT	1169
DB	1272	TATCAGAGTCCCTGGAAAGAAATCTTGGAGAGTTTGTGTGTGTCAGTGGAAATTTCTATT	1331
QY	1170	GGCATTTACCTATCACTTTTATCTACCATAGCTTTTGTGTCAGTGTATCATGAGCTCAAGTT	1229
DB	1332	GGCATTTACCTATCACTTTTATCTACCATAGCTTTTGTGTCAGTGTATCATGAGCTCAAGTT	1391
QY	1230	TAGATCTGCTAGG	1242
DB	1392	TAGATCTGCTAGG	1404

RESULT 6

US-10-199-869-26
;; Sequence 26, Application US/10199869
;; Publication No. US20030152953A1
;; GENERAL INFORMATION:
;; APPLICANT: Bristol-Myers Squibb Company
;; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUB
;; FILE REFERENCE: D0161 NP
;; CURRENT APPLICATION NUMBER: US/10/199,869
;; PRIOR FILING DATE: 2002-07-19
;; PRIOR APPLICATION NUMBER: US 60/306,577
;; PRIOR FILING DATE: 2001-07-19
;; NUMBER OF SEQ ID NOS: 90
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 26
;; LENGTH: 594
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-199-869-26

Query Match 46.5%; Score 594; DB 15; Length 594;
Best Local Similarity 100.0%; Pred. No. 2;le-305;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	634	ATAATTGAAGCTATCTGCATAGTTTGTTCACCTCCGAGTGCATCGTGAGTTTCATTGTC	693
DB	1	ATAATTGAAGCTATCTGCATAGTTTGTTCACCTCCGAGTGCATCGTGAGTTTCATTGTC	60
QY	694	TCCAAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTACTGGCAATC	753
DB	61	TCCAAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTACTGGCAATC	120
QY	754	ACGCGGTATTACATCTCTGTTCATGACAGTGTTCACGCGGAGAACTCTCAACTCCAG	813
DB	121	ACGCGGTATTACATCTCTGTTCATGACAGTGTTCACGCGGAGAACTCTCAACTCCAG	180
QY	814	AGGCTGGAGTCACTTGGAGGTACTTAGAATGATGAGGATTTTGGGTGATTAAGCTT	873
DB	181	AGGCTGGAGTCACTTGGAGGTACTTAGAATGATGAGGATTTTGGGTGATTAAGCTT	240
QY	874	GCCGCTCACTTCACTTGGTCTTCAGACACTCGGTTTGAATCTCAAACTGCTACCGAG	933
DB	241	GCCGCTCACTTCACTTGGTCTTCAGACACTCGGTTTGAATCTCAAACTGCTACCGAG	300
QY	934	ATGGTTATGTTACTTGTCTTCACTTGTGTGCCATGGCAATCTTTAGTGCATTTCTCAG	993
DB	301	ATGGTTATGTTACTTGTCTTCACTTGTGTGCCATGGCAATCTTTAGTGCATTTCTCAG	360
QY	994	CTTCTTGAACATGGCTGGACCTCGAAACATCCAAAGGACTTTACAGCAATCTCTGCT	1053
DB	361	CTTCTTGAACATGGCTGGACCTCGAAACATCCAAAGGACTTTACAGCAATCTCTGCT	420
QY	1054	GCCTGCTGGTGGTGAATATCTCTATGACTACAGTGGCTATGAGATATGATCTATC	1113
DB	421	GCCTGCTGGTGGTGAATATCTCTATGACTACAGTGGCTATGAGATATGATCTATC	480
QY	1114	ACAGTGCCTGGAAGAAATCTTTGGAGGAGTTTGTGTGTGTCAGTGGAAATTTCTATTG	1173
DB	481	ACAGTGCCTGGAAGAAATCTTTGGAGGAGTTTGTGTGTGTCAGTGGAAATTTCTATTG	540
QY	1174	TTACCTATCACTTTTATCTACCATAGCTTTTGTGTCAGTGTATCATGAGCTCAAG	1227
DB	541	TTACCTATCACTTTTATCTACCATAGCTTTTGTGTCAGTGTATCATGAGCTCAAG	594

RESULT 7
US-10-199-869-27
;; Sequence 27, Application US/10199869
;; Publication No. US20030152953A1
;; GENERAL INFORMATION:
;; APPLICANT: Bristol-Myers Squibb Company
;; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUB
;; FILE REFERENCE: K-alpha2

FILE REFERENCE: D0161 NP
 CURRENT APPLICATION NUMBER: US/10/199,869
 CURRENT FILING DATE: 2002-07-19
 PRIOR APPLICATION NUMBER: US 60/306,577
 PRIOR FILING DATE: 2001-07-19
 NUMBER OF SEQ ID NOS: 90
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 27
 LENGTH: 417
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-199-869-27

Query Match 31.3%; Score 400; DB 15; Length 417;
 Best Local Similarity 100.0%; Pred. No. 4.2e-202;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 31 GTGGTGTGAACGTGGCGGCGCCGCTATTTCGCTGCCCGGAGCTGCTGAAGGACTTC 90
 Db 1 GTGGTGTGAACGTGGCGGCGCCGCTATTTCGCTGCCCGGAGCTGCTGAAGGACTTC 60
 QY 91 CCGCTGCCCGCGTGAACCGCGCTGACCGCTGCGCTCCGAGCGCGAGCTGCTCGAGGTG 150
 Db 61 CCGCTGCCCGCGTGAACCGCGCTGACCGCTGCGCTCCGAGCGCGAGCTGCTCGAGGTG 120
 QY 151 TGGAGCACTACGACCGCGGCGCGAGTACTTCTTCGACCGGCACTCGGAGGCTTC 210
 Db 121 TGGAGCACTACGACCGCGGCGAGTACTTCTTCGACCGGCACTCGGAGGCTTC 180
 QY 211 GGCTTCATCTGCTTACGTGCGCGGCGCGCAAGCTGCGCTTCGCGCGCGGATGTC 270
 Db 181 GGCTTCATCTGCTTACGTGCGCGGCGCGCAAGCTGCGCTTCGCGCGCGGATGTC 240
 QY 271 GAGCTTCCTTACACGAGATGATCTACTGGGCGCTGAGGCGCGGACCTCGAGTAC 330
 Db 241 GAGCTTCCTTACACGAGATGATCTACTGGGCGCTGAGGCGCGGACCTCGAGTAC 300
 QY 331 TGTGTCGAGCGCGCGCTCGACGACCGCATGTCGCGACACCTTACCTCGGCGGAC 390
 Db 301 TGTGTCGAGCGCGCGCTCGACGACCGCATGTCGCGACACCTTACCTCGGCGGAC 360
 QY 391 GAGCGCGCGTGTGGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 430
 Db 361 GAGCGCGCGTGTGGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 400

RESULT 8
 US-09-852-386-25
 Sequence 25, Application US/09852386
 Publication No. US2003006443A1
 GENERAL INFORMATION:
 APPLICANT: Robeids, Steven L.
 APPLICANT: Benjamin, Christopher
 APPLICANT: Karneovsky, Alla M.
 APPLICANT: Ruble, Cara L.
 TITLE OF INVENTION: Human Ion Channels
 FILE REFERENCE: 00133.US1
 CURRENT APPLICATION NUMBER: US/09/852,386
 CURRENT FILING DATE: 2001-05-10
 PRIOR APPLICATION NUMBER: 60/203,305
 PRIOR FILING DATE: 2000-05-10
 PRIOR APPLICATION NUMBER: 60/207,092
 PRIOR FILING DATE: 2000-05-25
 PRIOR APPLICATION NUMBER: 60/206,526
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,033
 PRIOR FILING DATE: 2000-05-25
 PRIOR APPLICATION NUMBER: 60/207,093
 PRIOR FILING DATE: 2000-05-25
 PRIOR APPLICATION NUMBER: 60/216,893
 PRIOR FILING DATE: 2000-07-17
 PRIOR APPLICATION NUMBER: 60/237,873
 PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: 60/223,245
 PRIOR FILING DATE: 2000-08-04
 NUMBER OF SEQ ID NOS: 88
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 25
 LENGTH: 461
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-852-386-25

Query Match 27.2%; Score 347; DB 13; Length 461;
 Best Local Similarity 100.0%; Pred. No. 7e-174;
 Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 932 AGATGGTTATGTACTTCTTCTTCTTCTTGTGTTGCGCATGGCAATCTTTAGTCACATTTCTC 991
 Db 49 AGATGGTTATGTACTTCTTCTTCTTCTTGTGTTGCGCATGGCAATCTTTAGTCACATTTCTC 108
 QY 992 AGCTTTTGAACATGGCGTGGACCTGGAAACATCCACAGGACTTTACGAGCATTCCTG 1051
 Db 109 AGCTTTTGAACATGGCGTGGACCTGGAAACATCCACAGGACTTTACGAGCATTCCTG 168
 QY 1052 CTGCTGCTGGTGGGTGATTAATCTCTATGACTACAGTTGGCTATGGAGATATGATCTTA 1111
 Db 169 CTGCTGCTGGTGGGTGATTAATCTCTATGACTACAGTTGGCTATGGAGATATGATCTTA 228
 QY 1112 TCACAGTCCCTGGAAGAAATCTTGGAGAGTTTGTGTGTCAGTGGAAATTTCTTATGG 1171
 Db 239 TCACAGTCCCTGGAAGAAATCTTGGAGAGTTTGTGTGTCAGTGGAAATTTCTTATGG 288
 QY 1172 CATTACCTATCATTCTTATCTACCATAGCTTTGTCAGTGTATCATGAGCTCAAGTTTA 1231
 Db 289 CATTACCTATCATTCTTATCTACCATAGCTTTGTCAGTGTATCATGAGCTCAAGTTTA 348
 QY 1232 GATCTGTAGTATAGTAGGAGCTCTCCACTGAATTCCTGAATTA 1278
 Db 349 GATCTGTAGTATAGTAGGAGCTCTCCACTGAATTCCTGAATTA 395

RESULT 9
 US-09-989-920-7/c
 Sequence 7, Application US/09989920
 Patent No. US20020172957A1
 GENERAL INFORMATION:
 APPLICANT: Macina, Roberto
 APPLICANT: Recipon, Herve
 APPLICANT: Chen, Sei-yu
 APPLICANT: Sun, Yungming
 APPLICANT: Liu, Chenghua
 TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prote
 FILE REFERENCE: DEX-0291
 CURRENT APPLICATION NUMBER: US/09/989,920
 CURRENT FILING DATE: 2001-11-21
 PRIOR APPLICATION NUMBER: 60/252,500
 PRIOR FILING DATE: 2000-11-22
 NUMBER OF SEQ ID NOS: 284
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 7
 LENGTH: 777
 TYPE: DNA
 ORGANISM: Homo sapien
 US-09-989-920-7

Query Match 25.9%; Score 331; DB 9; Length 777;
 Best Local Similarity 100.0%; Pred. No. 2.3e-165;
 Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 948 TGCTTCATTGTGTTCCCATGGCAATCTTGTAGTGCACATTTCTCAGCTTCTTGAACATGG 1007
 Db 662 TGCTTCATTGTGTTCCCATGGCAATCTTGTAGTGCACATTTCTCAGCTTCTTGAACATGG 603
 QY 1008 GCTGAGCTGGAACATCCCAAGGACTTTACGAGCATTCCTGCTGCTGCTGGGT 1067

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Db 602 GCTGGACCTGGAAACATCCACAGGACTTTTACCAGCAATTCCTGCTGCTGCTGGGT 543
QY 1068 GATTATCTCTATGACTACAGTTGGCTATGGAGATATGATCTATCATCAGTGCCTGGAG 1127
Db 542 GATTATCTCTATGACTACAGTTGGCTATGGAGATATGATCTATCATCAGTGCCTGGAG 483
QY 1128 AATCTTGGAGAGTTGTGTGTGTCAGTGGAAATGTTCTATTGGCAATACCTATCATT 1187
Db 482 AATCTTGGAGAGTTGTGTGTGTCAGTGGAAATGTTCTATTGGCAATACCTATCATT 423
QY 1188 TATCTACCATAGCTTTGTGTCAGTGTATCATGAGTCAAGTTTAGATCTGCTAGTATAG 1247
Db 422 TATCTACCATAGCTTTGTGTCAGTGTATCATGAGTCAAGTTTAGATCTGCTAGTATAG 363
QY 1248 TAGGAGCCTCTCCACTGAATTCCTGAATTA 1278
Db 362 TAGGAGCCTCTCCACTGAATTCCTGAATTA 332

RESULT 10
US-09-989-920-8
; Sequence 8, Application US/09989920
; Patent No. US20020172957A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prob
; FILE REFERENCE: DEX-0291
; CURRENT APPLICATION NUMBER: US/09/989,920
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,500
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 911
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-989-920-8

Query Match 17.0%; Score 217; DB 9; Length 911;
Best Local Similarity 100.0%; Pred. No. 1.1e-104;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1062 GTGGTGATATCTCTATGACTACAGTGTGGCTATGGAGATATGATCTATCAGTGC 1121
Db 229 GTGGTGATATCTCTATGACTACAGTGTGGCTATGGAGATATGATCTATCAGTGC 288
QY 1122 TGGAGAAATCTTGGAGAGTTTGTGTGTCAGTGGAAATGTTCTATTGGCAATACCTAT 1181
Db 289 TGGAGAAATCTTGGAGAGTTTGTGTGTCAGTGGAAATGTTCTATTGGCAATACCTAT 348
QY 1182 CACTTTTATACCATAGCTTTTGGCAGTGTATATGAGTCAAGTTTAGATCTGCTAG 1241
Db 349 CACTTTTATACCATAGCTTTTGGCAGTGTATATGAGTCAAGTTTAGATCTGCTAG 408
QY 1242 GTATAGTAGAGCTCTCCACTGAATTCCTGAATTA 1278
Db 409 GTATAGTAGAGCTCTCCACTGAATTCCTGAATTA 445

RESULT 11
US-10-199-869-28
; Sequence 28, Application US/10199869
; Publication No. US20030152953A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUB
; FILE REFERENCE: D0161 NP
; CURRENT APPLICATION NUMBER: US/10/199,869

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; CURRENT APPLICATION NUMBER: US/10/199,869
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/306,577
; PRIOR FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 138
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-199-869-28

Query Match 10.8%; Score 138; DB 15; Length 138;
Best Local Similarity 100.0%; Pred. No. 1.4e-62;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 454 CGCTGGCTGAGCGCATGCGCGGACCTTCGAGAGCCACGTCGTCGTCGCGCCGAG 513
Db 1 CGCTGGCTGAGCGCATGCGCGGACCTTCGAGAGCCACGTCGTCGTCGCGCCGAG 60
QY 514 ATCCTGCTAGCGTGTGCGTGGTGTTCGTCGATCGTGTCCATGGTGTGTCGTCGCGCCAGC 573
Db 61 ATCCTGCTAGCGTGTGCGTGGTGTTCGTCGATCGTGTCCATGGTGTGTCGTCGCGCCAGC 120
QY 574 ACCTTGCCCGACTGCGCGC 591
Db 121 ACCTTGCCCGACTGCGCGC 138

RESULT 12
US-10-199-869-30/c
; Sequence 30, Application US/10199869
; Publication No. US20030152953A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUB
; FILE REFERENCE: D0161 NP
; CURRENT APPLICATION NUMBER: US/10/199,869
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/306,577
; PRIOR FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 80
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-199-869-30

Query Match 6.3%; Score 80; DB 15; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.1e-31;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 751 ATCAGCGCGTATTACATCTCTGTTGATGACAGTGTTCAGGCGAGAACTCTCAACTC 810
Db 80 ATCAGCGCGTATTACATCTCTGTTGATGACAGTGTTCAGGCGAGAACTCTCAACTC 21
QY 811 CAGAGGGCTGGAGTCACCTT 830
Db 20 CAGAGGGCTGGAGTCACCTT 1

RESULT 13
US-10-199-869-89/c
; Sequence 89, Application US/10199869
; Publication No. US20030152953A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUB
; FILE REFERENCE: D0161 NP
; CURRENT APPLICATION NUMBER: US/10/199,869

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; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/306,577
; PRIOR FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 89
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-199-869-89

Query Match      2.3%; Score 30; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.9e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 931 GAGATGGTATGTTACTTGTTCTTCATTGT 960
    |||||
Db 30 GAGATGGTATGTTACTTGTTCTTCATTGT 1

RESULT 14
US-10-114-270-268
; Sequence 268, Application US/10114270
; Publication No. US20040030110A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kexuda, Ramesh
; APPLICANT: Miller, Charles E.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Patturajan, Meera
; APPLICANT: Liu, Zhaozhong
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Li, Li
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Gorman, Linda
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Smithson, Glenda
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Ji, Weizhen
; APPLICANT: Anderson, David W.
; APPLICANT: Liette, Mario W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Stone, David J.
; APPLICANT: Macdougall, John R.
; APPLICANT: Rothenberg, Mark E.
; TITLE OF INVENTION: No. US20040030110A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-322C
; CURRENT APPLICATION NUMBER: US/10/114,270
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/281,086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10

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; PRIOR APPLICATION NUMBER: 60/283,512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 470
; SEQ ID NO 268
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: probe
US-10-114-270-268

Query Match      2.0%; Score 26; DB 13; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 865 ATTAGCTTGCCCGTCACTTCATTGG 890
    |||||
Db 1 ATTAGCTTGCCCGTCACTTCATTGG 26

RESULT 15
US-10-199-869-38/c
; Sequence 38, Application US/10199869
; Publication No. US20030152953A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUB
; FILE REFERENCE: D0161 NP
; CURRENT APPLICATION NUMBER: US/10/199,869
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/306,577
; PRIOR FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 38
; LENGTH: 37
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-199-869-38

Query Match      2.0%; Score 25; DB 15; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1251 GAGCCTCTCCACTGAATTCCTGAAT 1275
    |||||
Db 37 GAGCCTCTCCACTGAATTCCTGAAT 13

Search completed: April 19, 2004, 21:05:18
Job time : 590 secs

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OM nucleic - nucleic search, using sw model

Run on: April 19, 2004, 15:32:13 ; Search time 5116 Seconds
(without alignments)
10827.286 Million cell updates/sec

Title: US-10-016-647-1

Perfect score: 1278
Sequence: 1 atgaccttcggcgagcggg.....ccactgaattcctgaattaa 1278

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 24

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1278	100.0	1278	6	AX511260	AX511260 Sequence
2	1278	100.0	1844	6	AX511262	AX511262 Sequence
3	1278	100.0	3670	9	AF454547	AF454547 Homo sapi
4	840	65.7	2312	6	AX392945	AX392945 Sequence
5	729	57.0	2235	6	AX478109	AX478109 Sequence
6	649	50.8	151367	9	AC025750	AC025750 Homo sapi
7	647	50.6	1311	9	AB070604	AB070604 Homo sapi
8	647	50.6	1947	6	AX641934	AX641934 Sequence
9	647	50.6	1947	9	AF348982	AF348982 Homo sapi
10	647	50.6	3703	9	AF454548	AF454548 Homo sapi
11	347	27.2	461	6	AX319980	AX319980 Sequence
12	331	25.9	777	6	AX534980	AX534980 Sequence
13	217	17.0	911	6	AX534981	AX534981 Sequence
14	80	6.3	1302	9	AF450110	AF450110 Homo sapi
15	80	6.3	1744	10	AF454549	AF454549 Rattus no
16	80	6.3	1777	10	AF454550	AF454550 Rattus no
17	80	6.3	219807	2	AC098764	AC098764 Rattus no
18	80	6.3	259704	2	AC112092	AC112092 Rattus no
19	80	6.3	288099	2	AC133407	AC133407 Rattus no
20	78	6.1	702	9	HS325071	HS325071 Homo sapi
21	71	5.6	3323	10	AF454551	AF454551 Mus muscu
22	71	5.6	3356	10	AF454552	AF454552 Mus muscu
23	71	5.6	5775	6	AX641960	AX641960 Sequence
24	71	5.6	68831	2	AC101224	AC101224 Mus muscu
25	71	5.5	209523	10	AC084386	AC084386 Mus muscu
26	70	5.5	1038	10	AB070605	AB070605 Rattus no

ALIGNMENTS

RESULT 1	AX511260	1278 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	Sequence 1 from Patent WO0250271.				
DEFINITION	AX511260				
ACCESSION	AX511260.1				
VERSION	GI:23392138				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Fridde, C.J., Hilbun, E. and Turner, C.A.				
TITLE	Novel human ion channel protein and polynucleotides encoding the same				
JOURNAL	Patent: WO 0250271-A 1 27-JUN-2002;				
FEATURES	Lexicon Genetics Incorporated (US)				
SOURCE	Location/Qualifiers				
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	/mol_type="unassigned DNA"				
	/db_xref="taxon:9606"				
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Best Local Similarity	100.0%;	Pred. No. 0;			
Matches 1278;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1	ATGACCTTCGGCGCAGCGGGCGGCTCGTGGTGTGCTGAACGTGGCGGCCGGTAT	60		
Db	1	ATGACCTTCGGCGCAGCGGGCGGCTCGTGGTGTGCTGAACGTGGCGGCCGGTAT	60		
Qy	61	TCGCTGTCGGCGAGCTGCTGAAGGACTTCCCGTCGCCCGCGTGCACGCGCTCAGCGC	120		

Pred. No. is the number of results predicted by chance to have a

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 Qy 121 TCGCGCTCCAGCGCGAGCTGCTCGAGGTGTGGACGACTACGACCGCGAGCGCAACGAG 180
 Db 121 TCGCGCTCCAGCGCGAGCTGCTCGAGGTGTGGACGACTACGACCGCGAGCGCAACGAG 180
 Qy 181 TACTTCTTCACCGGCACTCGAGGCTTCGGCTTCACTCTGCTCTACGTCGCGCGCCAC 240
 Db 181 TACTTCTTCACCGGCACTCGAGGCTTCGGCTTCACTCTGCTCTACGTCGCGCGCCAC 240
 Qy 241 GGCAGCTGCGCTTCGCGCGCGAGATGCGAGCTTCCTTCTACAAAGAGATGATCTAC 300
 Db 241 GGCAGCTGCGCTTCGCGCGCGAGATGCGAGCTTCCTTCTACAAAGAGATGATCTAC 300
 Qy 301 TGGGCTCTGGAGGCGCGCACTCGAGTACTGTGCGAGCGCGCTTCGACGACCGCATG 360
 Db 301 TGGGCTCTGGAGGCGCGCACTCGAGTACTGTGCGAGCGCGCTTCGACGACCGCATG 360
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 Db 361 TCCGACACCTACACCTTCTACTCGCGCGAGCGCGGCTGCTGGCGCGCGACGAGCGC 420
 Qy 421 CGCCCGCGCGCGAGCGGCTCCCTCCAGGCTGCTGCGAGCGCATGCGCGCGAC 480
 Db 421 CGCCCGCGCGCGAGCGGCTCCCTCCAGGCTGCTGCGAGCGCATGCGCGCGAC 480
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 Db 601 GCGCACAACCGCAGCTGAGTACCGGAGCAGGATTAATGAAGCTATCTGATAGTTGG 660
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 Db 721 AGACCCCTGAGCACTATGATTTACTGGCAATCACCGCTATTACATCTCTGTTGATG 780
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 Qy 841 AGAATGATGAGGATTTTGGGTGATTAAGCTTCCCGCTCACTTCAATGGTCTTCAGACA 900
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 Qy 1081 ACTACAGTTGGCTATGAGATATGATTCCTATCACAGTGCCTGGAAAGATTTCTGGAGGA 1140
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 Db 1141 GTTGTGCTGTCAGTGAATTTCTATTGGCAATTAACCTATCACTTTTATACCATAGC 1200

Qy 1201 TTTGTGCACTTATCATGAGCTCAAGTTAGATCTCTAGGTATAGTAGAGCCTCTCC 1260
 Db 1201 TTTGTGCACTTATCATGAGCTCAAGTTAGATCTCTAGGTATAGTAGAGCCTCTCC 1260
 Qy 1261 ACTGAATTCCTCAATTA 1278
 Db 1261 ACTGAATTCCTCAATTA 1278
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 AX511262 1844 bp DNA linear PAT 27-SEP-2002
 LOCUS Sequence 3 from Patent WO0250271.
 DEFINITION AX511262
 ACCESSION AX511262
 VERSION AX511262.1 GI:23392139
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Fridele, C.J., Hilbun, E. and Turner, C.A.
 TITLE Novel human ion channel protein and polynucleotides encoding the same
 JOURNAL Patent: WO 0250271-A 3 27-JUN-2002;
 Lexicon Genetics Incorporated (US)
 FEATURES
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 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
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 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATGACCTTCGGCGCGAGCGGCGGCTCGGTGTGTGTGAACGTGGCGGCGCGCGGTAT 60
 Db 457 ATGACCTTCGGCGCGAGCGGCGGCTCGGTGTGTGTGAACGTGGCGGCGCGCGGTAT 516
 Qy 61 TCGCTGTCCCGGAGCTGCTGAAGGACTTCCCGCTGCGCGCGGTGAGCCGGCTGCACGGC 120
 Db 517 TCGCTGTCCCGGAGCTGCTGAAGGACTTCCCGCTGCGCGCGGTGAGCCGGCTGCACGGC 576
 Qy 121 TCGCGCTCCGAGCGGAGCTGCTCGAGGTGTGAGCACTACGACCGCGAGCGCAACGAG 180
 Db 577 TCGCGCTCCGAGCGGAGCTGCTCGAGGTGTGAGCACTACGACCGCGAGCGCAACGAG 636
 Qy 181 TACTTCTTCGACCGGCACTCGAGGCTTCGGCTTCACTCTGCTCTACGTCGCGCGCCAC 240
 Db 637 TACTTCTTCGACCGGCACTCGAGGCTTCGGCTTCACTCTGCTCTACGTCGCGCGCCAC 696
 Qy 241 GGCAGCTGCGCTTCGCGCGCGGATGTGCGAGCTCTCTTCTACAAAGAGATGATCTAC 300
 Db 697 GGCAGCTGCGCTTCGCGCGCGGATGTGCGAGCTCTCTTCTACAAAGAGATGATCTAC 756
 Qy 301 TGGGCTCTGGAGGCGCGGACCTCGAGTACTGTGCGAGCGCGCTTCGACGACCGCATG 360
 Db 757 TGGGCTCTGGAGGCGCGGACCTCGAGTACTGTGCGAGCGCGCTTCGACGACCGCATG 816
 Qy 361 TCCGACACCTACACCTTCTACTCGCGCGAGCGAGCGCGGCTGCTGGCGCGCGAGCGC 420
 Db 817 TCCGACACCTACACCTTCTACTCGCGCGAGCGAGCGCGGCTGCTGGCGCGCGAGCGC 876
 Qy 421 CGCCCGCGCGCGGCGGAGCGGCTCCCTCCAGGCTGCTGCGAGCGCATGCGCGCGAC 480
 Db 877 CGCCCGCGCGCGGCGGAGCGGCTCCCTCCAGGCTGCTGCGAGCGCATGCGCGCGAC 936
 Qy 481 TTCGAGGAGCGCACTGCTGCTGCTGCGCGCGAGATCCTGCTAGCGTGTGCTGCTTC 540
 Db 937 TTCGAGGAGCGCACTGCTGCTGCTGCGCGCGAGATCCTGCTAGCGTGTGCTGCTTC 996

Qy	601	GCCGACAA	CCGAGCCTTGGATGACCGGAGCAGGATAAATTGAAGCTATCTGCATAGGTTGG	660
Db	1078	GCCGACAA	CCGAGCCTGGATGACCGGAGCAGGATAAATTGAAGCTATCTGCATAGGTTGG	1137
Qy	661	TTCACTGCCGAGTGCATCGTAGGTTCAATTGTTCTCCAAAACAAGTGTGAGTTTGTCAAG	720	
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Qy	721	AGACCCCTGGAACATCATTTGATTTTACTGGCAATCACGCCGTATTACATCTCTGTGTTGATG	780	
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Qy	781	ACAGTGTTTACAGCGAGAACTCTCAACTCCAGAGGCTGGAGTCACTTGAGGGTACTTT	840	
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Qy	841	AGAATGATGAGGATTTTTTGGGTGATTAAGCTTTGCCCGTCACTTCATTGGTCTTTCAGACA	900	
Db	1318	AGAATGATGAGGATTTTTTGGGTGATTAAGCTTTGCCCGTCACTTCATTGGTCTTTCAGACA	1377	
Qy	901	CTCGGTTTGACTCTCAAACTTGCTACCGAGAGATGGTTAGTTACTTTHCTTCATTGTT	960	
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Qy	1021	ACATCCAA	CAAGGACTTTACAGATTTCTGCTGCTGCTGGTGGGTGATTAATCTCTATG	1080
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Qy	1261	ACTGAATTCCTGAAATTA	1278	
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LOCUS	AX392945	Sequence 47 from Patent WO0212340.	2312 bp	DNA	linear
DEFINITION	AX392945				
ACCESSION	AX392945				
VERSION	AX392945.1				
		GI:19700992			

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Tang, Y.T., Yue, H., Nguyen, D.B., Hafalia, A.J., Elliott, V.S., Lu, Y.,
 Walia, N.K., Yao, M.G., Raughn, M.R., Gandhi, A.R., Ding, L.,
 Sanjanwala, M., Ramkumar, J., Arvizu, C., Gietzen, K.J., Lai, P.G.,
 Azimzai, Y., Khan, F.A., Thangavelu, K., Thornton, M., Lu, D.A.,
 Tribouley, C.M., Warren, B.A., Ison, C.H., Das, D., Raumann, B.E.,
 Policky, J.L. and Kearney, L.
 TITLE Transposers and ion channels
 JOURNAL Patent: WO 0240541-A 39 23-MAY-2002;
 Incyte Genomics, Inc. (US)

FEATURES
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 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 574 AGTTGCCGACTGCGCAACGACCCCGACACACCGACCGTGGATGACCGAGCAGG 633
 Db 980 AGTTGCCGACTGCGCAACGACCCCGACACACCGACCGTGGATGACCGAGCAGG 1039

QY 634 ATAATTGAAGCTATCTGATAGTGTGTTCTGTCGCGAGTGCATGCTGATGTTGTC 693
 Db 1040 ATAATTGAAGCTATCTGATAGTGTGTTCTGTCGCGAGTGCATGCTGATGTTGTC 1099

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QY 814 AGGGCTGAGTCACTTGGAGGTACTTAGAATGATGAGATTTTGGGTGATTAAGCTT 873
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QY 1234 TCTGCTAGG 1242
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RESULT 6
 AC025750/c
 LOCUS AC025750 151367 bp DNA linear PRI 09-JAN-2002
 DEFINITION Homo sapiens BAC clone RP11-804P20 from 2, complete sequence.
 AC025750
 ACCESSION AC025750
 VERSION AC025750.10 GI:18098549
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 151367)
 AUTHORS Sulston, J.E. and Waterston, R.
 TITLE Toward a complete human genome sequence
 JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
 MEDLINE 93063792
 PUBMED 9847074

REFERENCE 2 (bases 1 to 151367)
 AUTHORS Tomlinson, C., Cotton, M. and Doeber, A.
 TITLE The sequence of Homo sapiens BAC clone RP11-804P20
 JOURNAL Unpublished (2002)
 REFERENCE 3 (bases 1 to 151367)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (13-MAR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 4 (bases 1 to 151367)
 AUTHORS Waterston, R.
 TITLE Direct Submission
 JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Jan 9, 2002 this sequence version replaced gi:13431263.

COMMENT ----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc
 Contact: sapiens@wustl.edu
 Summary Statistics
 Center project name: H_NH0804P20

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
 Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
 The RP11 human BAC library was made from the blood of one male donor, as described by Osada, K., Woon, P.Y., Zhao, B., Frengen, E., Tateo, M., Cateneese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong

and coworkers at the Roswell Park Cancer Institute
(http://baopac.med.buffalo.edu)

VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-299C5, 2000 bp overlap; the clone sequenced to the right is RP11-729W8. Actual start of this clone is at base position 157736 of RP11-299C5; actual end is at base position 151367 of RP11-804P20.

Data from AC074375 and AC006038 was used to finish this clone, AC025750. Polymorphisms have been identified between AC025750 and AC074375. The sequence from 40567 to 41115, from 40991 to 41115 are covered only by PCR products from clone DNA. There is an unresolved homopolymeric run between 39229 and 39243. There is an unresolved region between 13476 and 132479.

FEATURES

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Query Match 50.8%; Score 649; DB 9; Length 151367;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 649; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 630 CAGGATAATTGAAGCTATCTGCATAGGTTGGTTCACCTGCCGAGTGATCGTGAGTTTCAT 689

Db 8482 CAGGATAATTGAAGCTATCTGCATAGGTTGGTTCACCTGCCGAGTGATCGTGAGTTTCAT 8423

QY 690 TGCTCCAAAACAAGTGTCAGTTTGTCAAGAGACCCCTCAACATCATTTGATTTTACTGGC 749

Db 8422 TGCTCCAAAACAAGTGTCAGTTTGTCAAGAGACCCCTCAACATCATTTGATTTTACTGGC 8363

QY 750 AATCAGCGGTATACATCTCTGTGTTGATGACAGTGTTCACGGCGAGAACTCTCAACT 809
DB 8362 AATCAGCGGTATACATCTCTGTGTTGATGACAGTGTTCACGGCGAGAACTCTCAACT 8303
QY 810 CCAGAGGCTGGAGTCACTTGGAGGTACTTAGAATGATGAGGATTTTTCGGTGATTA 869
DB 8302 CCAGAGGCTGGAGTCACTTGGAGGTACTTAGAATGATGAGGATTTTTCGGTGATTA 8243
QY 870 GCTTCCCGTCACTTCACTTGGTCTTCAGACACTGGTGTGACTCTCAACGTTGCTACCG 929
DB 8242 GCTTCCCGTCACTTCACTTGGTCTTCAGACACTGGTGTGACTCTCAACGTTGCTACCG 8183
QY 930 AGAGATGTTTATGTTTACTTGTCTTCAATTTGTGTTGCCATGGCAATCTTTAGTGCACTTTC 989
DB 8182 AGAGATGTTTATGTTTACTTGTCTTCAATTTGTGTTGCCATGGCAATCTTTAGTGCACTTTC 8123
QY 990 TCAGTCTTCTGAAATGAGGCTGGAGCTGGAACATCCGAAGACATTTACAGCATTC 1049
DB 8122 TCAGTCTTCTGAAATGAGGCTGGAGCTGGAACATCCGAAGACATTTACAGCATTC 8063
QY 1050 TGCTCCCTGCTGGTGGGTGATTAATCTCTATGACTACAGTTGGCTATGGAGATATGATCC 1109
DB 8062 TGCTCCCTGCTGGTGGGTGATTAATCTCTATGACTACAGTTGGCTATGGAGATATGATCC 8003
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DB 8002 TATCAGTGGCTGGAAGAAATTTTGGAGGATTTGTGTTGTGAGTGAATTTGTTCTATT 7943
QY 1170 GGCATTACCTATCACTTTTACTACCATAGCTTTGTGAGGATTTATCATGAGCTCAAGTT 1229
DB 7942 GGCATTACCTATCACTTTTACTACCATAGCTTTGTGAGGATTTATCATGAGCTCAAGTT 7883
QY 1230 TAGATCTGCTAGGTATAGTAGGAGCTCTCCACTGAATTCCTGAATTA 1278
DB 7882 TAGATCTGCTAGGTATAGTAGGAGCTCTCCACTGAATTCCTGAATTA 7834

RESULT 7
LOCUS AB070604 1311 bp mRNA linear PRI 23-MAR-2002
DEFINITION Homo sapiens KV6.3 mRNA for voltage-gated K+ channel 6.3, complete cds.
ACCESSION AB070604
VERSION AB070604.1 GI:19916472
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 Sano, Y., Mochizuki, S., Miyake, A., Kitada, C., Inamura, K., Yokoi, H., Nozawa, K., Matsushima, H. and Furuichi, K.
TITLE Molecular cloning and characterization of Kv6.3, a novel modulatory subunit for voltage-gated K+ channel Kv2.1
JOURNAL FEBS Lett. 513, 230-234 (2002)
REFERENCE 2 (bases 1 to 1311)
AUTHORS Sano, Y. and Mochizuki, S.
TITLE Direct Submission
JOURNAL Submitted (24-AUG-2001) Yorikata Sano, Yamanouchi Pharmaceutical Co., Ltd, Molecular Medicine Laboratories; 21 Miyukigaoka, Tsukuba, Ibaraki 305-8585, Japan (E-mail: sano.yorikata@yamanouchi.co.jp, Tel:81-298-52-5111, Fax:81-298-52-2965).

FEATURES
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CVVSGIVLLALPITFIYHSPVQCYHELKFRSARYSRSLSTEFIN"

ORIGIN
Query Match 50.6%; Score 647; DB 9; Length 1311;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 632 GGATATTTAGACTATCGCATAGGTTGGTTCACTCCCGAGTGCATCGTGAGGTTCAATG 691
DB 665 GGATATTTAGACTATCGCATAGGTTGGTTCACTCCCGAGTGCATCGTGAGGTTCAATG 724
QY 692 TCTCCAAAACAACTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTACTGGCAA 751
DB 725 TCTCCAAAACAACTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTACTGGCAA 784
QY 752 TCACGGCGTATACATCTCTGTGTTGATGACAGTGTTTACAGCGAGAACTCTCAACTCC 811
DB 785 TCACGGCGTATACATCTCTGTGTTGATGACAGTGTTTACAGCGAGAACTCTCAACTCC 844
QY 812 AGAGGGCTGAGTCACTTGTGAGGTTACTTAGAATGATGAGGATTTTGGTGGTCAATAGC 871
DB 845 AGAGGGCTGAGTCACTTGTGAGGTTACTTAGAATGATGAGGATTTTGGTGGTCAATAGC 904
QY 872 TTCCCGTCACTTCAATGGTCTTCAGACACTCGGTTTGACTCTCAACGTTGCTACCGAG 931
DB 905 TTCCCGTCACTTCAATGGTCTTCAGACACTCGGTTTGACTCTCAACGTTGCTACCGAG 964
QY 932 AGATGTTTGTACTTGTCTTCAATTTGTGTTGCCATGGCAATCTTTAGTGCACTTCTC 991
DB 965 AGATGTTTGTACTTGTCTTCAATTTGTGTTGCCATGGCAATCTTTAGTGCACTTCTC 1024
QY 992 AGCTTCTTGAAACATGGCTGGACCTGGAACATCCCAAGAGACTTTACCAGATTCCTG 1051
DB 1025 AGCTTCTTGAAACATGGCTGGACCTGGAACATCCCAAGAGACTTTACCAGATTCCTG 1084
QY 1052 CTGCTGCTGGTGGGTGATTAATCTCTATGACTACAGTTGGCTATGGAGATATGATCCTTA 1111
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QY 1112 TCACAGTGGCTGGAAGAAATTTTGGAGGATTTGTGTTGTGCTAGTGAATTTCTATTGG 1171
DB 1145 TCACAGTGGCTGGAAGAAATTTTGGAGGATTTGTGTTGTGCTAGTGAATTTCTATTGG 1204
QY 1172 CATTACCTATCACTTTTATCTACATAGCTTTGTGAGGATTTATCATGAGCTCAAGTTTA 1231
DB 1205 CATTACCTATCACTTTTATCTACATAGCTTTGTGAGGATTTATCATGAGCTCAAGTTTA 1264
QY 1232 GATCTGCTAGGTATAGTAGGAGCTCTCCACTGAATTCCTGAATTA 1278
DB 1265 GATCTGCTAGGTATAGTAGGAGCTCTCCACTGAATTCCTGAATTA 1311

RESULT 8
LOCUS AX641934 1947 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3 from Patent WO02096944.
ACCESSION AX641934
VERSION AX641934.1 GI:28474564
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.


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Query Match      27.2%; Score 347; DB 6; Length 461;
Best Local Similarity 100.0%; Pred. No. 9.6e-170;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 932 AGATGGTTATGTTACTTGTCTTCAATTTGTTGGCCATGGAATCTTTAGTGCACCTTTCTC 991
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QY 992 AGCTTTCTGACATGGCTGGACCTGGAACATCCCAAGGACTTTTACCACATCTCTG 1051
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DB 169 CTGCTGCTGGTGGGTGATTATCTCTATGACATACAGTTGGCTATGGAGATATGTATCTCTA 228

QY 1112 TCACAGTGGCTGGAAGAAATCTTTGGAGGAGTTTGTCTCAGTGGAAATTTCTTATGG 1171
DB 229 TCACAGTGGCTGGAAGAAATCTTTGGAGGAGTTTGTCTCAGTGGAAATTTCTTATGG 288

QY 1172 CATTACCTATCACTTTTACTTACCATAGCTTTGTGCAGGTATCATGAGCTCAAGTTTA 1231
DB 289 CATTACCTATCACTTTTACTTACCATAGCTTTGTGCAGGTATCATGAGCTCAAGTTTA 348

QY 1232 GATCTCTAGGTATAGTAGGAGCTCTCCACTGAATTCCTGAATTA 1278
DB 349 GATCTCTAGGTATAGTAGGAGCTCTCCACTGAATTCCTGAATTA 395

RESULT 12
AX534980/c
LOCUS
DEFINITION Sequence 7 from Patent WO02068633.
ACCESSION AX534980
VERSION AX534980.1 GI:25261559
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Macina, R.A., Recipon, H., Chen, S.Y., Sun, Y. and Liu, C.
TITLE Compositions and methods relating to lung specific genes and proteins
JOURNAL Patent: WO 02068633-A 7 06-SEP-2002;
Diadexus, Inc. (US)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 2.2e-161;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 948 TGCTTCATTTGTTGGCCATGGAATCTTTAGTGCACCTTTCTCAGCTTTCTGAACTGG 1007
DB 662 TGCTTCATTTGTTGGCCATGGAATCTTTAGTGCACCTTTCTCAGCTTTCTGAACTGG 603

QY 1008 GCTGACCTGGAAACATCAACAGGACTTTACAGCAATCTCTGCTGCTCTGCTGGGT 1067
DB 602 GCTGACCTGGAAACATCAACAGGACTTTACAGCAATCTCTGCTGCTCTGCTGGGT 543

QY 1068 GATTATCTATGATACAGTTGGCTATGGAGATATGATCTATCAAGTGGCTGGAAG 1127
DB 542 GATTATCTATGATACAGTTGGCTATGGAGATATGATCTATCAAGTGGCTGGAAG 483

QY 1128 AATTCTTGAGGAGTTGTTGTTCAGTGGAAATTTCTTATGGCAATTAACCTATCACTTT 1187
DB 482 AATTCTTGAGGAGTTGTTGTTCAGTGGAAATTTCTTATGGCAATTAACCTATCACTTT 423

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QY 1188 TATCTACATAGCTTTTGTGAGTGTATCATGAGCTCAAGTTTAGATCTCTAGGTATAG 1247
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QY 1248 TAGGAGCTCTCCACTGAATTCCTGAATTA 1278
DB 362 TAGGAGCTCTCCACTGAATTCCTGAATTA 332

RESULT 13
AX534981
LOCUS
DEFINITION Sequence 8 from Patent WO02068633.
ACCESSION AX534981
VERSION AX534981.1 GI:25261562
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Macina, R.A., Recipon, H., Chen, S.Y., Sun, Y. and Liu, C.
TITLE Compositions and methods relating to lung specific genes and proteins
JOURNAL Patent: WO 02068633-A 8 06-SEP-2002;
Diadexus, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 1.1e-101;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1242 GTATAGTAGGAGCTCTCCACTGAATTCCTGAATTA 1278
DB 409 GTATAGTAGGAGCTCTCCACTGAATTCCTGAATTA 445

RESULT 14
AF450110
LOCUS
DEFINITION Homo sapiens voltage-gated potassium channel subunit Kv6.4 mRNA, complete cds.
ACCESSION AF450110
VERSION AF450110.1 GI:31295623
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1302)
AUTHORS Preisig-Muller, R., Derst, C., Mederos Y Schnitzler, M. and Daut, J.
TITLE Cloning and characterization of two novel gamma Kv subunits
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 1302)
REFERENCE Preisig-Muller, R., Derst, C., Mederos Y Schnitzler, M. and Daut, J.
TITLE Direct Submission

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JOURNAL Submitted (23-NOV-2001) University of Marburg, Institute of Physiology, Deutschhausstrasse 1-2, Marburg 35037, Germany

FEATURES Location/Qualifiers

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/tissue_type="brain"

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/db_xref="GI:31295624"

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ORIGIN

Query Match 6.3%; Score 80; DB 9; Length 1302;
Best Local Similarity 100.0%; Pred. No. 5.8e-30;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 AAGCTCGCCTTCGCGCGCGGATGCGAGCTCTCTTCTACAACGAGATGATCTACTGG 303

DB 244 AAGCTCGCCTTCGCGCGCGGATGCGAGCTCTCTTCTACAACGAGATGATCTACTGG 303

QY 304 GGCCTGGAGGGCGGCACCT 323

DB 304 GGCCTGGAGGGCGGCACCT 323

RESULT 15

AF454549 1744 bp mRNA linear ROD 09-AUG-2002

LOCUS Rattus norvegicus voltage-gated potassium channel subunit Kv10.1a

DEFINITION mRNA, complete cds, alternatively spliced.

ACCESSION AF454549

VERSION AF454549.1 GI:22164085

KEYWORDS

SOURCE Rattus norvegicus (Norway rat)

ORGANISM

Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

1 (bases 1 to 1744)

Vega-Saenz de Miera, E.C. and Rudy, B.

Kv10.1a and Kv10.1b: Two novel alternatively spliced potassium

channel subunits

Unpublished

2 (bases 1 to 1744)

Vega-Saenz de Miera, E.C. and Rudy, B.

Direct Submission

Submitted (04-DEC-2001) Physiology and Neuroscience, New York

University School of Medicine, 550 First Avenue, New York, NY

10016, USA

FEATURES

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ORIGIN

Query Match 6.3%; Score 80; DB 10; Length 1744;
Best Local Similarity 100.0%; Pred. No. 5.8e-30;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 470 AAGCTCGCCTTCGCGCGCGGATGCGAGCTCTCTTCTACAACGAGATGATCTACTGG 529

QY 304 GGCCTGGAGGGCGGCACCT 323

DB 530 GGCCTGGAGGGCGGCACCT 549

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Job time : 5126 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
9360.685 Million cell updates/sec

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Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 24

Total number of hits satisfying chosen parameters: 19

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

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1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002s.*
7: Geneseqn2003as.*
8: Geneseqn2003bs.*
9: Geneseqn2003cs.*
10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1278	100.0	1844	6	Abn83931 Human vol
3	840	65.7	2312	6	Ad33662 Human TRI
4	729	57.0	2235	6	Abk83228 Human tra
5	647	50.6	1947	7	Abz24711 Human pot
6	647	50.6	5174	9	Abd01447 Human TCH
7	644	50.4	1308	9	Abd01427 Human TCH
8	613	48.0	1651	7	Abx72192 Human NOV
9	347	27.2	461	6	Abk27494 DNA encod
c 10	331	25.9	777	6	Abx91965 Lung spec
11	217	17.0	911	6	Abx91966 Lung spec
12	71	5.6	5775	9	Abz24716 Murine po
13	70	5.5	950	9	Abd01469 Mouse TCH
14	29	2.3	1634	6	Abq49122 Oligonucl
c 15	29	2.3	1634	6	Abq49123 Oligonucl
16	26	2.0	26	7	Abx72331 Human NOV
c 17	24	1.9	24	9	Abd01432 Human TCH
c 18	24	1.9	1634	6	Abq49124 Oligonucl
19	24	1.9	1634	6	Abq49125 Oligonucl

ALIGNMENTS

RESULT 1
ABN83930 standard; cDNA; 1278 BP.
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AC ABN83930;
XX
06-SEP-2002 (first entry)
XX
Human voltage-gated potassium channel-like protein encoding cDNA.
XX
Human; voltage-gated potassium channel; ion channel; neuroprotective;
KW therapeutic; diagnostic; pharmacogenic; gene therapy; SNP;
KW single nucleotide polymorphism; foetal brain; brain; cerebellum;
KW pituitary; prostate; thymus; lymph node; bone marrow; trachea;
KW foetal liver; liver; testis; thyroid; salivary gland; stomach;
KW skeletal muscle; heart; uterus; adipose; hypothalamus; ovary; aorta;
KW 12 week old embryo; adenocarcinoma; osteosarcoma; Gene; ss.
OS Homo sapiens.
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PH Key Location/Qualifiers
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FT variation replace(432,C)
FT /*tag= b
FT /standard_name= "single nucleotide polymorphism"
XX
XX WO200250271-A2.
XX
XX 27-JUN-2002.
XX
XX 10-DEC-2001; 2001WO-US048050.
XX
XX 20-DEC-2000; 2000US-0257932P.
XX
XX (LEXI-) LEXICON GENETICS INC.
XX
XX Fiddle CJ, Hilbun E, Turner CA;
XX
XX WPI; 2002-508799/54.
DR P-PSDB; ABB83073.
XX
XX Human ion channel polynucleotide useful in therapeutic, diagnostic and pharmacogenic applications.
XX
XX Claim 1; Page 34; 36pp; English.
XX
XX The invention relates to a novel human ion channel polynucleotide that shares structural similarity with voltage-gated potassium channel proteins. The activity of the protein of the invention may be described as neuroprotective. The protein of the invention is useful in therapeutic, diagnostic and pharmacogenic applications, for example to identify mutations associated with a particular disease, as a diagnostic or prognostic assay, or in gene therapy. The protein of the invention has been found to be expressed in human foetal brain, brain, cerebellum, pituitary, prostate, thymus, lymph node, bone marrow, trachea, foetal liver, liver, testis, thyroid, salivary gland, stomach, skeletal muscle, heart, uterus, adipose, hypothalamus, ovary, aorta, 12 week old embryo, adenocarcinoma and osteosarcoma cells. The current sequence represents the human voltage-gated potassium channel-like protein encoding cDNA

XX Sequence 1278 BP; 237 A; 349 C; 376 G; 316 T; 0 U; 0 Other;

Query Match 100.0%; Score 1278; DB 6; Length 1278;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGACCTTCGGCGCAGCGGGCGCTCGGTGGTCTGAACGTGGCGCGCCGGTAT 60
DB 1 ATGACCTTCGGCGCAGCGGGCGCTCGGTGGTCTGAACGTGGCGCGCCGGTAT 60

61 TCGCTGTCGGGAGCTGCTGAAGACTTCCGGCTCGCGCGTGAGCGGCTGCACGGC 120
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61 TCGCTGTCGGGAGCTGCTGAAGACTTCCGGCTCGCGCGTGAGCGGCTGCACGGC 120
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121 TCGCGCTCGAGCGGCGACGCTGCTGAGGTGTCGAGACTACGACCGGAGCGGCGAAGAG 180
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121 TCGCGCTCGAGCGGCGACGCTGCTGAGGTGTCGAGACTACGACCGGAGCGGCGAAGAG 180
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181 TACTTCTTCGACCGGCACTCGAGGCGCTTCGGGCTTCATCTCTCTACGTGCGCGCCAC 240
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181 TACTTCTTCGACCGGCACTCGAGGCGCTTCGGGCTTCATCTCTCTACGTGCGCGCCAC 240
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241 GGAAGCTCGCTTCGGCGCGGAGATGTCGAGCTCTCTCTTACAAAGAGATGATCTAC 300
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241 GGAAGCTCGCTTCGGCGCGGAGATGTCGAGCTCTCTCTTACAAAGAGATGATCTAC 300
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301 TGGGCGCTCGAGCGGCGCACCTCGAGTACTCTGTCAGCGCGGCTCGACACCGCATG 360
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301 TGGGCGCTCGAGCGGCGCACCTCGAGTACTCTGTCAGCGCGGCTCGACACCGCATG 360
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361 TCGACACCTACACCTTCTACTCGGCGGAGCGGCGGCTGCTGGGCGGCGAGCGG 420
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421 CGCGCGGCGGCGGCGGCGGCTGCTCGAGCGGCTGCTCGAGCGGCTGCGGCGGCGG 480
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481 TCGAGGAGCGGCGGCGGCGGCTGCTCGAGCGGCTGCTCGAGCGGCTGCTCGAGG 540
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481 TCGAGGAGCGGCGGCGGCGGCTGCTCGAGCGGCTGCTCGAGCGGCTGCTCGAGG 540
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541 GTGATCGTGTCTGATGCTGCTGCGCGGAGCAAGTTCGCGGCTGCGGCGGCGGCGG 600
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601 GCGGCAACCGGCGGCTGATGCTGCGGCGGAGCAAGTTCGCGGCTGCGGCGGCGG 660
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721 AGACCGCTGACATCATGATGCTGCGGCGGAGCAAGTTCGCGGCTGCGGCGGCGG 780
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721 AGACCGCTGACATCATGATGCTGCGGCGGAGCAAGTTCGCGGCTGCGGCGGCGG 780
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781 ACAGTGTTCACGCGGAGCACTCTCAACTCGAGGCTGCGGCTGCGGCTGCGGCTG 840
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781 ACAGTGTTCACGCGGAGCACTCTCAACTCGAGGCTGCGGCTGCGGCTGCGGCTG 840
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841 AGAATGATGAGGATTTTGGGAGTAAAGCTTGGCGGCTGCGGCTGCGGCTGCGG 900
Db
841 AGAATGATGAGGATTTTGGGAGTAAAGCTTGGCGGCTGCGGCTGCGGCTGCGG 900
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901 CTCGGTTTCACTCTCAAAAGTGTCTACCGAGAGATGTTTATGTTACTTCTCTCTT 960
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901 CTCGGTTTCACTCTCAAAAGTGTCTACCGAGAGATGTTTATGTTACTTCTCTCTT 960
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961 GTTGCCATGCAATCTTTAGTACCTTCTCAGCTTCTTGAACATGGGCTGCACTGGA 1020
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961 GTTGCCATGCAATCTTTAGTACCTTCTCAGCTTCTTGAACATGGGCTGCACTGGA 1020
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1021 ACATCAACAGGACTTTTACCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Db
1021 ACATCAACAGGACTTTTACCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Qy
1081 ACTACAGTTGGCTATGGAGATGATGATCTCTATCAGAGTCCCTGGAAGATTTCTG 1140
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1081 ACTACAGTTGGCTATGGAGATGATGATCTCTATCAGAGTCCCTGGAAGATTTCTG 1140
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1141 GTTGTGTTGTGCTAGTGAATTTGTTCTATTGGCAATACCTATACATTTTCTACCATAGC 1200

Db 1141 GTTGTGTTGTGCTAGTGAATTTGTTCTATTGGCAATACCTATACATTTTCTACCATAGC 1200
Qy 1201 TTTGTGTCAGTGTATCATGAGCTCAAGTTTAGATCTGCTAGTATAGTAGGAGCCTCTCC 1260
Db 1201 TTTGTGTCAGTGTATCATGAGCTCAAGTTTAGATCTGCTAGTATAGTAGGAGCCTCTCC 1260
Qy 1261 ACTGAATTCCTGAATTA 1278
Db 1261 ACTGAATTCCTGAATTA 1278

RESULT 2
ABN83931
ID ABN83931 standard; DNA; 1844 BP.
AC ABN83931;
XX
DT 06-SEP-2002 (first entry)
XX Human voltage-gated potassium channel-like protein encoding sequence.
XX Human; voltage-gated potassium channel; ion channel; neuroprotective;
KW therapeutic; diagnostic; pharmacogenomic; gene therapy; SNP;
KW single nucleotide polymorphism; foetal brain; brain; cerebellum;
KW pituitary; prostate; thymus; lymph node; bone marrow; trachea;
KW foetal liver; liver; testis; thyroid; salivary gland; stomach;
KW skeletal muscle; heart; uterus; adipose; hypophalamus; ovary; aorta;
KW 12 week old embryo; adenocarcinoma; osteosarcoma; Gene; ds.
XX Homo sapiens.

Key Location/Qualifiers
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CDS 457..1734
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WO200250271-A2.

27-JUN-2002.

10-DEC-2001; 2001WO-US048050.

20-DEC-2000; 2000US-0257932P.

(LEXI-) LEXICON GENETICS INC.

Friedle CJ, Hilbun E, Turner CA;

WPI; 2002-508799/54.

P-PSDB; ABB83073.

Human ion channel polynucleotide useful in therapeutic, diagnostic and pharmacogenomic applications.

Disclosure; Page 36; 36pp; English.

The invention relates to a novel human ion channel polynucleotide that shares structural similarity with voltage-gated potassium channel proteins. The activity of the protein of the invention may be described as neuroprotective. The protein of the invention is useful in therapeutic, diagnostic and pharmacogenomic applications, for example to identify mutations associated with a particular disease, as a diagnostic or prognostic assay, or in gene therapy. The protein of the invention has been found to be expressed in human foetal brain, brain, cerebellum, pituitary, prostate, thymus, lymph node, bone marrow, trachea, foetal

PR 03-NOV-2000; 2000US-0245904P.
PR 09-NOV-2000; 2000US-0247673P.
PR 17-NOV-2000; 2000US-0249661P.
PR 20-NOV-2000; 2000US-0252232P.
PR 01-DEC-2000; 2000US-0250790P.
XX (INCY-) INCYTE GENOMICS INC.
PA Tang YT, Yue H, Nguyen DB, Hafalia AJA, Elliott VS, Lu Y;
XX Wallia NK, Yao MG, Baughn MR, Gandhi AR, Ding L, Sanjanwala M;
PI Ramkumar J, Arvizu C, Gietzen KU, Lal PG, Azimzai Y, Khan FA;
PI Thangavelu K, Thornton M, Lu DAM, Tribouley CM, Warren BA, Ison CH;
PI Das D, Raumann BE, Policky JL, Kearney L;
XX WPI: 2002-463570/49.
DR P-PSDB; ABG61549.
XX New transporters and ion channels (TRICH) polypeptides, useful for
PT diagnosing, preventing, and treating disorders associated with an
PT abnormal expression or activity of TRICH, e.g. immunological, muscular or
PT renal disorders.
XX Claim 5; Page 176-177; 178pp; English.
XX The invention relates to human transporters and ion channels (TRICH)
CC polypeptides, a naturally occurring amino acid sequence 90 % identical to
CC TRICH, a biologically active fragment of TRICH or an immunogenic fragment
CC of TRICH. Also included are an isolated polynucleotide encoding TRICH, a
CC recombinant polynucleotide comprising a promoter sequence operably linked
CC to the TRICH polynucleotide, a cell transformed with the recombinant
CC polynucleotide, a transgenic organism comprising the recombinant
CC polynucleotide, an isolated antibody that binds specifically to TRICH,
CC and screening for compounds which bind to TRICH, modulate TRICH, modulate
CC TRICH expression or are ant/agonists of TRICH. The polypeptides are
CC useful for diagnosing, treating, and preventing transport, neurological,
CC muscle, immunological disorders (e.g. scleroderma, systemic lupus
CC erythematosus, allergies), cell proliferative disorders such as cancers
CC (e.g. leukemia, cervical or breast cancers), neurodegenerative disorders
CC (e.g. Parkinson's disease, Alzheimer's disease), muscular disorders (e.g.
CC myotonic dystrophy, catatonias), endocrine disorders (e.g. diabetes,
CC Grave's disease), gastrointestinal disorders (e.g. Crohn's disease),
CC renal disorders (e.g. Good pasture's syndrome), viral, bacterial, fungal,
CC parasitic, protozoal and helminthic infections, cardiovascular disorders
CC (e.g. atherosclerosis), or hepatic diseases (e.g. cirrhosis) and many
CC other diseases and disorders detailed in the specification. They can also
CC be used in assessing the effects of exogenous compounds on the expression
CC of nucleic acid and amino acid sequences of transporters and ion
CC channels. TRICH or its fragments may also be used in screening for
CC compounds that specifically bind to and modulate the activity of TRICH.
CC The polynucleotides can be used to create knock-in humanised animals or
CC transgenic animals to model human disease. The present sequence encodes a
CC TRICH protein
XX Sequence 2235 BP; 395 A; 657 C; 715 G; 468 T; 0 U; 0 Other;
Query Match 57.0%; Score 729; DB 6; Length 2235;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 920 ATCTGCTAGCGTGTGCGTGTGTTGCTGATCGTGTGCTGATCGTGTGCGCCAGC 979
QY 574 AGTTTCCCGACTGGCGCAACGAGCCGCGCAACCGCAGCGCTGATGACCGAGCAGG 633
DB 980 AGTTTCCCGACTGGCGCAACGAGCCGCGCAACCGCAGCGCTGATGACCGAGCAGG 1039
QY 634 ATAATTGAAGCTATCTGCTAGTGTGTTGCTGATCGTGTGCTGATGCTGCTGCTG 693
DB 1040 ATAATTGAAGCTATCTGCTAGTGTGTTGCTGATCGTGTGCTGATGCTGCTGCTG 1099
QY 694 TCAAAAAACAAGTGTGAGTTTGTCAAGACACCCCTGAAACATCATTTACTGCGAATC 753

DB 1100 -TCCAAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTACTTGGCAATC 1159
QY 754 AGCCGCTATTACATCTCTGTGTTGATGACAGAGTGTTTACAGGCGAGACTCTCAACTCCAG 813
DB 1160 AGCCGCTATTACATCTCTGTGTTGATGACAGAGTGTTTACAGGCGAGACTCTCAACTCCAG 1219
QY 814 AGGCGCTGGAGTCACTTGGGTGATTTAGAAATGATGAGGATTTTGGGTGATTAAGCTT 873
DB 1220 AGGCGTGGAGTCACTTGGGTGATTTAGAAATGATGAGGATTTTGGGTGATTAAGCTT 1279
QY 874 GCGCGTCACTTCACTTGGTCTTACAGACCTCGGTTTACCTCTCAAAAGTGTGCTACCGAGAG 933
DB 1280 GCGCGTCACTTCACTTGGTCTTACAGACCTCGGTTTACCTCTCAAAAGTGTGCTACCGAGAG 1339
QY 934 ATGCTTATGTTACTTGTCTTCTTCTTGTGCTGATGCTGCAATCTTTAGTGCACATTTCTCAG 993
DB 1340 ATGCTTATGTTACTTGTCTTCTTCTTGTGCTGATGCTGCAATCTTTAGTGCACATTTCTCAG 1399
QY 994 CTTCTTGAACATCGGCTGGACCTGGAACAAATCATCAAGGACTTTTACCGAGCATTCCTGCT 1053
DB 1400 CTTCTTGAACATCGGCTGGACCTGGAACAAATCATCAAGGACTTTTACCGAGCATTCCTGCT 1459
QY 1054 GCCTGCTGCTGGGTGATTTCTCTATGACTACAGTTGGCTATGAGATATGATCTCTATC 1113
DB 1460 GCCTGCTGCTGGGTGATTTCTCTATGACTACAGTTGGCTATGAGATATGATCTCTATC 1519
QY 1114 ACACTGCTCGGAAGAAATTTCTTGGAGGAGTTTGTGTTTCTCAGTGGAAATTTCTTATTGGCA 1173
DB 1520 ACACTGCTCGGAAGAAATTTCTTGGAGGAGTTTGTGTTTCTCAGTGGAAATTTCTTATTGGCA 1579
QY 1174 TTACCTATCACTTTTATCTACCACTAGTTTGTGAGTGTATCATGAGCTCAAGTTTGA 1233
DB 1580 TTACCTATCACTTTTATCTACCACTAGTTTGTGAGTGTATCATGAGCTCAAGTTTGA 1639
QY 1234 TCTGCTAGG 1242
DB 1640 TCTGCTAGG 1648
RESULT 5
ABZ24711
ID ABZ24711 standard; cDNA; 1947 BP.
XX AC ABZ24711;
XX DT 07-APR-2003 (first entry)
XX DE Human potassium channel subunit Kv10.1 cDNA.
XX KW Potassium channel; Kv10.1; human; anticonvulsant; antiarrhythmic;
XX KW tranquilizer; cytostatic; virucide; neurotropic; neuroprotective;
XX KW epilepsy; long QT syndrome; muscular ataxia; arrhythmia; gene therapy;
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
XX FT CDS 596..1906
XX FT /*tag= a
XX FT /note= "Human Kv10.1"
XX PN WO200296944-A2.
XX PD 05-DEC-2002.
XX PF 31-MAY-2002; 2002WO-EP006082.
XX PR 31-MAY-2001; 2001EP-00202060.
XX PA (VLAAs-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX PI Snyder DJ, Ottschytch N, Raes A, Van Hoorick D;
XX

DR WPI: 2003-140443/13.
XX P-PSDB; ABP59352.

PT Novel voltage-gated heterotetrameric potassium channel useful for
PT diagnosing, preventing and/or treating excitability disorders, comprises
PT Kv2.1, Kv3.1, Kv5.1, Kv6.3, Kv10.1 or Kv11.1 potassium channel subunits.
XX
XX
PS Claim 3; Page 50-53; 93pp; English.

XX The present sequence is that of cDNA encoding human potassium channel
CC subunit Kv10.1. The cDNA was obtained by PCR from a brain library. The
CC invention relates to the cloning and characterisation of 3 novel voltage-
CC gated potassium channel subunits that were identified in the human
CC genome: Kv6.3 (located at 16q24.1), Kv10.1 (2p21) and Kv11.1 (9p24.2).
CC Yeast two-hybrid and co-immunoprecipitation experiments showed that these
CC subunits do not form homotetrameric channels, but do form
CC heterotetrameric channels with Kv2.1, Kv3.1 and/or Kv5.1. Co-expression
CC of each of the novel subunits with Kv2.1, Kv3.1 and/or Kv5.1 results in
CC currents that differ from typical Kv2.1 currents. Kv6.3, Kv10.1 and
CC Kv11.1 alone do not reach the plasma membrane but are retained in the
CC endoplasmic reticulum. Co-expression with Kv2.1 results in transport to
CC the plasma membrane. The invention provides novel, voltage-gated
CC heterotetrameric potassium channels comprising Kv2.1, Kv3.1, Kv5.1,
CC Kv6.3, Kv10.1 or Kv11.1. These are useful for identifying a molecule that
CC increases or decreases ion flux through the potassium channel. Nucleic
CC acids encoding the heterotetrameric potassium channels are used in gene
CC therapy to prevent or treat congenital or acquired excitability disorders
CC including epilepsy, long QT syndrome, muscular ataxia, arrhythmia (all
CC claimed), as well as hyperactivity disorders, mental disorders, mood
CC disorders, behavioural disorders, anxiety disorders, hypokalaemia,
CC periodic paralysis, spasticity disorders, myotonia and paramyotonia. The
CC nucleic acids can be used to transfect cells. For example, stem cells are
CC used in ex vivo procedures for cell transfection and gene therapy. The
CC nucleic acids are also useful in diagnosis, and in the creation of
CC transgenic or knockout animals

XX Sequence 1947 BP; 324 A; 596 G; 644 G; 383 T; 0 U; 0 Other;

Query Match 50.6%; Score 647; DB 7; Length 1947;
Best Local Similarity 100.0%; Pred. No. 2.9e-313;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 632 GGATAATTGAGCTACTGCATAGTTGGTTCCTCCTCCAGTGCATCGAGGTTCAATG 691
DB 1260 GGATAATTGAGCTACTGCATAGTTGGTTCCTCCTCCAGTGCATCGAGGTTCAATG 1319
QY 692 TCTCCAAAACAAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTACTGGCAA 751
DB 1320 TCTCCAAAACAAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTACTGGCAA 1379
QY 752 TCACGGCGATTACATCTCTGTTGATCAGAGTGTTCACAGCGAGACTCTCAACTCC 811
DB 1380 TCACGGCGATTACATCTCTGTTGATCAGAGTGTTCACAGCGAGACTCTCAACTCC 1439
QY 812 ACAGGGCTGGAGTCACTTGGAGGTACTTAGATGATGAGGATTTTGGGTGATTAGC 871
DB 1440 AGAGGGCTGGAGTCACTTGGAGGTACTTAGATGATGAGGATTTTGGGTGATTAGC 1499
QY 872 TTGCGCGTCACTTCACTTGGTTCACAGACTCGTTGATCTCAAAAGTTCCTACCGAG 931
DB 1500 TTGCGCGTCACTTCACTTGGTTCACAGACTCGTTGATCTCAAAAGTTCCTACCGAG 1559
QY 932 AGATGGTTAGTTACTTGTCTTCACTTGTGTTGCCATGCAATCTTTAGTGCACTTCTC 991
DB 1560 AGATGGTTAGTTACTTGTCTTCACTTGTGTTGCCATGCAATCTTTAGTGCACTTCTC 1619
QY 992 AGCTTCTTGAACATGGGTGGACCTGGAAACATCCAAAGGACATTTACAGCATTCCTG 1051
DB 1620 AGCTTCTTGAACATGGGTGGACCTGGAAACATCCAAAGGACATTTACAGCATTCCTG 1679
QY 1052 CTGSCCTGCTGGTGGGTGATTATCTCTATGACTACAGTGTGGCTATGGAGATGTATCTCTA 1111
DB 1680 CTGSCCTGCTGGTGGGTGATTATCTCTATGACTACAGTGTGGCTATGGAGATGTATCTCTA 1739

QY 1112 TCACAGTCCCTGGGAAGAAATCTTGGAGAGTTTGTGTGTTCAGTGAATTTCTTATGG 1171
DB 1740 TCACAGTCCCTGGGAAGAAATCTTGGAGAGTTTGTGTGTTCAGTGAATTTCTTATGG 1799
QY 1172 CATTACCTATCACATTTTATCTACCATAGCTTTGTGCAGTGTATCATGAGCTCAAGTTTA 1231
DB 1800 CATTACCTATCACATTTTATCTACCATAGCTTTGTGCAGTGTATCATGAGCTCAAGTTTA 1859
QY 1232 GATCTGTAGTATAGTAGAGGCTCTCCACTGAATTCCTGAATTA 1278
DB 1860 GATCTGTAGTATAGTAGAGGCTCTCCACTGAATTCCTGAATTA 1906

RESULT 6

ID ADD01447 standard; cDNA; 5174 BP.
AC ADD01447;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human TCHI36 cDNA sequence.

ds; gene; antidiabetic; antilipemic; antiarteriosclerotic; nootropic;
neuroprotective; anabolic; antiinflammatory; immunosuppressive;
cytostatic; antiasthmatic; antiarthritic; cerebroprotective;
antiallergic; dermatological; cardiant; antiparkinsonian; neuroleptic;
glucose transporter; potassium ion channel protein; diabetes;
hyperlipemia; arteriosclerosis; digestive disorder; Crohn's disease;
colitis; gastritis; ileitis; rectal inflammation; inflammatory disease;
sepsis; prostatic hypertrophy; reproductive disorder; pneumonia;
meningitis; hepatitis; myocarditis; asthma; immune disorder;
multiple sclerosis; rheumatoid arthritis; Sjogren's disease; lupus;
allergy; hay fever; allergic rhinitis; anaphylactic shock;
atopic dermatitis; circulatory disorder; heart failure; cancer;
Alzheimer's disease; Parkinson's disease; schizophrenia;
hyperprolactinemia; Cushing's disease; vesicular glutamate transporter.

Homo sapiens.

WO2003054190-A1.

03-JUL-2003.

19-DEC-2002; 2002WO-JP013290.

21-DEC-2001; 2001JP-00389361.

25-DEC-2001; 2001JP-00392577.

26-DEC-2001; 2001JP-00394947.

26-DEC-2001; 2001JP-00395467.

06-FEB-2002; 2002JP-00030010.

08-FEB-2002; 2002JP-00033095.

06-JUN-2002; 2002JP-00165336.

(TAKE) TAKEDA CHEM IND LTD.

Nakanishi A, Sagiya Y, Uno Y;

WPI; 2003-541817/51.

Glucose transporter TCH099, vesicular glutamate transporter TCHI177 and

potassium channel protein TCHI36 and DNA encoding them for diagnosis,

treatment and prevention of diabetes, hyperlipemia, arteriosclerosis and

digestive disorders.

Claim 62; SEQ ID NO 83; 221pp; Japanese.

The invention relates to a novel glucose transporter TCH099, vesicular

glutamate transporter TCHI177 and voltage-dependent potassium ion channel

protein TCHI36. The sequences are useful in the treatment, prevention and

diagnosis of a broad range of diseases including diabetes, hyperlipemia,

arteriosclerosis, digestive disorders (such as Crohn's disease, colitis,

CC gastritis, ileitis and rectal inflammation), inflammatory diseases,
 CC sepsis, prostatic hypertrophy, reproductive disorders, pneumonia,
 CC meningitis, hepatitis, myocarditis, asthma, immune disorders (such as
 CC allergies (such as hay fever, allergic rhinitis, Sjogren's disease and lupus),
 CC atopic dermatitis), circulatory disorders (such as heart failure), cancer
 CC (such as cancer of the lung, kidney, liver, ovary, prostate, stomach,
 CC pancreas, bladder, breast, fallopian tubes or colon), central nervous
 CC system diseases (such as Alzheimer's, Parkinson's and schizophrenia) and
 CC secretory disorders (such as hyperprolactinemia and Cushing's disease). This
 CC sequence represents the cDNA sequence for the novel human voltage-gated
 XX potassium ion channel protein TCH136.
 XX
 SQ Sequence 5174 BP; 1335 A; 1139 C; 1257 G; 1443 T; 0 U; 0 Other;
 Query Match 50.6%; Score 647; DB 9; Length 5174;
 Best Local Similarity 100.0%; Pred. No. 2.9e-313; Indels 0; Gaps 0;
 Matches 647; Conservative 0; Mismatches 0;
 QY 632 GGATAATTGAAGCTATCTGATGAGTGGTTCACATGCCGAGTGCACTCGAGGTTCAATTG 691
 Db 1149 GGATAATTGAAGCTATCTGATGAGTGGTTCACATGCCGAGTGCACTCGAGGTTCAATTG 1208
 QY 692 TCTCCAAAACAAAGTGTGAGTTGTTCAGAGACCCCTGAAACATCATTTACTTACGGCAA 751
 Db 1209 TCTCCAAAACAAAGTGTGAGTTGTTCAGAGACCCCTGAAACATCATTTACTTACGGCAA 1268
 QY 752 TCACGCCGATTAACATCTCTGTGTTGATGACAGTCTTTACAGGCCGAGAACTCTCAACTCC 811
 Db 1269 TCACGCCGATTAACATCTCTGTGTTGATGACAGTCTTTACAGGCCGAGAACTCTCAACTCC 1328
 QY 812 AGAGGGCTGGAGTACCTTGAGGGTACTTAGAATGATGAGGATTTTGGGTGATTAAGC 871
 Db 1329 AGAGGGCTGGAGTACCTTGAGGGTACTTAGAATGATGAGGATTTTGGGTGATTAAGC 1388
 QY 872 TTGCCCGTCACTTTCATTTGTTCTTACAGACCTCGGTTTGAATCTCAAGCTTCTCAACCAG 931
 Db 1389 TTGCCCGTCACTTTCATTTGTTCTTACAGACCTCGGTTTGAATCTCTCAAGCTTCTCAACCAG 1448
 QY 932 AGATGGTTATGTTACTTGTCTTCAATTTGTTGGTCAATGCAATCTTTAGTCACTTCTC 991
 Db 1449 AGATGGTTATGTTACTTGTCTTCAATTTGTTGGTCAATGCAATCTTTAGTCACTTCTC 1508
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 QY 1052 CTGCTCTGCTGGTGGTGAATTTATCTCTATGACATACAGTTGGCTATGAGATATGATCCTA 1111
 Db 1569 CTGCTCTGCTGGTGGTGAATTTATCTCTATGACATACAGTTGGCTATGAGATATGATCCTA 1628
 QY 1112 TCACAGTGCCTGGAGAAATCTTGAGGAGTTGTGTGTGTCAGTGAATTTCTATTGG 1171
 Db 1629 TCACAGTGCCTGGAGAAATCTTGAGGAGTTGTGTGTGTCAGTGAATTTCTATTGG 1689
 QY 1172 CATTACTATCACTTTTATCTACCATAGCTTTGTGAGGTTTATCATGAGCTCAAGTTTA 1231
 Db 1689 CATTACTATCACTTTTATCTACCATAGCTTTGTGAGGTTTATCATGAGCTCAAGTTTA 1748
 QY 1232 GATCTCTAGGTATAGTAGAGCCTTCCATCGAATTCCTGAATTA 1278
 Db 1749 GATCTCTAGGTATAGTAGAGCCTTCCATCGAATTCCTGAATTA 1795
 RESULT 7
 ADD01427
 ID ADD01427 standard; DNA; 1308 BP.
 XX
 AC ADD01427;
 XX
 DT 01-JAN-2004 (first entry)
 XX Human TCH136 coding sequence.

XX ds; gene; antidiabetic; antilipemic; antiarteriosclerotic; nootropic;
 KW neuroprotective; anabolic; antiinflammatory; immunosuppressive;
 KW cycostatic; aniasthmatic; antiarthritic; cerebroprotective;
 KW antiallergic; dermatological; cardiant; antiparkinsonian; neuroleptic;
 KW glucose transporter; potassium ion channel protein; diabetes;
 KW hyperlipemia; arteriosclerosis; digestive disorder; Crohn's disease;
 KW colitis; gastritis; ileitis; rectal inflammation; inflammatory disease;
 KW sepsis; prostatic hypertrophy; reproductive disorder; pneumonia;
 KW meningitis; hepatitis; myocarditis; asthma; immune disorder;
 KW multiple sclerosis; rheumatoid arthritis; Sjogren's disease; lupus;
 KW allergy; hay fever; allergic rhinitis; anaphylactic shock;
 KW atopic dermatitis; circulatory disorder; heart failure; cancer;
 KW Alzheimer's disease; Parkinson's disease; schizophrenia;
 KW hyperprolactinemia; Cushing's disease; vesicular glutamate transporter.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 CDS 1..1308
 FT /*tag= a
 FT /product= "human TCH136 protein"
 FT /function= "voltage-dependent potassium ion channel"
 PN W02003054190-A1.
 XX 03-JUL-2003.
 PD 19-DEC-2002; 2002WO-JP013290.
 XX 21-DEC-2001; 2001JP-00389361.
 PR 25-DEC-2001; 2001JP-00392577.
 PR 26-DEC-2001; 2001JP-00394947.
 PR 06-FEB-2002; 2001JP-00395467.
 PR 08-FEB-2002; 2002JP-00030010.
 PR 08-FEB-2002; 2002JP-00033095.
 PR 06-JUN-2002; 2002JP-00165336.
 XX (TAKE) TAKEDA CHEM IND LTD.
 XX Nakanishi A, Sagiya Y, Uno Y;
 FI WPI; 2003-541817/51.
 DR P-PSDB; ADD01426.
 XX
 PT Glucose transporter TCH099, vesicular glutamate transporter TCH177 and
 PT potassium channel protein TCH136 and DNA encoding them for diagnosis,
 PT treatment and prevention of diabetes, hyperlipemia, arteriosclerosis and
 PT digestive disorders.
 XX
 PS Claim 62; SEQ ID NO 63; 221pp; Japanese.
 XX
 CC The invention relates to a novel glucose transporter TCH099, vesicular
 CC glutamate transporter TCH177 and voltage-dependent potassium ion channel
 CC protein TCH136. The sequences are useful in the treatment, prevention and
 CC diagnosis of a broad range of diseases including diabetes, hyperlipemia,
 CC arteriosclerosis, digestive disorders (such as Crohn's disease, colitis,
 CC gastritis, ileitis and rectal inflammation), inflammatory diseases,
 CC sepsis, prostatic hypertrophy, reproductive disorders, pneumonia,
 CC meningitis, hepatitis, myocarditis, asthma, immune disorders (such as
 CC multiple sclerosis, rheumatoid arthritis, Sjogren's disease and lupus),
 CC allergies (such as hay fever, allergic rhinitis, anaphylactic shock and
 CC atopic dermatitis), circulatory disorders (such as heart failure), cancer
 CC (such as cancer of the lung, kidney, liver, ovary, prostate, stomach,
 CC pancreas, bladder, breast, fallopian tubes or colon), central nervous
 CC system diseases (such as Alzheimer's, Parkinson's and schizophrenia) and
 CC secretory disorders (such as hyperprolactinemia and Cushing's disease). This
 CC sequence represents the coding sequence for the novel human voltage-gated
 CC potassium ion channel protein TCH136.
 XX
 SQ Sequence 1308 BP; 238 A; 362 C; 389 G; 319 T; 0 U; 0 Other;
 Query Match 50.4%; Score 644; DB 9; Length 1308;

Best Local Similarity 100.0%; Pred. No. 9.3e-312;

Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

632 GGATAATTGAAGCTATCTGCATAGGTTGGTTCACTGCCGAGTGCATCGTGAGGTTCAATTG 691

665 GGATAATTGAAGCTATCTGCATAGGTTGGTTCACTGCCGAGTGCATCGTGAGGTTCAATTG 724

692 TCTCCAAAAACAAGGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTACTTGCCAA 751

725 TCTCCAAAAACAAGGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTACTTGCCAA 784

752 TCACGCCGATTAACATCTCTGTCTGTATGACAGTGGTTTACAGCGGAGAACTCTCAACTCC 811

785 TCACGCCGATTAACATCTCTGTCTGTATGACAGTGGTTTACAGCGGAGAACTCTCAACTCC 844

812 AGAGGGCTGGAGTCACTTCAAGGGTACTTAAATGATGAGAAATTTTGGTGCAATTAAGC 871

845 AGAGGGCTGGAGTCACTTCAAGGGTACTTAAATGATGAGAAATTTTGGTGCAATTAAGC 904

872 TTGCCCGTCACTTCATTGGTCTTCAGACACTCGGTTTGACTCTCAACAGTTGTACCCGAG 931

905 TTGCCCGTCACTTCATTGGTCTTCAGACACTCGGTTTGACTCTCAACAGTTGTACCCGAG 964

932 AGATGGTTATGTTACTTGTCTTCAATTTGGTGTGCGATGGCAATCTTTAGTGCATTTCTC 991

965 AGATGGTTATGTTACTTGTCTTCAATTTGGTGTGCGATGGCAATCTTTAGTGCATTTCTC 1024

992 AGCTTCTTGAACATGGGCTGGACCTGGAAACATCCAAACAGGACTTTACCAGCAATTCCTG 1051

1025 AGCTTCTTGAACATGGGCTGGACCTGGAAACATCCAAACAGGACTTTACCAGCAATTCCTG 1084

1052 CTGGCTCTCGGTGGTGGAATATCTCTATGACTACAGTTGGCTATGAGATATGTATCTCTA 1111

1085 CTGGCTCTCGGTGGTGGAATATCTCTATGACTACAGTTGGCTATGAGATATGTATCTCTA 1144

1112 TCACAGTGCCTGGAAGAAATCTTTGGAGGAGTTGTGTGTTCAGTGGAAATTTGTTCTATTGG 1171

1145 TCACAGTGCCTGGAAGAAATCTTTGGAGGAGTTGTGTGTTCAGTGGAAATTTGTTCTATTGG 1204

1172 CATTACCTATCACTTTTATCTACATAGCTTTGTGCAGTGTATCATGAGCTCAAGTTTA 1231

1205 CATTACCTATCACTTTTATCTACATAGCTTTGTGCAGTGTATCATGAGCTCAAGTTTA 1264

1232 GATCTGCTAGGATAGTAGGAGGCTCTCCACTGAAATTCCTGAAT 1275

1265 GATCTGCTAGGATAGTAGGAGGCTCTCCACTGAAATTCCTGAAT 1308

RESULT a

ABX72192

ID ABX72192 standard: cDNA: 1651 BP.

XXXX

AC ABX72192;

XX

DT 03-JUN-2003 (first entry)

XX

Human NOVX polynucleotide #23.

XX

Human; NOVX; gene; ss; metabolic disorder; cardiomyopathy; diabetes; ASD
hypertension; congenital heart defect; aortic stenosis; valve disease;
atrial septal defect; atrioventricular canal defect; ductus arteriosus;
pulmonary stenosis; subaortic stenosis; ventricular septal defect; VSD;
tuberculous sclerosis; scleroderma; atherosclerosis; infectious disease;
obesity; anorexia; neurodegenerative disorder; Alzheimer's disease;
parkinson's disease; immune disorder; haematopoietic disorder;
haemophilia; hypercoagulation; Crohn's disease; cancer.

X

SCS Home

[illegible]

WOMEN

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466
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17-0

PF	03-APR-2002	2002MO-US010780.
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03-APR-2001	2001US-0281086P.	
03-APR-2001	2001US-0281136P.	
05-APR-2001	2001US-0281963P.	
05-APR-2001	2001US-0281506P.	
06-APR-2001	2001US-0282020P.	
10-APR-2001	2001US-0282930P.	
10-APR-2001	2001US-0282934P.	
12-APR-2001	2001US-0283512P.	
13-APR-2001	2001US-0283710P.	
17-APR-2001	2001US-0284234P.	
19-APR-2001	2001US-0285325P.	
20-APR-2001	2001US-0285381P.	
20-APR-2001	2001US-0285609P.	
23-APR-2001	2001US-0285748P.	
23-APR-2001	2001US-0285890P.	
24-APR-2001	2001US-0286068P.	
25-APR-2001	2001US-0286292P.	
27-APR-2001	2001US-0286521P.	
02-MAY-2001	2001US-0288953P.	
02-MAY-2001	2001US-0293416P.	
30-MAY-2001	2001US-0294488P.	
30-MAY-2001	2001US-02948952P.	
18-JUN-2001	2001US-02969237P.	
19-JUN-2001	2001US-0299276P.	
19-JUN-2001	2001US-0318750P.	
12-SEP-2001	2001US-0324800P.	
25-SEP-2001	2001US-0324802P.	
25-SEP-2001	2001US-0325664P.	
27-SEP-2001	2001US-0330143P.	
17-OCT-2001	2001US-0332131P.	
14-NOV-2001	2001US-0332240P.	
14-NOV-2001	2001US-0332779P.	
21-NOV-2001	2001US-0332115P.	
04-DEC-2001	2001US-0337621P.	
03-JAN-2002	2002US-0345783P.	
16-JAN-2002	2002US-0350251P.	
02-APR-2002	2002US-00114270.	
XX		
	(CURA-) CURAGEN CORP.	

(CURA-) CURAGEN CORP.

Guo X, Kekuda R, Miller CE, Malyankar UM, Speyck KA;
Ratnatrayan M, Liu X, Gusev VI, Li L, Vernet CAW, Zerkusen BD;
Corman L, Shenoy SG, Pena CE, Smithson G, Burgess CE, Gerlach V;
Shankets RA, Gangoli EA, Taupier RU, Casman SJ, Ji W;
Leite MW, Rastelli E, Edinger SR, Stone DJ;
Vaccadogall JR, Rothenberg ME, Mazur A, Millet I, Peyman JA;
Ellerman K;

WPT: 2003-046858/04

P-PSDB: ABU54564.

New isolated NOVX polypeptide useful for treating atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease and cancer.

Claim 17: Page 136: 666pp: English:

The invention relates to human polypeptides, termed NOVX, and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for diagnosing disease, and screening for potential therapeutic agents. The sequences are useful for treating metabolic disorders, cardiomyopathy, diabetes, hypertension, congenital heart defects, aortic stenosis, atrial septal defect (ASD), atrioventricular canal defect, aortic regurgitation, aortic stenosis, subaortic stenosis, ventricular septal defect (VSD), valve diseases, tuberosclerosis, scleroderma, atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's disease, immune disorders, haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease and cancer. Sequences ABX72170-ABX72275 represent human NOVX polynucleotides of the invention.

XX

SQ	Sequence 1651 BP; 292 A; 476 C; 510 G; 373 T; 0 U; 0 Other;	
Query Match	48.0%; Score 613; DB 7; Length 1651;	
Best Local Similarity	100.0%; Pred. No. 3.1e-296;	
Matches 613; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	630 CAGGATAATTGAAGCTATCTGCATAGGTGGTTCTACTCCGAGTCATCGTGAGTTTCAT	689
DB	792 CAGGATATTGAGCTATCTGCATAGGTGGTTCTACTCCGAGTCATCGTGAGTTTCAT	851
QY	690 TGTCTCCAAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGGAACATCATTTGATCTGGC	749
DB	852 TGTCTCCAAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGGAACATCATTTGATCTGGC	911
QY	750 ATCAAGCGGTATTACATCTCTGCTTGTATGACAGTGTTTACAGCGAGAACTCTCAACT	809
DB	912 AATCAGCGGTATTACATCTCTGCTTGTATGACAGTGTTTACAGCGAGAACTCTCAACT	971
QY	810 CCAGAGGGCTGGAGTCACCTTGGAGGTACTTAGAATGATGAGGATTTTTTGGGTGATTAA	869
DB	972 CCAGAGGGCTGGAGTCACCTTGGAGGTACTTAGAATGATGAGGATTTTTTGGGTGATTAA	1031
QY	870 GCTTCCCGTCACTTCATTTGCTTCAGACATCTCGTTGACTCTCAACGTTGCTACCG	929
DB	1032 GCTTCCCGTCACTTCATTTGCTTCAGACATCTCGTTGACTCTCAACGTTGCTACCG	1091
QY	930 AGAGATGGTTATGTACTTGTCTTCAATTTGTTGCCATGGCAATCTTTAGTGCACTTTC	989
DB	1092 AGAGATGGTTATGTACTTGTCTTCAATTTGTTGCCATGGCAATCTTTAGTGCACTTTC	1151
QY	990 TCAGCTTCTTGAACATGGCTGGACCTGGAAACATCCCAAGAGCTTTACAGCAATTC	1049
DB	1152 TCAGCTTCTTGAACATGGCTGGACCTGGAAACATCCCAAGAGCTTTACAGCAATTC	1211
QY	1050 TGTCTGCTGCTGGTGGTGAATTTCTATGACTACAGTTGGCTATGAGATATGTATCC	1109
DB	1212 TGTCTGCTGCTGGTGGTGAATTTCTATGACTACAGTTGGCTATGAGATATGTATCC	1271
QY	1110 TATCAGTGGCTGGAAGAAATCTTGGAGGATTTGTGTTCAGTGAATTTGTCTATT	1169
DB	1272 TATCAGTGGCTGGAAGAAATCTTGGAGGATTTGTGTTCAGTGAATTTGTCTATT	1331
QY	1170 GCATTACTATCACTTTATACATAGCTTCTGAGAGCTTTATCATGAGCTCAAGTT	1229
DB	1332 GCATTACTATCACTTTATACATAGCTTCTGAGAGCTTTATCATGAGCTCAAGTT	1391
QY	1230 TAGATCTGTAGG 1242	
DB	1392 TAGATCTGTAGG 1404	
RESULT 9		
ID	ABK27494	
XX	ABK27494 standard; cDNA; 461 BP.	
AC	ABK27494;	
XX		
DT	09-APR-2002 (first entry)	
XX		
DE	DNA encoding novel human ion channel protein #25.	
XX		
KW	Human; ion channel; anti-HIV; analgesic; cytostatic; antidiabetic;	
KW	anorectic; metabolic; hypertensive; hypotensive; thrombolytic; cardiant;	
KW	antiatherosclerotic; neuroleptic; antimigraine; antiparkinsonian;	
KW	tranquilliser; antidepressant; neuroprotective; anticonvulsant; pain;	
KW	antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;	
KW	psychiatric disorder; asthmatic; vulnery; neurological disorder; obesity;	
KW	human immunodeficiency virus; HIV-1; HIV-2; cancer; diabetes; anorexia;	
KW	myocardial infarction; Parkinson's disease; schizophrenia; anxiety;	
KW	dementia; Huntington's disease; thyroid disorder; inflammation;	
KW	autoimmune disorder; hormonal disorder; renal failure; psoriasis;	
KW	movement disorder; gene; ss.	

XX	Homo sapiens.	
OS		
FN	W0200185788-A2.	
XX		
PD	15-NOV-2001.	
XX		
PF	10-MAY-2001; 2001WO-US014965.	
XX		
PR	10-MAY-2000; 2000US-0203305P.	
PR	23-MAY-2000; 2000US-0206526P.	
PR	25-MAY-2000; 2000US-0207033P.	
PR	25-MAY-2000; 2000US-0207092P.	
PR	25-MAY-2000; 2000US-0207093P.	
PR	07-JUL-2000; 2000US-0216893P.	
PR	04-AUG-2000; 2000US-0223245P.	
PR	04-OCT-2000; 2000US-0237873P.	
XX		
PA	(PHAA) PHARMACIA & UPJOHN CO.	
XX		
PI	Roberts SL, Benjamin CW, Karnovsky AM, Ruble CL;	
XX		
DR	WPI; 2002-062237/08.	
DR	P-PSDB; AAU81345.	
XX		
PT	New polynucleotied, useful for identifying ion channel activity	
PT	modulators that are used for treating Parkinson's disease, schizophrenia,	
PT	migraine, anxiety, manic depression, encodes the ion channel polypeptide.	
XX		
PS	Claim 1; Page 86; 172pp; English.	
XX		
CC	The invention relates to an isolated nucleic acid molecule (I) which	
CC	encodes a novel ion channel protein, ion-x (II). The nucleic acid,	
CC	protein and antibody are useful for identifying a compound which binds a	
CC	nucleic acid molecule encoding ion-x. These are useful for treatment of a	
CC	neurological or psychiatric disorder which modulates ligand binding to	
CC	ion-x in neurons of the mammal; in gene therapy to restore ion-x activity	
CC	in certain disease states; for treating asthma, traumatic brain injury,	
CC	etc; modulators of ion-x activity or expression are useful for treating	
CC	diseases such as viral infections caused by human immunodeficiency virus	
CC	(HIV)-1 or HIV-2, pain, cancers, diabetes, obesity, anorexia,	
CC	hypotension, hypertension, thrombosis, myocardial infarction,	
CC	cardiomyopathies, atherosclerosis, Parkinson's disease, schizophrenia,	
CC	migraine, anxiety, manic depression, dementia, Huntington's disease,	
CC	thyroid disorders, inflammatory conditions, rheumatoid arthritis, and	
CC	autoimmune disorders, hormonal disorders, renal failure, psoriasis, and	
CC	movement disorders. ABK27470-ABK27517 represent human ion channel protein	
CC	coding sequences and PCR primers of the invention	
XX		
SQ	Sequence 461 BP; 109 A; 93 C; 98 G; 161 T; 0 U; 0 Other;	
Query Match	27.2%; Score 347; DB 6; Length 461;	
Best Local Similarity	100.0%; Pred. No. 4.6e-163;	
Matches 347; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	932 AGATGGTTATGTACTTGTCTTCTTCTTGTGCTGCAATCTTTAGTGCACTTTCTC	991
DB	49 AGATGGTTATGTACTTGTCTTCTTCTTGTGCTGCAATCTTTAGTGCACTTTCTC	108
QY	992 AGCTTCTTGAACATGGCTGGAAACATCCCAAGAGCTTTACCAGCAATTCCTG	1051
DB	109 AGCTTCTTGAACATGGCTGGAAACATCCCAAGAGCTTTACCAGCAATTCCTG	169
QY	1052 CTGCTGCTGCTGGTGAATTTCTTATGACTACAGTTGGCTATGGAGATATGATCCTA	1111
DB	169 CTGCTGCTGCTGGTGAATTTCTTATGACTACAGTTGGCTATGGAGATATGATCCTA	228
QY	1112 TCACAGTGCCTGGAAGAAATCTTGGAGAGTTTGTGTGTGTCAGTGAATTTCTATTGG	1171
DB	229 TCACAGTGCCTGGAAGAAATCTTGGAGAGTTTGTGTGTGTCAGTGAATTTCTATTGG	288
QY	1172 CATTAACCTATCACTTTTATCTACCATAGCTTTGTGCACTTTATCATGACTCAAGTTA	1231

Db 289 CATTAAGTATCACTTTATCTACCATAGCTTTGTGAGTGTATCATGAGCTCAAGTTTA 348
 QY 1232 GATCTGCTAGGTATAGTAGGAGCTCTCCACTGAATTCCTGGAATTAA 1278
 Db 349 GATCTGCTAGGTATAGTAGGAGCTCTCCACTGAATTCCTGGAATTAA 395

RESULT 10
 ABX91965/c
 ID ABX91965 standard; cDNA; 777 BP.
 XX AC ABX91965;
 XX
 DT 08-MAY-2003 (first entry)
 XX
 DE Lung specific nucleic acid (LSNA) #7.
 XX
 KW Human; gene therapy; vaccine; lung specific antigen; cancer diagnosis;
 KW cancer monitoring; cancer staging; cancer imaging; lung cancer;
 KW non-cancerous diseases of the lung; transgenic animal; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200268633-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 21-NOV-2001; 2001WO-US043612.
 XX
 PR 22-NOV-2000; 2000US-0252500P.
 XX
 PA (DIAD-) DIADEXUS INC.
 XX
 PI Macina RA, Recipon H, Chen S, Sun Y, Liu C;
 XX
 DR WPI; 2002-713376/77.
 XX
 XX New isolated human nucleic acid molecule and polypeptide, useful for
 PT identifying, diagnosing, monitoring, staging, imaging and treating lung
 PT cancer and non-cancerous diseases of the lung.
 XX
 PS Claim 1; Page 163-164; 389pp; English.
 XX
 CC The invention describes an isolated human nucleic acid (I) encoding any
 CC of 120 10-1533 residue amino acid sequences (S1), given in the
 CC specification, comprising any of 164 179-12421 base pair sequences (S2),
 CC given in the specification. The methods and compositions of the present
 CC invention are useful for identifying, diagnosing, monitoring, staging,
 CC imaging and treating lung cancer and non-cancerous diseases of the lung.
 CC They are also used for identifying lung tissue, monitoring and
 CC identifying and/or designing antagonists of the polypeptide of the
 CC invention, gene therapy, production of transgenic animals and production
 CC of engineered lung tissue for treatment and research. This sequence
 CC encodes a lung specific nucleic acid
 XX
 SQ Sequence 777 BP; 250 A; 162 C; 158 G; 207 T; 0 U; 0 Other;
 Query Match 25.9%; Score 331; DB 6; Length 777;
 Best Local Similarity 100.0%; Pred. No. 4.7e-155;
 Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 948 TGCCTTCATTTGGTGGCAGTATCTTGTAGTGCATCTTCTCAGCTTCTTGACATGG 1007
 Db 662 TGCCTTCATTTGGTGGCAGTATCTTGTAGTGCATCTTCTCAGCTTCTTGACATGG 603
 QY 1008 GCTGGACCTGGAAACATCCAAAGGACTTTACCAGCATTCCTGCTGCTGTGGGT 1067
 Db 602 GCTGGACCTGGAAACATCCAAAGGACTTTACCAGCATTCCTGCTGCTGTGGGT 543
 QY 1068 GATTATCTCTATGACTACAGTTGGCTATGAGATATGATATCCTATCAGAGTCCGGAAG 1127
 Db 542 GATTATCTCTATGACTACAGTTGGCTATGAGATATGATATCCTATCAGAGTCCGGAAG 483

QY 1128 AATCTTGGAGAGTTTGTGTGTGTCAGTGAATTTCTATTGGCATTACCTATCACTTT 1187
 Db 482 AATCTTGGAGAGTTTGTGTGTGTCAGTGAATTTCTATTGGCATTACCTATCACTTT 423
 QY 1188 TATCTACCATAGCTTTGTGAGTGTATCATGAGCTCAAGTTTAGATCTCTAGGTATAG 1247
 Db 422 TATCTACCATAGCTTTGTGAGTGTATCATGAGCTCAAGTTTAGATCTCTAGGTATAG 363

QY 1248 TAGGAGCTCTCCACTGAATTCCTGGAATTAA 1278
 Db 362 TAGGAGCTCTCCACTGAATTCCTGGAATTAA 332

RESULT 11
 ABX91966
 ID ABX91966 standard; cDNA; 911 BP.
 XX AC ABX91966;
 XX
 DT 08-MAY-2003 (first entry)
 XX
 DE Lung specific nucleic acid (LSNA) #8.
 XX
 KW Human; gene therapy; vaccine; lung specific antigen; cancer diagnosis;
 KW cancer monitoring; cancer staging; cancer imaging; lung cancer;
 KW non-cancerous diseases of the lung; transgenic animal; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200268633-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 21-NOV-2001; 2001WO-US043612.
 XX
 PR 22-NOV-2000; 2000US-0252500P.
 XX
 PA (DIAD-) DIADEXUS INC.
 XX
 PI Macina RA, Recipon H, Chen S, Sun Y, Liu C;
 XX
 DR WPI; 2002-713376/77.
 XX
 XX New isolated human nucleic acid molecule and polypeptide, useful for
 PT identifying, diagnosing, monitoring, staging, imaging and treating lung
 PT cancer and non-cancerous diseases of the lung.
 XX
 PS Claim 1; Page 164; 389pp; English.
 XX
 CC The invention describes an isolated human nucleic acid (I) encoding any
 CC of 120 10-1533 residue amino acid sequences (S1), given in the
 CC specification, comprising any of 164 179-12421 base pair sequences (S2),
 CC given in the specification. The methods and compositions of the present
 CC invention are useful for identifying, diagnosing, monitoring, staging,
 CC imaging and treating lung cancer and non-cancerous diseases of the lung.
 CC They are also used for identifying lung tissue, monitoring and
 CC identifying and/or designing antagonists of the polypeptide of the
 CC invention, gene therapy, production of transgenic animals and production
 CC of engineered lung tissue for treatment and research. This sequence
 CC encodes a lung specific nucleic acid
 XX
 SQ Sequence 911 BP; 249 A; 168 C; 181 G; 313 T; 0 U; 0 Other;
 Query Match 17.0%; Score 217; DB 6; Length 911;
 Best Local Similarity 100.0%; Pred. No. 5.6e-98;
 Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1062 GTGGGTGATTTATCTCTATGACTACAGTTGGCTATGGAGATATGATCCTATCAGTGCC 1121
 Db 229 GTGGGTGATTTATCTCTATGACTACAGTTGGCTATGGAGATATGATCCTATCAGTGCC 288
 QY 1122 TGAAGAAATCTTGGAGAGTTTGTGTGTGTCAGTGAATTTCTATTGGCATACCTAT 1181

Db 289 TGAAGAATCTTGGAGAGTTTGTGTGTCAGTGAATTTGTTCTATTGGCATTTACCTAT 348
1182 CACTTTTATCTACCATAGCTTTGTGTCAGTGTATCATGAGCTCAAGTTTATAGATCTGCTAG 1241
Db 349 CACTTTTATCTACCATAGCTTTGTGTCAGTGTATCATGAGCTCAAGTTTATAGATCTGCTAG 408
QY 1242 GTATAGTAGGACCTCTCCACTGAATTTCTGAAATTAA 1278
Db 409 GTATAGTAGGACCTCTCCACTGAATTTCTGAAATTAA 445
RESULT 12
ABZ24716
ID ABZ24716 standard; cDNA; 5775 BP.
XX
AC ABZ24716;
XX
DT 07-APR-2003 (first entry)
DE Murine potassium channel subunit Kv10.1 - flag sequence.
XX
KW Potassium channel; Kv10.1; mouse; transgenic mouse; gene; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT misc_feature 3424..4749
FT /tag= "a"
FT /note= "flag"
XX
PN WO200296944-A2.
XX
PD 05-DEC-2002.
XX
PF 31-MAY-2002; 2002WO-EP006082.
XX
PR 31-MAY-2001; 2001EP-00202060.
XX
PA (VLAAs) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
PI Snyders DJ, Ottechytsch N, Raes A, Van Hoorick D;
XX
XX WPI; 2003-140443/13.
DR
XX Novel voltage-gated heterotetrameric potassium channel useful for
PT diagnosing, preventing and/or treating excitability disorders, comprises
PT Kv2.1, Kv3.1, Kv5.1, Kv6.3, Kv10.1 or Kv11.1 potassium channel subunits.
XX
XX Example; Page 80-82; 93pp; English.
XX
CC The present sequence is that of a construct used in the creation of a
CC potassium channel subunit Kv10.1 transgenic mouse. In an example from the
CC invention, the construct was microinjected into the pronucleus of a one-
CC cell embryo, and then incubated in a foster mother of the FVB/Nlco mouse
CC strain. The invention provides novel, voltage-gated heterotetrameric
CC potassium channels comprising Kv2.1, Kv3.1, Kv5.1, Kv6.3, Kv10.1 or
CC Kv11.1. These are useful for identifying a molecule that increases or
CC decreases ion flux through the potassium channel (claimed). Nucleic acids
CC encoding the heterotetrameric potassium channels are used in gene therapy
CC to prevent or treat congenital or acquired excitability disorders
CC including epilepsy, long QT syndrome, muscular ataxia, and arrhythmia
CC (all claimed)
XX
SQ Sequence 5775 BP; 1327 A; 1530 C; 1532 G; 1386 T; 0 U; 0 Other;
Query Match 5.6%; Score 71; DB 7; Length 5775;
Best Local Similarity 100.0%; Pred. No. 6.8e-25;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 244 AAGCTGCGTTTCGCGCGGATGTGCGAGCTCTCTTCTACACGAGATGATCTACTGG 303
Db 3667 AAGCTGCGTTTCGCGCGGATGTGCGAGCTCTCTTCTACACGAGATGATCTACTGG 3726

QY 304 GGCTGTGAGGG 314
Db 3727 GGCTGTGAGGG 3737
RESULT 13
ADD01469
ID ADD01469 standard; cDNA; 950 BP.
XX
AC ADD01469;
XX
DT 01-JAN-2004 (first entry)
DE Mouse TCH136 cDNA sequence fragment.
XX
KW ds; antidiabetic; antilipemic; antiarteriosclerotic; nootropic;
KW neuroprotective; anabolic; antiinflammatory; immunosuppressive;
KW cyostatic; antiasthmatic; antiarthritic; cerebrotective;
KW antiallergic; dermatological; cardiant; antiparkinsonian; neuroleptic;
KW glucose transporter; potassium ion channel protein; diabetes;
KW hyperlipemia; arteriosclerosis; digestive disorder; Crohn's disease;
KW colitis; gastritis; ileitis; rectal inflammation; inflammatory disease;
KW sepsis; prostatic hypertrophy; reproductive disorder; pneumonia;
KW meningitis; hepatitis; myocarditis; asthma; immune disorder;
KW multiple sclerosis; rheumatoid arthritis; Sjogren's disease; lupus;
KW allergy; hay fever; allergic rhinitis; anaphylactic shock;
KW atopic dermatitis; circulatory disorder; heart failure; cancer;
KW Alzheimer's disease; Parkinson's disease; schizophrenia;
KW hyperprolactinemia; Cushing's disease; vesicular glutamate transporter.
XX
OS Mus sp.
XX
PN WO2003054190-A1.
XX
PD 03-JUL-2003.
XX
PF 19-DEC-2002; 2002WO-JP013290.
XX
PR 21-DEC-2001; 2001JP-00389361.
PR 25-DEC-2001; 2001JP-00392577.
PR 26-DEC-2001; 2001JP-00394947.
PR 26-DEC-2001; 2001JP-00395467.
PR 06-FEB-2002; 2002JP-00030010.
PR 08-FEB-2002; 2002JP-00033095.
PR 06-JUN-2002; 2002JP-00165336.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
PI Nakanishi A, Sagiya Y, Uno Y;
XX
XX WPI; 2003-541817/51.
XX
CC Glucose transporter TCH099, vesicular glutamate transporter TCH177 and
CC potassium channel protein TCH136 and DNA encoding them for diagnosis,
CC treatment and prevention of diabetes, hyperlipemia, arteriosclerosis and
CC digestive disorders.
XX
XX Example 21; SEQ ID NO 105; 221pp; Japanese.
XX
CC The invention relates to a novel glucose transporter TCH099, vesicular
CC glutamate transporter TCH177 and voltage-dependent potassium ion channel
CC protein TCH136. The sequences are useful in the treatment, prevention and
CC diagnosis of a broad range of diseases including diabetes, hyperlipemia,
CC arteriosclerosis, digestive disorders (such as Crohn's disease, colitis,
CC gastritis, ileitis and rectal inflammation), inflammatory diseases,
CC sepsis, prostatic hypertrophy, reproductive disorders, pneumonia,
CC meningitis, hepatitis, myocarditis, asthma, immune disorders (such as
CC multiple sclerosis, rheumatoid arthritis, Sjogren's disease and lupus),
CC allergies (such as hay fever, allergic rhinitis, anaphylactic shock and
CC atopic dermatitis), circulatory disorders (such as heart failure), cancer
CC (such as cancer of the lung, kidney, liver, ovary, prostate, stomach,
CC pancreas, bladder, breast, fallopian tubes or colon), central nervous
CC system diseases (such as Alzheimer's, Parkinson's and schizophrenia) and

CC secretory disorders (such hyperprolactinemia and Cushing's disease). This
 CC sequence represents a fragment of the cDNA sequence for the novel mouse
 CC voltage-dependent potassium ion channel protein TCH136.

XX
 SQ Sequence 950 BP; 182 A; 263 C; 269 G; 230 T; 0 U; 6 Other;

Query Match 5.5%; Score 70; DB 9; Length 950;
 Best Local Similarity 100.0%; Pred. No. 2.2e-24;
 Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 452 GGGCTGGCTGGAGCGATCGCGCGACCTTCGAGAGCCACGTCGTCGTCGGCGCGC 511
 Db 150 GGGCTGGCTGGAGCGATCGCGCGACCTTCGAGAGCCACGTCGTCGTCGGCGCGC 209

QY 512 AGATCCTGGC 521

Db 210 AGATCCTGGC 219

RESULT 14

ABQ49122
 ID ABQ49122 standard; DNA; 1634 BP.

XX AC ABQ49122;

XX DT 12-JUL-2002 (first entry)

XX DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 35713.

XX KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
 KW drug; side effect; cancer; central nervous system; cardiovascular;
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;
 KW SNP; cell differentiation; ds.

XX OS Homo sapiens.

XX PN WO200218632-A2.

XX PD 07-MAR-2002.

XX PF 01-SEP-2001; 2001WO-EP010074.

XX PR 01-SEP-2000; 2000DE-01043826.

XX PR 05-SEP-2000; 2000DE-01044543.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K, Guetig D;

XX DR WPI; 2002-371829/40.

XX PT Determining the degree of cytosine methylation in genomic DNA, useful for
 PT diagnosis and prognosis, comprises selective hybridization of amplicons
 PT from chemically treated DNA.

XX PS Claim 12; 56pp + Sequence Listing; 56pp; German.

XX This invention describes a novel method for determining the degree of
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
 CC genomic sample of DNA. The sample is treated chemically to convert
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic
 CC DNA that contains the target C is amplified to form a labeled amplicon.
 CC The amplicon is hybridised to two classes, each with at least one member,
 CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
 CC degree of hybridisation to both classes is determined from the label on
 CC the amplicon. From the ratio of labels hybridised to the two classes of
 CC oligomers, the degree of methylation is calculated. The method is used:
 CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
 CC and of a wide range of diseases, e.g. cancer, disorders of the central
 CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
 CC particularly by detecting mutations or single nucleotide polymorphisms
 CC (SNPs); and (ii) for differentiation of cell or tissue types and for
 CC investigating cell differentiation. The method allows the methylation

CC status of many C residues to be determined simultaneously. ABQ13410-
 CC ABQ54121 represent genomic DNA sequences used to illustrate the method
 CC for determining the degree of cytosine methylation described in the
 CC disclosure of the invention

XX SQ Sequence 1634 BP; 212 A; 232 C; 624 G; 566 T; 0 U; 0 Other;

Query Match 2.3%; Score 29; DB 6; Length 1634;

Best Local Similarity 100.0%; Pred. No. 0.00073;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 522 TAGCGTTCGGTGGTGTTCGTGATCGTGT 550

Db 1244 TAGCGTTCGGTGGTGTTCGTGATCGTGT 1272

RESULT 15

ABQ49123/c

ID ABQ49123 standard; DNA; 1634 BP.

XX AC ABQ49123;

XX DT 12-JUL-2002 (first entry)

XX DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 35714.

XX KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
 KW drug; side effect; cancer; central nervous system; cardiovascular;
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;
 KW SNP; cell differentiation; ds.

XX OS Homo sapiens.

XX PN WO200218632-A2.

XX PD 07-MAR-2002.

XX PF 01-SEP-2001; 2001WO-EP010074.

XX PR 01-SEP-2000; 2000DE-01043826.

XX PR 05-SEP-2000; 2000DE-01044543.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K, Guetig D;

XX DR WPI; 2002-371829/40.

XX PT Determining the degree of cytosine methylation in genomic DNA, useful for
 PT diagnosis and prognosis, comprises selective hybridization of amplicons
 PT from chemically treated DNA.

XX PS Claim 12; 56pp + Sequence Listing; 56pp; German.

XX This invention describes a novel method for determining the degree of
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
 CC genomic sample of DNA. The sample is treated chemically to convert
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic
 CC DNA that contains the target C is amplified to form a labeled amplicon.
 CC The amplicon is hybridised to two classes, each with at least one member,
 CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
 CC degree of hybridisation to both classes is determined from the label on
 CC the amplicon. From the ratio of labels hybridised to the two classes of
 CC oligomers, the degree of methylation is calculated. The method is used:
 CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
 CC and of a wide range of diseases, e.g. cancer, disorders of the central
 CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
 CC particularly by detecting mutations or single nucleotide polymorphisms
 CC (SNPs); and (ii) for differentiation of cell or tissue types and for
 CC investigating cell differentiation. The method allows the methylation
 CC status of many C residues to be determined simultaneously. ABQ13410-
 CC ABQ54121 represent genomic DNA sequences used to illustrate the method
 CC for determining the degree of cytosine methylation described in the

CC disclosure of the invention
 XX
 SQ Sequence 1634 BP; 566 A; 624 C; 232 G; 212 T; 0 U; 0 Other;
 Query Match 2.3%; Score 29; DB 6; Length 1634;
 Best Local Similarity 100.0%; Pred. No. 0.00073;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 522 TAGCGTGTCCGTGGTTCGTGATCGTGT 550
 Db 391 TAGCGTGTCCGTGGTTCGTGATCGTGT 363

Search completed: April 19, 2004, 17:06:05
 Job time : 589 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 19, 2004, 16:49:26 ; Search time 117 Seconds
(without alignments)
6061.771 Million cell updates/sec

Title: US-10-016-647-1
Perfect score: 1278
Sequence: 1 atgaccttcggcgcgagcgg.....ccactgaattcctgaattaa 1278

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 24

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query			
No.	Score	Match	Length	ID
Description				

No matches found

Search completed: April 19, 2004, 19:34:58
Job time : 117 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 19, 2004, 16:57:24 ; Search time 4632 Seconds
(without alignment)

9708.087 Million cell updates/sec

Title: US-10-016-647-1

Perfect score: 1278

Sequence: 1 atgaccttcggcgagcggg.....ccactgaattccgtaattaa 1278

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 37577330 seqs, 17593059518 residues

Word size : 24

Total number of hits satisfying chosen parameters: 72

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1278	100.0	1844	43	US-10-016-647-3	Sequence 3, Appli
3	1227	96.0	3215	1	PCT-US02-23407-1	Sequence 1, Appli
4	1227	96.0	3215	46	US-10-199-869-1	Sequence 1, Appli
5	1227	96.0	3215	87	US-60-306-577-1	Sequence 1, Appli
6	840	65.7	2312	49	US-10-343-903-47	Sequence 47, Appl
7	834	65.3	1416	46	US-10-170-235-1828	Sequence 1828, Ap
8	729	57.0	2235	51	US-10-415-378-39	Sequence 39, Appl
9	729	57.0	2405	1	PCT-US03-28227-1172	Sequence 1172, Ap
10	649	50.8	695	75	US-60-196-712-1268	Sequence 1268, Ap
11	647	50.6	2204	1	PCT-US03-33087-85	Sequence 85, Appl
12	613	48.0	1651	1	PCT-US02-10780-45	Sequence 45, Appl
13	613	48.0	1651	45	US-10-114-270-45	Sequence 45, Appl
14	594	46.5	594	1	PCT-US02-23407-26	Sequence 26, Appl
15	594	46.5	594	46	US-10-199-869-26	Sequence 26, Appl
16	594	46.5	594	87	US-60-306-577-26	Sequence 26, Appl
17	582	45.5	1315	79	US-60-230-445-2448	Sequence 2448, Ap
18	562	44.0	1147	79	US-60-230-445-2449	Sequence 2449, Ap
19	519	40.6	520	77	US-60-113-177-1094	Sequence 1094, Ap
20	495	38.7	649	75	US-60-195-134-392	Sequence 392, App
21	495	38.7	649	75	US-60-195-134-393	Sequence 393, App
22	495	38.7	649	75	US-60-195-134-394	Sequence 394, App
23	495	38.7	649	75	US-60-195-134-395	Sequence 395, App
24	495	38.7	649	75	US-60-195-134-396	Sequence 396, App
25	495	38.7	649	75	US-60-195-134-397	Sequence 397, App
26	495	38.7	649	75	US-60-195-333-36	Sequence 36, Appl
27	430	33.6	1317	31	US-09-745-064-4	Sequence 4, Appli
28	430	33.6	1317	45	US-10-141-622-4	Sequence 4, Appli
29	400	31.3	417	1	PCT-US03-23407-27	Sequence 27, Appl
30	400	31.3	417	46	US-10-199-869-27	Sequence 27, Appl
31	400	31.3	417	87	US-60-306-577-27	Sequence 27, Appl
32	347	27.2	461	1	PCT-US01-14365-25	Sequence 25, Appl
33	347	27.2	461	34	US-09-852-386-25	Sequence 25, Appl
34	347	27.2	461	73	US-60-171-487-127	Sequence 127, App
35	331	25.9	777	42	US-09-989-920-7	Sequence 7, Appli
36	277	21.7	355	72	US-60-163-080-230	Sequence 230, App
37	277	21.7	355	72	US-60-169-841-1270	Sequence 1270, Ap
38	276	21.6	354	72	US-60-162-244-85	Sequence 85, Appl
39	276	21.6	354	72	US-60-162-357-739	Sequence 739, App
40	252	19.7	582	73	US-60-171-487-87	Sequence 87, Appl
41	228	17.8	1103	28	US-09-570-045-6	Sequence 6, Appli
42	217	17.0	911	42	US-09-389-920-8	Sequence 8, Appli
43	138	10.8	138	1	PCT-US02-23407-28	Sequence 28, Appl
44	138	10.8	138	46	US-10-199-869-28	Sequence 28, Appl
45	138	10.8	138	87	US-60-306-577-28	Sequence 28, Appl

ALIGNMENTS

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RESULT 1
US-10-016-647-1
; Sequence 1, Application US/10016647
; GENERAL INFORMATION:
; APPLICANT: Fiddler, Carl Johan
; APPLICANT: Hilbun, Erin
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0284-USA
; CURRENT APPLICATION NUMBER: US/10/016,647
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/257,932
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1278
; TYPE: DNA
; ORGANISM: homo sapiens

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RESULT 2
US-10-016-647-3
; Sequence 3, Application US/10016647
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Hilbun, Erin
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0284-USA
; CURRENT APPLICATION NUMBER: US/10/016,647
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/257,932
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1844
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-016-647-3

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Matches 1278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 TCGCGCTCCGAGCGGACGCTGCTCGAGGTGTGCGAGCTACGACCGCGAGCGCAACGAG 180
Db 577 TCGCGCTCCGAGCGGACGCTGCTCGAGGTGTGCGAGCTACGACCGCGAGCGCAACGAG 636
QY 181 TACTTCTTCGACGGCACTCGAGGCGCTTCGCTTCATCTGCTTCATCTGCTGCGCGGCAC 240
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RESULT 3
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; Sequence 1, Application PC/TUS0223407
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUB
; TITLE OF INVENTION: K-alphaM2
; FILE REFERENCE: D0161 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/23407
; CURRENT FILING DATE: 2002-07-19

; PRIOR APPLICATION NUMBER: US 60/306,577
 ; PRIOR FILING DATE: 2001-07-19
 ; NUMBER OF SEQ ID NOS: 90
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 3215
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1275)
 ; OTHER INFORMATION:
 PCT-US02-23407-1

Query Match 96.0%; Score 1227; DB 1; Length 3215;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1277; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	ATGACCTTCGGGCGCAGCGGGCGGCTCGGTGGTGTGAGTGGCGGCGCGCGGAT	60
Db	1	ATGACCTTCGGGCGCAGCGGGCGGCTCGGTGGTGTGAGTGGCGGCGCGCGGAT	60
QY	61	TCGCTGTCCGGGAGCTGTGAAGGACTTCCCGCTCGCGCGGTGAGCGCGGTGCAACGGC	120
Db	61	TCGCTGTCCGGGAGCTGTGAAGGACTTCCCGCTCGCGCGGTGAGCGCGGTGCAACGGC	120
QY	121	TGGCGCTCCAGCGCGAGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGG	180
Db	121	TGGCGCTCCAGCGCGAGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGG	180
QY	181	TACTTCTTCGACCGGCACTCGGAGGCTTCGGGCTTCATCTGCTTACGTCGCGGCCAC	240
Db	181	TACTTCTTCGACCGGCACTCGGAGGCTTCGGGCTTCATCTGCTTACGTCGCGGCCAC	240
QY	241	GGCAAGCTGGCTTCGGGCGCGGAGTGTGAGGCTTCCTTTACAAAGAGATGATCTAC	300
Db	241	GGCAAGCTGGCTTCGGGCGCGGAGTGTGAGGCTTCCTTTACAAAGAGATGATCTAC	300
QY	301	TGGGGCTGGAGGCGCGACCTCGAGTACTGTGCGAGCGCGGCTCGACCGCGCATG	360
Db	301	TGGGGCTGGAGGCGCGACCTCGAGTACTGTGCGAGCGCGGCTCGACCGCGCATG	360
QY	361	TCCGACCACTTACTTACTGGCGCGAGCGCGGCGTGTGGCGCGCGACGAGCGG	420
Db	361	TCCGACCACTTACTTACTGGCGCGAGCGCGGCGTGTGGCGCGCGACGAGCGG	420
QY	421	CGCGCGCGCGCGCGAGCGGCTTCCTCCAGCGCTGTGAGGCTGTGAGGCTGTGAGG	480
Db	421	CGCGCGCGCGCGCGAGCGGCTTCCTCCAGCGCTGTGAGGCTGTGAGGCTGTGAGG	480
QY	481	TTGAGGAGCGCCACGTCGCTGTGGCGCGAGATCTTGGCTAGCGTGTGGTGTTC	540
Db	481	TTGAGGAGCGCCACGTCGCTGTGGCGCGAGATCTTGGCTAGCGTGTGGTGTTC	540
QY	541	GTGATCGTTCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	600
Db	541	GTGATCGTTCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	600
QY	601	GCGGACAAACCGAGCTGTGATGACCGGAGCAGATAATTGAAGCTATCTGATAGTTGG	660
Db	601	GCGGACAAACCGAGCTGTGATGACCGGAGCAGATAATTGAAGCTATCTGATAGTTGG	660
QY	661	TTCACTGCGGAGTGATGTGAGTTTCAATGTCTCAAAAAAAGAGTGTGAGTTGTCAAG	720
Db	661	TTCACTGCGGAGTGATGTGAGTTTCAATGTCTCAAAAAAAGAGTGTGAGTTGTCAAG	720
QY	721	AGACCCCTGAAATCATTTGATTTACTGGCAATTCAGCGGTATCATCTGTGTGTGTG	780
Db	721	AGACCCCTGAAATCATTTGATTTACTGGCAATTCAGCGGTATCATCTGTGTGTGTG	780
QY	781	ACAGTGTTCAGGCGAGAACTCTCAACTCCAGGGGTGAGTCACTTTCAGGGTACTT	840
Db	781	ACAGTGTTCAGGCGAGAACTCTCAACTCCAGGGGTGAGTCACTTTCAGGGTACTT	840

QY	841	AGAATGATGAGGATTTTTTGGTGATTAAGCTTCCCGTCACTTTCATTTGGTCTTCAGACA	900
Db	841	AGAATGATGAGGATTTTTTGGTGATTAAGCTTCCCGTCACTTTCATTTGGTCTTCAGACA	900
QY	901	CTCGTTTGACTCTCAAAAGCTTGTACCGAGAGATGGTATGTTACTTGTCTTCAATTTGT	960
Db	901	CTCGTTTGACTCTCAAAAGCTTGTACCGAGAGATGGTATGTTACTTGTCTTCAATTTGT	960
QY	961	GTTGCCATGGCAATCTTTAGTGCACTTCTCAGCTTCTTGAACATGGGCTGGACCTGGAA	1020
Db	961	GTTGCCATGGCAATCTTTAGTGCACTTCTCAGCTTCTTGAACATGGGCTGGACCTGGAA	1020
QY	1021	ACATCCAAAGAGACTTTTACCGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1080
Db	1021	ACATCCAAAGAGACTTTTACCGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1080
QY	1081	ACTCAGTTGGCTATGAGATATGATATCTATCATCAGTGCCTGGAAGAATCTTGGAGGA	1140
Db	1081	ACTCAGTTGGCTATGAGATATGATATCTATCATCAGTGCCTGGAAGAATCTTGGAGGA	1140
QY	1141	GTTTGTGTGTGCTGAGGAAATTTCTATTTGGCATTACCTATCATTCTTATCTACCATAGC	1200
Db	1141	GTTTGTGTGTGCTGAGGAAATTTCTATTTGGCATTACCTATCATTCTTATCTACCATAGC	1200
QY	1201	TTTGTGAGTGTATCATAGAGCTCAAGTTTGTAGTCTGCTAGGTATAGTAGAGCTCTCC	1260
Db	1201	TTTGTGAGTGTATCATAGAGCTCAAGTTTGTAGTCTGCTAGGTATAGTAGAGCTCTCC	1260
QY	1261	ACTCAATTCCTGGAATTA 1278	
Db	1261	ACTCAATTCCTGGAATTA 1278	

RESULT 4

US-10-199-869-1

; Sequence 1, Application US/10199869

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUB

; FILE REFERENCE: D0161 NP

; CURRENT APPLICATION NUMBER: US/10/199,869

; PRIOR FILING DATE: 2002-07-19

; PRIOR APPLICATION NUMBER: US 60/306,577

; PRIOR FILING DATE: 2001-07-19

; NUMBER OF SEQ ID NOS: 90

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 3215

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(1275)

; OTHER INFORMATION:

US-10-199-869-1

Query Match 96.0%; Score 1227; DB 46; Length 3215;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1277; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	ATGACCTTCGGGCGCAGCGGGCGGCTCGGTGGTGTGCTGAAAGTGGCGGCGCGCGCGAT	60
Db	1	ATGACCTTCGGGCGCAGCGGGCGGCTCGGTGGTGTGCTGAAAGTGGCGGCGCGCGAT	60
QY	61	TCGCTGTCCGGAGCTGTGAGGACTTCCCGCTCGCGCGGTGAGCGCGGTGACCGGC	120
Db	61	TCGCTGTCCGGAGCTGTGAGGACTTCCCGCTCGCGCGGTGAGCGCGGTGACCGGC	120
QY	121	TGCGGTCCGAGCGCGACCTGTCTCCAGGTGTGCGAGCTACGACCGCGGCGCAACGAG	180
Db	121	TGCGGTCCGAGCGCGACCTGTCTCCAGGTGTGCGAGCTACGACCGCGGCGCAACGAG	180

Db 1666 GATATGATCTTATCACAGTGCCTGGAAGATTCTTGGAGAGTTTGTGTGTCAGTGA 1725
QY 1159 ATTGTTCTATTGGCAATACCTATCACTTTATCTACCACTAGCTTTGTGTCAGTGTATCAT 1218
Db 1726 ATTGTTCTATTGGCAATACCTATCACTTTATCTACCACTAGCTTTGTGTCAGTGTATCAT 1785
QY 1219 GAGCTCAAGTTTAGATCTGCTAGGTATAGTAGGAGCTCTCCACTGAATTCCTGAATAA 1278
Db 1786 GAGCTCAAGTTTAGATCTGCTAGGTATAGTAGGAGCTCTCCACTGAATTCCTGAATAA 1845
RESULT 7
US-10-170-235-1828
; Sequence 1828, Application US/10170235
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
; FILE REFERENCE: CL001380
; CURRENT APPLICATION NUMBER: US/10/170,235
; CURRENT FILING DATE: 2003-03-17
; NUMBER OF SEQ ID NOS: 42514
; SEQ ID NO 1828
; LENGTH: 1416
; TYPE: DNA
; ORGANISM: HUMAN
US-10-170-235-1828
Query Match 65.3%; Score 834; DB 46; Length 1416;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 834; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGACCTTCGGCGCAGCGCGGCGCTCGGTGCTGAACGTGGGGCGGCCCGGTAT 60
Db 1 ATGACCTTCGGCGCAGCGCGGCGGCTCGGTGCTGAACGTGGGGCGGCCCGGTAT 60
QY 61 TCGCTGTCGGGAGCTGTGAAGNCTTCCGCTGCGCGCGGTGAGCGGCTGACCGC 120
Db 61 TCGCTGTCGGGAGCTGTGAAGNCTTCCGCTGCGCGCGGTGAGCGGCTGACCGC 120
QY 121 TCGCGCTCCGAGCGCAGCTGTCTGAGGTGTGCGAGCTACGACCGCGAGCGCAACGAG 180
Db 121 TCGCGCTCCGAGCGCAGCTGTCTGAGGTGTGCGAGCTACGACCGCGAGCGCAACGAG 180
QY 181 TACTTCTTCGACCGGCACTCGAGGCTTCGGTTCATCTGCTTACGTCGCGGCCAC 240
Db 181 TACTTCTTCGACCGGCACTCGAGGCTTCGGTTCATCTGCTTACGTCGCGGCCAC 240
QY 241 GCGAGCTGCTTCGCGCGCGGAGTGTGCGAGCTCTCTTCTACAAAGATGATCTAC 300
Db 241 GCGAGCTGCTTCGCGCGCGGAGTGTGCGAGCTCTCTTCTACAAAGATGATCTAC 300
QY 301 TGGGCGCTGGAGGCGCGCACTCTCGAGTACTGTGTCAGCGCGGCTTCGACCGCGCATG 360
Db 301 TGGGCGCTGGAGGCGCGCACTCTCGAGTACTGTGTCAGCGCGGCTTCGACCGCGCATG 360
QY 361 TCCGACACCTACACCTTCTACTCGCGCGCAGCGCGGCTGTCGCGCGCGCAGCGGCG 420
Db 361 TCCGACACCTACACCTTCTACTCGCGCGCAGCGCGGCTGTCGCGCGCGCAGCGGCG 420
QY 421 CGCCCGCGCGCGCGCGCGGCTCCCTCCAGCGCTGCTGAGCGCGCATGCGCGCGGACC 480
Db 421 CGCCCGCGCGCGCGCGGCTCCCTCCAGCGCTGCTGAGCGCGCATGCGCGCGGACC 480
QY 481 TTCGAGAGCCCACTGCTGCTGCGCGCGCAGATCTGCGCTAGCGTGTGCGGTGTC 540
Db 481 TTCGAGAGCCCACTGCTGCTGCGCGCGCAGATCTGCGCTAGCGTGTGCGGTGTC 540
QY 541 GTATGCTGTCCATGTTGTTGCTGTGCGCGCAGCAGCTTGGCCGACCTGGCGCAGCGC 600
Db 541 GTATGCTGTCCATGTTGTTGCTGTGCGCGCAGCAGCTTGGCCGACCTGGCGCAGCGC 600

QY 601 GCCGACAAACCGAGCCTGGATGACCGGAGCAGGATAATTGAAGCTATCTGCATAGTTGG 660
Db 601 GCCGACAAACCGAGCCTGGATGACCGGAGCAGGATAATTGAAGCTATCTGCATAGTTGG 660
QY 661 TTCACTGCCAGTGCATCGTGAAGTTTCATTCCTCCAAAACCAAGTGTGAGTTTGTCAAG 720
Db 661 TTCACTGCCAGTGCATCGTGAAGTTTCATTCCTCCAAAACCAAGTGTGAGTTTGTCAAG 720
QY 721 AGACCCCTGAACATCATTTACTGGCAATCACGCGTATTACATCTCTGTGTTGATG 780
Db 721 AGACCCCTGAACATCATTTACTGGCAATCACGCGTATTACATCTCTGTGTTGATG 780
QY 781 ACAGTGTTCACGCGGAGAACTCTCACTCCAGAGGCTGGAGTCACTTTGAGG 834
Db 781 ACAGTGTTCACGCGGAGAACTCTCACTCCAGAGGCTGGAGTCACTTTGAGG 834

RESULT 8
US-10-415-378-39
; Sequence 39, Application US/10415378
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; TANG, Y. Tom
; APPLICANT: YUE, Henry; NGUYEN, Damiel B.;
; APPLICANT: HAPALIA, April J.A.; ELLIOTT, Vicki S.;
; APPLICANT: LU, Yan; CHAWLA, Narinder K.;
; APPLICANT: YAO, Monique G.; BAUGHN, Mariah R.;
; APPLICANT: GANDHI, Ameena R.; DING, Li;
; APPLICANT: SANJANWALA, Madhusudan M.; RAMKUMAR, Jayalaxmi;
; APPLICANT: ARVIZU, Chandra S.; GIEZEN, Kimberly J.;
; APPLICANT: LAL, Preeti G.; AZIMZAI, Yalda;
; APPLICANT: KHAN, Farrah A.; THANGAVELU, Kavitha;
; APPLICANT: THORNTON, Michael B.; LU, Dying Aina M.;
; APPLICANT: TRIBOULEY, Catherine M.; WARREN, Bridget A.;
; APPLICANT: ISON, H. Craig; DAS, Debopriya;
; APPLICANT: RAMMANN, Brigitte E.; POLICKY, Jennifer L.;
; APPLICANT: KEARNEY, Liam
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PI-0270 USN
; CURRENT APPLICATION NUMBER: US/10/415,378
; CURRENT FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: PCT/US01/46055
; PRIOR FILING DATE: 2001-10-27
; PRIOR APPLICATION NUMBER: US 60/250,790
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/252,232
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/249,661
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/247,673
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/245,904
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/243,989
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PERL Program
; SEQ ID NO 39
; LENGTH: 2235
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7482060CB1
US-10-415-378-39

Query Match 57.0%; Score 729; DB 51; Length 2235;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 514 ATCTGGTAGCGTGTGCGTGGTGTGTCGATCGTCCATGCTGCTGCGCCAGC 573
Db 920 ATCTGGTAGCGTGTGCGTGGTGTGTCGATCGTCCATGCTGCTGCGCCAGC 979


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RESULT 11
PCT-US03-33087-95
; GENERAL INFORMATION:
; Sequence 85, Application PC/TUS0333087
; APPLICANT: INCYTE CORPORATION; Hafalia, April J.A.;
; APPLICANT: KHARE, Reena; LAL, Preeti G.;
; APPLICANT: YUE, Henry; BAUGHN, Mariiah R.;
; APPLICANT: THORNTON, Michael B.; LU, Dyang Aina M.;
; APPLICANT: ISON, Craig H.; BECHA, Shanya D.;
; APPLICANT: DING, Li; WARREN, Bridget A.;
; APPLICANT: LEE, Soo Yeun; SWARNAKAR, Anita;
; APPLICANT: ELLIOTT, Vicki S.; RICHARDSON, Thomas W.;
; APPLICANT: NARQUIS, Joseph P.; RAMKUMAR, Jayalakmi;
; APPLICANT: MURAGE, Jaji; RAUMANN, Brigitte E.;
; APPLICANT: YAO, Monique G.; LU, Yan;
; APPLICANT: GRIETZEN, Kimberly J.; YANG, Yonghong G.;
; APPLICANT: CHANG, Hsin-Ru; CHAWLA, Narinder K.;
; APPLICANT: TRAN, Uyen K.; LEE, Sally;
; APPLICANT: YANG, Junming; GANDHI, Ameena R.;
; APPLICANT: TRIBOLESY, Catherine M.; POLICKY, Jennifer L.;
; APPLICANT: RING, Huijun Z.; LEE, Ernestine A.
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PF-1591 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/33087
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: US 60/419,313
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/421,033
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 60/421,349
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/423,516
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PERL Program
; SEQ ID NO 85
; LENGTH: 2204
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7523683CB1
PCT-US03-33087-85

Query Match 50.8%; Score 647; DB 1; Length 2204;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 632 GGATAATTGAAGCTATCTGCATAGGTTGGTTCACTCCGAGTGCATCTGAGGTTCAATG 691
Db 1091 GGATAATTGAAGCTATCTGCATAGGTTGGTTCACTCCGAGTGCATCTGAGGTTCAATG 1150
Qy 692 TCTCCAAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTGATTTACTGGCAA 751
Db 1151 TCTCCAAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTGATTTACTGGCAA 1210
Qy 752 TCAGCCGGTATTACATCTCTGTCTCATGACAGTGTTCACAGCGAGAGAATCTTCAACTCC 811
Db 1211 TCAGCCGGTATTACATCTCTGTCTCATGACAGTGTTCACAGCGAGAGAATCTTCAACTCC 1270
Qy 812 AGAGGGCTGGAGTCACCTTCGAGGGTACTTAGAATGATGAGGATTTTTTGGTGATTAAGC 871
Db 1271 AGAGGGCTGGAGTCACCTTCGAGGGTACTTAGAATGATGAGGATTTTTTGGTGATTAAGC 1330
Qy 872 TTGCCCGTCACTTCATTTGGTCTTCAGACATCGTTTGACTCTCAACGTTGCTACCGAG 931
Db 1331 TTGCCCGTCACTTCATTTGGTCTTCAGACATCGTTTGACTCTCAACGTTGCTACCGAG 1390
Qy 932 AGATGGTTATGTTACTTGTCTTCATTTGTTGCCATGGCAATCTTTAGTGCACTTTCTC 991
Db 1391 AGATGGTTATGTTACTTGTCTTCATTTGTTGCCATGGCAATCTTTAGTGCACTTTCTC 1450
Qy 992 AGCTTCTTGAACATGGGCTGGACCTGGAAACATCCAAAGAGACTTTCACGAGTTCCTG 1051

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/ APPLICANT: Malyankar, Uriel M.
/ APPLICANT: Spytek, Kimberly A.
/ APPLICANT: Patturajan, Meera
/ APPLICANT: Liu, Zhaozhong
/ APPLICANT: Gusev, Vladimir Y.
/ APPLICANT: Li, Li
/ APPLICANT: Vernet, Corine
/ APPLICANT: Zerhusen, Bryan D.
/ APPLICANT: Gorman, Linda
/ APPLICANT: Shenoy, Suresh G.
/ APPLICANT: Pena, Carol E.A.
/ APPLICANT: Smithson, Glenda
/ APPLICANT: Burgess, Catherine E.
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Shinkets, Richard A.
/ APPLICANT: Gangolli, Esha A.
/ APPLICANT: Taupier Jr., Raymond J.
/ APPLICANT: Casman, Stacie J.
/ APPLICANT: Ji, Weizhen
/ APPLICANT: Anderson, David W.
/ APPLICANT: Liette, Mario W.
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Edinger, Shlomit R.
/ APPLICANT: Stone, David J.
/ APPLICANT: MacDougall, John R.
/ APPLICANT: Rothenberg, Mark E.
/ TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-322C
/ CURRENT APPLICATION NUMBER: US/10/114,270
/ CURRENT FILING DATE: 2002-11-27
/ PRIOR APPLICATION NUMBER: 60/281,086
/ PRIOR FILING DATE: 2001-04-03
/ PRIOR APPLICATION NUMBER: 60/281,136
/ PRIOR FILING DATE: 2001-04-03
/ PRIOR APPLICATION NUMBER: 60/281,863
/ PRIOR FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: 60/281,906
/ PRIOR FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: 60/282,020
/ PRIOR FILING DATE: 2001-04-06
/ PRIOR APPLICATION NUMBER: 60/282,930
/ PRIOR FILING DATE: 2001-04-10
/ PRIOR APPLICATION NUMBER: 60/282,934
/ PRIOR FILING DATE: 2001-04-10
/ PRIOR APPLICATION NUMBER: 60/283,512
/ PRIOR FILING DATE: 2001-04-12
/ PRIOR APPLICATION NUMBER: 60/283,710
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 60/284,234
/ PRIOR FILING DATE: 2001-04-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 470
/ SEQ ID NO 45
/ LENGTH: 1651
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(1642)
US-10-114-270-45

Query Match      48.0%; Score 613; DB 45; Length 1651;
Best Local Similarity 100.0%; Pred. No. 1.6e-309;
Matches 613; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 630 CAGGATAATTGAAGCTATCGCATAGTTGGTTCACTGCCGAGTGCATCGTCAGGTTTCAT 689
DB 792 CAGGATAATTGAAGCTATCGCATAGTTGGTTCACTGCCGAGTGCATCGTCAGGTTTCAT 851
QY 690 TGTCTCCAAAACAAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTGATTCTGGC 749
DB 852 TGTCTCCAAAACAAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTGATTCTGGC 911
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QY 750 AATCAGCGCCGTATTACATCTCTGTGTATGACAGTGTTTACAGGCGAGAACTCTCAACT 809
DB 912 AATCAGCGCCGTATTACATCTCTGTGTATGACAGTGTTTACAGGCGAGAACTCTCAACT 971
QY 810 CCAGAGGGCTGGAGTACACCTTGAGGGTACTTAGAATGATGAGGATTTTTGGGTGATTAA 869
DB 972 CCAGAGGGCTGGAGTACACCTTGAGGGTACTTAGAATGATGAGGATTTTTGGGTGATTAA 1031
QY 870 GCTTGGCCGTCACCTTCAATCGTCTTCAGACACACCTCGGTTTGACTCTCAAAAGCTGCTACCG 929
DB 1032 GCTTGGCCGTCACCTTCAATCGTCTTCAGACACACCTCGGTTTGACTCTCAAAAGCTGCTACCG 1091
QY 930 AGAGATGGTATTGTTACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 989
DB 1092 AGAGATGGTATTGTTACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1151
QY 990 TCAGCTTTCTTTGAACATGGGCTGGACCTGGAAACATCCAAACAGGACTTTTACCAGCAATTC 1049
DB 1152 TCAGCTTTCTTTGAACATGGGCTGGACCTGGAAACATCCAAACAGGACTTTTACCAGCAATTC 1211
QY 1050 TGTGCTCTGCTGGTGGTGAATTAATCTATGACTACAGTTGGCTATGGAGATATGTATCC 1109
DB 1212 TGTGCTCTGCTGGTGGTGAATTAATCTATGACTACAGTTGGCTATGGAGATATGTATCC 1271
QY 1110 TATCACAGTGCCTGGAAGAAATTTCTTGAGGAGTTTGTGTGTGTCAGTGGAAATTTCTTATT 1169
DB 1272 TATCACAGTGCCTGGAAGAAATTTCTTGAGGAGTTTGTGTGTGTCAGTGGAAATTTCTTATT 1331
QY 1170 GGCATTAACCTATACATCTTTTATCTACCATAGCTTTGTCAGTGTATCATGAGCTCAAGTT 1229
DB 1332 GGCATTAACCTATACATCTTTTATCTACCATAGCTTTGTCAGTGTATCATGAGCTCAAGTT 1391
QY 1230 TAGATCTGCTAGG 1242
DB 1392 TAGATCTGCTAGG 1404
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RESULT 14

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PCT-US02-23407-26
; Sequence 26, Application PC/TUS0223407
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUB-
; TITLE OF INVENTION: K-alpha2
; FILE REFERENCE: D0161 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/23407
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/306,577
; PRIOR FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 26
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-23407-26
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Query Match      46.5%; Score 594; DB 1; Length 594;
Best Local Similarity 100.0%; Pred. No. 1.5e-299;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 634 ATAATTGAAGCTATCTGCATAGTTGGTTCACTGCCGAGTGCATCGTCAGGTTTCATTTGC 693
DB 1 ATAATTGAAGCTATCTGCATAGTTGGTTCACTGCCGAGTGCATCGTCAGGTTTCATTTGC 60
QY 694 TCCAAAACAAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTGATTCTAGTGCATC 753
DB 61 TCCAAAACAAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTGATTCTAGTGCATC 120
QY 754 AGCGCGTATTAATCTCTGTGTGTGATGACAGTGTTTTACGCGGAGAACTCTCAACTCGAG 813
DB 121 AGCGCGTATTAATCTCTGTGTGTGATGACAGTGTTTTACGCGGAGAACTCTCAACTCGAG 180
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QY 814 AGGCTGGAGTCACTTGGAGTACTTAGAATGATGAGGATTTTGGGTGATTAAGCTT 873
Db 181 AGGCTGGAGTCACTTGGAGTACTTAGAATGATGAGGATTTTGGGTGATTAAGCTT 240
QY 874 GCCCGTCACTTCACTTCTTTCAGACACTCGGTTTGACCTCTCAAGCTTCTACCGAGAG 933
Db 241 GCCCGTCACTTCACTTCTTTCAGACACTCGGTTTGACCTCTCAAGCTTCTACCGAGAG 300
QY 934 ATGGTTATGTTACTTGTCTTCACTTGTGTTGCCATGCGCAATCTTTAGTGCATTTCTCAG 993
Db 301 ATGGTTATGTTACTTGTCTTCACTTGTGTTGCCATGCGCAATCTTTAGTGCATTTCTCAG 360
QY 994 CTTCCTGAAACATGGGCTGGACCTGGAACATCCAAACAGGACTTTACCGAGCTTCTCTGCT 1053
Db 361 CTTCCTGAAACATGGGCTGGACCTGGAACATCCAAACAGGACTTTACCGAGCTTCTCTGCT 420
QY 1054 GCCTGCTGGTGGGTGATTTCTCTATGACTACAGTTGGCTATCGAGATATGTATCCTATC 1113
Db 421 GCCTGCTGGTGGGTGATTTCTCTATGACTACAGTTGGCTATCGAGATATGTATCCTATC 480
QY 1114 ACAGTGCTGGAAGAAATCTTGGAGGAGTTTGTGTTGTCAGTGGAAATTTCTATTGGCA 1173
Db 481 ACAGTGCTGGAAGAAATCTTGGAGGAGTTTGTGTTGTCAGTGGAAATTTCTATTGGCA 540
QY 1174 TTACCTATCACTTTTATCTACCATAGCTTTGTGAGTGTATCATGAGCTCAAG 1227
Db 541 TTACCTATCACTTTTATCTACCATAGCTTTGTGAGTGTATCATGAGCTCAAG 594

RESULT 15

US-10-199-869-26
; Sequence 26, Application US/10199869
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUB
; TITLE OF INVENTION: K α 1pham2
; FILE REFERENCE: D0161 NP
; CURRENT APPLICATION NUMBER: US/10/199,869
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/306,577
; PRIOR FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-199-869-26

Query Match 46.5%; Score 594; DB 46; Length 594;
Best Local Similarity 100.0%; Pred. No. 1.5e-299;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 634 ATAATTGAAGCTATCTGCATAGGTGGTTCACCTGCCGAGTGCATCGTGAGGTTCAATTGTC 693
Db 1 ATAATTGAAGCTATCTGCATAGGTGGTTCACCTGCCGAGTGCATCGTGAGGTTCAATTGTC 60
QY 694 TCCAAAACAAAGTGTGAGTTGTCAAGAGACCCCTGAAATCATGATTTACTGGCAATC 753
Db 61 TCCAAAACAAAGTGTGAGTTGTCAAGAGACCCCTGAAATCATGATTTACTGGCAATC 120
QY 754 ACCCGGTATTACATCTCTGTGTTGATGACAGTGTTCACAGGCGAGAACTCTCAACTCCAG 813
Db 121 ACCCGGTATTACATCTCTGTGTTGATGACAGTGTTCACAGGCGAGAACTCTCAACTCCAG 180
QY 814 AGGGCTGGAGTCACTTGGGTGATTTAGATGATGAGGATTTTGGGTGATTAAGCTT 873
Db 181 AGGGCTGGAGTCACTTGGGTGATTTAGATGATGAGGATTTTGGGTGATTAAGCTT 240
QY 874 GCCCGTCACTTCACTTCTTTCAGACACTCGGTTTGACCTCTCAAGCTTCTACCGAGAG 933
Db 241 GCCCGTCACTTCACTTCTTTCAGACACTCGGTTTGACCTCTCAAGCTTCTACCGAGAG 300

Search completed: April 19, 2004, 20:52:38
Job time : 4640 secs


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QY 459 GCTGAGCGCATGCGCGGACCTTCGAGGAGCCACGTCGCTGCTGCGCGCGAGATCCT 518
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QY 519 GCCTAGCGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 578
    |||
Db 121 GCCTAGCGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
    |||
QY 579 GCCGACTGCGCGCAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 638
    |||
Db 181 GCCGACTGCGCGCAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
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QY 639 TGAAGCTATCGCATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 698
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QY 699 AAACAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTACTGCGCAATCACGCC 758
    |||
Db 301 AAACAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTACTGCGCAATCACGCC 360
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QY 759 GTATTACATCTCTGTGTGATGACAGTGTGTACAGGCGAAGTCTCAATCCAGAGGCG 818
    |||
Db 361 GTATTACATCTCTGTGTGATGACAGTGTGTACAGGCGAAGTCTCAATCCAGAGGCG 420
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QY 819 TGGAGTCACCTTGAGG 834
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Db 421 TGGAGTCACCTTGAGG 436
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RESULT 5
US-60-545-213-26268
; Sequence 26268, Application US/60545213
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042099)
; CURRENT APPLICATION NUMBER: US/60/545,213
; CURRENT FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26268
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-60-545-213-26268

```

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Query Match
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 927 CCGAGAGATGTTATGTTACTTCTC 951
    |||
Db 1  CCGAGAGATGTTATGTTACTTCTC 25
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RESULT 6
US-60-545-213-26269
; Sequence 26269, Application US/60545213
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042099)
; CURRENT APPLICATION NUMBER: US/60/545,213
; CURRENT FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26269
; LENGTH: 25
; TYPE: DNA

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```

; ORGANISM: probe
US-60-545-213-26269
Query Match
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 928 CGAGAGATGTTATGTTACTTCTC 952
    |||
Db 1  CGAGAGATGTTATGTTACTTCTC 25
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RESULT 7
US-60-545-213-26270
; Sequence 26270, Application US/60545213
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042099)
; CURRENT APPLICATION NUMBER: US/60/545,213
; CURRENT FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26270
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-60-545-213-26270

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Query Match
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 931 GAGATGTTATGTTACTTCTTCA 955
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Db 1  GAGATGTTATGTTACTTCTTCA 25
    |||

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RESULT 8
US-60-545-213-26271
; Sequence 26271, Application US/60545213
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042099)
; CURRENT APPLICATION NUMBER: US/60/545,213
; CURRENT FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26271
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-60-545-213-26271

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Query Match
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 930 AGAGATGTTATGTTACTTCTTC 954
    |||
Db 1  AGAGATGTTATGTTACTTCTTC 25
    |||

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RESULT 9
US-60-545-213-26272
; Sequence 26272, Application US/60545213
; GENERAL INFORMATION:
; APPLICANT: Wyeth

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; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26277
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-60-545-213-26277

Query Match      2.0%; Score 25; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 941 TGTACTTGCTCTTCATTTGTGTGTC 965
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Db 1 TGTACTTGCTCTTCATTTGTGTGTC 25

RESULT 15
US-60-545-213-26278
; Sequence 26278, Application US/60545213
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042099)
; CURRENT APPLICATION NUMBER: US/60/545,213
; CURRENT FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26278
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-60-545-213-26278

Query Match      2.0%; Score 25; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 921 TTGCTACCGAGAGATGGTTATGTTA 945
    |||||||
Db 1 TTGCTACCGAGAGATGGTTATGTTA 25

Search completed: April 19, 2004, 20:55:14
Job time : 149 secs
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 6, 2004, 16:21:11 ; Search time 5112 seconds
(without alignments)
10835.758 Million cell updates/sec

Title: US-10-016-647-1
Perfect score: 1278
Sequence: 1 atgacctcgccgagcg...ccactgaattcctgaattaa 1278

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 1: gb_ba.*
- 2: gb_hg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
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- 34: em_hg_pin.*
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- 36: em_hg_man.*
- 37: em_hg_vrt.*
- 38: em_sy.*
- 39: em_hgo_hum.*
- 40: em_hgo_mus.*
- 41: em_hgo_other.*

Pred. No. is the number of results predicted by chance to have a

Result No.	Score	Match	Length	DB	ID	Description
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2	1278	100.0	1844	6	AX511262	Sequence
3	1278	100.0	3670	9	AF454547	Homo sapi
4	1235	96.6	1311	9	AB070604	Homo sapi
5	1235	96.6	1947	6	AX641934	Sequence
6	1235	96.6	1947	9	AF348982	Homo sapi
7	1235	96.6	3703	9	AF454548	Homo sapi
8	1178.4	92.2	2235	6	AX478109	Sequence
9	1115.6	87.3	3323	10	AF454551	Mus muscu
10	1099.6	86.0	1744	10	AF454549	Rattus no
11	1072.6	83.9	3356	10	AF454552	Mus muscu
12	1070	83.7	5775	6	AX641960	Sequence
13	1056.6	82.7	1302	9	AF450110	Homo sapi
14	1056.6	82.7	1777	10	AF454550	Rattus no
15	846.6	66.2	2312	6	AX392945	Sequence
16	805.4	63.0	1038	10	AB070605	Rattus no
17	649	50.8	151367	9	AC025750	Homo sapi
18	577	45.1	209523	10	AC084366	Mus muscu
19	553	43.3	219807	2	AC098764	Rattus no
20	553	43.3	259704	2	AC112092	Rattus no
21	553	43.3	268099	2	AC133407	Rattus no
22	383	30.0	461	6	AX319980	Sequence
23	377.8	29.6	6831	2	AC101224	Mus muscu
24	348.4	27.3	777	6	AX534980	Sequence
25	336.4	26.3	911	6	AX534981	Sequence
26	283.8	22.2	1401	9	HSA011021	Homo sapi
27	278.8	21.8	3348	10	RSRKLIPC	X16476 Rat drk1 ge
28	278.4	21.8	2203	9	BC045629	Homo sapi
29	277.4	21.7	1542	9	AF033383	Homo sapi
30	277.4	21.7	2127	6	I81198	Sequence 1
31	277.4	21.7	2127	6	BD14650	Potassium
32	264.4	20.7	2574	10	MUSSHAB	M64228 Mouse potas
33	264.4	20.7	2707	10	BC051422	Mus muscu
34	264.4	20.7	3525	10	BC031776	Mus muscu
35	264.4	20.7	3733	10	BC061501	Mus muscu
36	262	20.5	1560	6	AX641932	Sequence
37	262	20.5	1560	9	AF348984	Homo sapi
38	262	20.5	1560	9	AF450108	Homo sapi
39	260.6	20.4	2577	9	AF026005	Homo sapi
40	260.6	20.4	3054	9	HSDRK1	X68302 H.sapiens h
41	260.4	20.4	2523	10	RRA011020	RA011020 Rattus ra
42	260.2	20.4	3777	9	AX641938	Sequence
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44	258.8	20.3	2022	6	BD235203	Voltage g
45	253.6	19.8	2882	4	AF266507	Oryctolag

ALIGNMENTS

RESULT 1	AX511260	AX511260	1278 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	Sequence 1 from Patent WO0250271.					
DEFINITION	Sequence 1 from Patent WO0250271.					
ACCESSION	AX511260					
VERSION	AX511260.1	GI:23392138				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1					
AUTHORS	Friddle,C.J., Hilbun,E. and Turner,C.A.					
TITLE	Novel human ion channel protein and polynucleotides encoding the same					

JOURNAL Patent: WO 0250271-A 1 27-JUN-2002;
Lexicon Genetics Incorporated (US)
FEATURES Location/Qualifiers
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source
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match 100.0%; Score 1278; DB 6; Length 1278;
Best Local Similarity 100.0%; Pred. No. 7.8e-170;
Matches 1278; Conservative 0; Mismatches 0; Indels 0;

QY	1	ATGACCTTCGGGCGCAGCGGGCGGCTCGTGGTGTCTGAACGTGGCGCGCCCGGTAT	60
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QY	61	TCGCTGTCCCGGAGCTCTCTGAAGGACTTCCGCTGGCCGCGCGCTGAGCGGCTGCACGCG	120
Db	61	TCGCTGTCCCGGAGCTCTGAAGGACTTCCGCTGGCCGCGCGCTGAGCGGCTGCACGCG	120
QY	121	TGCGCCTCCGAGCGGACGTCTCGAGGTGTGCGAAGCTACGACCGCGAGCGCAACAG	180
Db	121	TGCGCCTCCGAGCGGACGTCTCGAGGTGTGCGAAGCTACGACCGCGAGCGCAACAG	180
QY	181	TACTTCTTCGACCGGCACTCGAGGCGCTTCGGCTTCATCTCTTACACGAGATGATCA	300
Db	181	TACTTCTTCGACCGGCACTCGAGGCGCTTCGGCTTCATCTCTTACACGAGATGATCA	300
QY	241	GCGAAGCTGCGCTTCGCGCGCGGATGTGCGAGCTCTCTTACACGAGATGATCA	300
Db	241	GCGAAGCTGCGCTTCGCGCGCGGATGTGCGAGCTCTCTTACACGAGATGATCA	300
QY	301	TGGGCGCTGGAGGGCGGCACCTCGAGTACTGTGCCAGCGCGCCTCGACGACCGCATG	360
Db	301	TGGGCGCTGGAGGGCGGCACCTCGAGTACTGTGCCAGCGCGCCTCGACGACCGCATG	360
QY	361	TCGACACCTACACCTTCTACTCGGCGGACGAGCGGGCGTGTGGGCGCGACGAGGGG	420
Db	361	TCGACACCTACACCTTCTACTCGGCGGACGAGCGGGCGTGTGGGCGCGACGAGGGG	420
QY	421	CGCCCGCGGGCGCGAGGCGGCTCCCTCCAGGCGCTGGCTGAGCGGCATTCGCGCGGAC	480
Db	421	CGCCCGCGGGCGCGAGGCGGCTCCCTCCAGGCGCTGGCTGAGCGGCATTCGCGCGGAC	480
QY	481	TTGAGGAGAGCCACGTCGTCTGCTGGCGCGCAGATCCTGGCTAGCGTGTGGTGGTTC	540
Db	481	TTGAGGAGAGCCACGTCGTCTGCTGGCGCGCAGATCCTGGCTAGCGTGTGGTGGTTC	540
QY	541	GTGATCGTGTCCATGTGGTGTCTGCGCAGACGTTGCCGACGTGGCGGCAACGCGAGCG	600
Db	541	GTGATCGTGTCCATGTGGTGTCTGCGCAGACGTTGCCGACGTGGCGGCAACGCGAGCG	600
QY	601	GCGGACAAACCGACGCTCGATGACCGGAGCAGGATTAATTGAAGCTATCTGCAATAGTTGG	660
Db	601	GCGGACAAACCGACGCTCGATGACCGGAGCAGGATTAATTGAAGCTATCTGCAATAGTTGG	660
QY	661	TTCAGTCGCGAGTGCACTGAGGTTCAATTGTCTCCAAAACAAAGTGTGAGTTGTCAAG	720
Db	661	TTCAGTCGCGAGTGCACTGAGGTTCAATTGTCTCCAAAACAAAGTGTGAGTTGTCAAG	720
QY	721	AGACCCCTGAACATCAATTGATTACTGGCAATCAGCGCGTATTACATCTCTGTGTTGATG	780
Db	721	AGACCCCTGAACATCAATTGATTACTGGCAATCAGCGCGTATTACATCTCTGTGTTGATG	780
QY	781	ACAGTGTTTACGCGGAGACTCTCACTCCAGGGGCTGGAGTCACTTGAGGAGTACTT	840
Db	781	ACAGTGTTTACGCGGAGAACTCTCACTCCAGGGGCTGGAGTCACTTGAGGAGTACTT	840
QY	841	AGAAATGATGAGGATTTTGTGGTGATTAAGCTTGGCCGTCACCTTCATTCGTCTTCAGACA	900
Db	841	AGAAATGATGAGGATTTTGTGGTGATTAAGCTTGGCCGTCACCTTCATTCGTCTTCAGACA	900

Qy	901	CTCGTTTGACTCTCAAACGTTGCTACCGAGAGATGGTTATGTTACTTGTTCTTCATTGTT	960
Db	901	CTCGTTTGACTCTCAAACGTTGCTACCGAGAGATGGTTATGTTACTTGTTCTTCATTGTT	960
Qy	961	GTTCGCATGGCAATCTTTAGTGACATTTCTCAGCTTCTTCAACATGGCTGGACCTGGAA	1020
Db	961	GTTCGCATGGCAATCTTTAGTGACATTTCTCAGCTTCTTCAACATGGCTGGACCTGGAA	1020
Qy	1021	ACATCCAAAGGACATTACACGATTCCTGCTGCCTGCTGGTGGTGATTACTCTATG	1080
Db	1021	ACATCCAAAGGACATTACACGATTCCTGCTGCCTGCTGGTGGTGATTACTCTATG	1080
Qy	1081	ACTACAGTTGGCTATGGAGATATGTAATCTTATCACAGTGCCTGGAGAAGATTCCTGGAGGA	1140
Db	1081	ACTACAGTTGGCTATGGAGATATGTAATCTTATCACAGTGCCTGGAGAAGATTCCTGGAGGA	1140
Qy	1141	GTTTGTGTTGTCAGTGGAAATGTTCTATTGGCAATTACCTATACATTTTATCTACCATAGC	1200
Db	1141	GTTTGTGTTGTCAGTGGAAATGTTCTATTGGCAATTACCTATACATTTTATCTACCATAGC	1200
Qy	1201	TTTGTGCAGTGGTTATCATGAGCTCAAGCTTTAGATCTGCTAGGTATAGTAGGAGCCTCTCC	1260
Db	1201	TTTGTGCAGTGGTTATCATGAGCTCAAGCTTTAGATCTGCTAGGTATAGTAGGAGCCTCTCC	1260
Qy	1261	ACTGAATTCCTGAAATAA	1278
Db	1261	ACTGAATTCCTGAAATAA	1278

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RESULT 2
AX511262
LOCUS      1844 bp          DNA          linear          PAT 27-SEP-2002
DEFINITION Sequence 3 from Patent WO0250271.
ACCESSION  AX511262
VERSION     AX511262.1  GI:233392139
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Fridde, C.J., Hilbun, E. and Turner, C.A.
TITLE       Novel human ion channel protein and polynucleotides encoding the
same
JOURNAL     Patent: WO 0250271-A 3 27-JUN-2002;
            Lexicon Genetics Incorporated (US)
FEATURES    Location/Qualifiers
             1..1844
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
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SOURCE

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	Query Match	100.0.0%;	Score 1278;	DB 6;	Length 1844;
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	Matches 1278;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	457	ATGACCTTCGGGCGGACGGGGCGGCTCGGTGGTGTCTGAACGTGGCGCGCGCCCGGTAT	516		
Qy	61	TGCTCTCCGGGAGTGCTGAAGGACTTTCGCGCTGCGCCGCGTGAGCCGGGTGCACGGC	120		
Db	517	TGCTCTCCGGGAGTGCTGAAGGACTTTCGCGCTGCGCCGCGTGAGCCGGGTGCACGGC	576		
Qy	121	TGCCGCTCCGAGCGGACGTCTCGAGGTGTCGACGACTACGACCGCGAGCGCAACGAG	180		
Db	577	TGCCGCTCCGAGCGGACGTCTCGAGGTGTCGACGACTACGACCGCGAGGCGCAACGAG	536		
Qy	181	TACTTCTTCGACCGGCACTTCGAGGCGCTTCGCGCTTCATCTCTACTGTCGGCGGCCAC	240		
Db	637	TACTTCTTCGACCGGCACTTCGAGGCGCTTCGCGCTTCATCTCTACTGTCGGCGGCCAC	596		

241	QY	GGCAAGCTGGCTTCGCGCGGGATGTGCGAGCTCTCTTTACAAACGAGATGATCTAC	300
697	Db	GGCAAGCTGGCTTCGCGCGGGATGTGCGAGCTCTCTTTACAAACGAGATGATCTAC	756
301	QY	TGSGGGCTGGAGGGCGGACACTCGAGTACTGTGCGCCAGCGCGCTTCGACGACCGCATG	360
757	Db	TGSGGGCTGGAGGGCGGACACTCGAGTACTGTGCGCCAGCGCGCTTCGACGACCGCATG	816
361	QY	TCCGACACCTTACACCTTTCTACTCGGCGGACGAGCCGGGCGTGTGGCCCGGACGAGGCG	420
817	Db	TCCGACACCTTACACCTTTCTACTCGGCGGACGAGCCGGGCGTGTGGCCCGGACGAGGCG	876
421	QY	CGCCCCGGGGCGGAGCGGGCTCCCTCCAGCGGTGCTGGAGCGCATGCGCGGACG	480
877	Db	CGCCCCGGGGCGGAGCGGGCTCCCTCCAGCGGTGCTGGAGCGCATGCGCGGACG	936
481	QY	TTCCGAGAGCCACGTCGTGCTGGCGCGCAGATCCTGCTAGCGTGTGCGTGTGTTTC	540
937	Db	TTCCGAGAGCCACGTCGTGCTGGCGCGCAGATCCTGCTAGCGTGTGCGTGTGTTTC	996
541	QY	GTGATCGTGTCCATGGTGTGCTGTGGCCAGACAGTGTGCCCGACTGGCGCAACGAGCC	600
997	Db	GTGATCGTGTCCATGGTGTGCTGTGGCCAGACAGTGTGCCCGACTGGCGCAACGAGCC	1056
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 linear
 PRI 23-MAR-2002

AB070604
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 Sano, Y., Mochizuki, S., Miyake, A., Kitada, C., Inamura, K., Yokoi, H.,
 Nozawa, K., Matsushima, H. and Furuichi, K.
 Molecular cloning and characterization of Kv6.3, a novel modulatory
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 FEBS Lett. 513, 230-234 (2002)
 2 (bases 1 to 1311)
 Sano, Y. and Mochizuki, S.
 Direct Submission
 Submitted (24-AUG-2001) Yorikata Sano, Yamanouchi Pharmaceutical
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AUTHORS
Snyders,D.J., Ottschyttsch,N., Raes,A. and van Hoorick,D.
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New heterotetrameric potassium channels and uses thereof
JOURNAL
Patent: WO 02096944-A 3 05-DEC-2002;
Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)
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New heterotetrameric potassium channels and uses thereof
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Ottschytch, N., Raes, A., Van Hoorick, D. and Snyder, D.J.			
Obligatory heterotetramerization of three previously uncharacterized Kv channel alpha-subunits identified in the human genome			
Proc. Natl. Acad. Sci. U.S.A. 99 (12), 7986-7991 (2002)			
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Ottschytch, N., van Hoorick, D., Raes, A.L. and Snyder, D.J.			
Direct Submission			
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Submitted (14-PEB-2001) Molecular Biophysics, VIB (Flanders Inst. Biotechnology & University of Antwerp, Universiteitsplein 1, Antwerp 2610, Belgium			

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Qy	1	ATGACCTTCGGGGCCAGCGGGCGGCTCGGTGGTGTGCTGAACGTTGGCGCGCGCCGGTAT	60
Db	596	ATGACCTTCGGGGCCAGCGGGCGGCTCGGTGGTGTGCTGAACGTTGGCGCGCGCCGGTAT	655
Qy	61	TCGTGTCCCGGGAGCTGTGAAGGACTTCGCGTGGCGCGCGTGAAGCCGGTGCACGC	120
Db	656	TCGTGTCCCGGGAGCTGTGAAGGACTTCGCGTGGCGCGCGTGAAGCCGGTGCACGC	715
Qy	121	TGCCGCTCCGAGCGCAGCTGCTCGAGGTGTGGACGACTACGACCGCGAGCGCAACGAG	180
Db	716	TGCCGCTCCGAGCGCAGCTGCTCGAGGTGTGGACGACTACGACCGCGAGCGCAACGAG	775
Qy	181	TACTTCTTCGACCGGCACTCGAGGCGCTTCGGGTTCACTCTGCTCTACGTCGCGGCCAC	240
Db	776	TACTTCTTCGACCGGCACTCGAGGCGCTTCGGGTTCACTCTGCTCTACGTCGCGGCCAC	835
Qy	241	GGCAAGCTGCGCTTCGCGCGCGGAGTGTGAGCTCTCCTTCTACACGAGATGATCTAC	300
Db	836	GGCAAGCTGCGCTTCGCGCGCGGAGTGTGAGCTCTCCTTCTACACGAGATGATCTAC	895
Qy	301	TGGGCGCTCGAGGCGCGCACCTCGAGTACTGTGTCGAGCGCGGCTTCGACGACCGCATG	360
Db	896	TGGGCGCTCGAGGCGCGCACCTCGAGTACTGTGTCGAGCGCGGCTTCGACGACCGCATG	955
Qy	361	TCGACACCTTACCTTCTACTCGCGCGCAGCGCGGCGTGTGGCGCGCAGAGGCG	420
Db	956	TCGACACCTTACCTTCTACTCGCGCGCAGCGCGGCGTGTGGCGCGCAGAGGCG	1015
Qy	421	CGCCCGCGCGCGCGGCGGCTCCCTCCAGCGCTGGCTGGAGCGCATGCGCGCGACC	480
Db	1016	CGCCCGCGCGCGCGGCGGCTCCCTCCAGCGCTGGCTGGAGCGCATGCGCGCGACC	1075
Qy	481	TTGAGAGAGCCCACTGCTGCTGGCGCGCGCAGATCTGGCTAGCGTGTGGTGTTC	540
Db	1076	TTGAGAGAGCCCACTGCTGCTGGCGCGCGCAGATCTGGCTAGCGTGTGGTGTTC	1135
Qy	541	GTGATCGTGTCCATGTTGTTGCTGTGCGCGCAGACGCTTCCCGACTGGCGCAACGAGCC	600
Db	1136	GTGATCGTGTCCATGTTGTTGCTGTGCGCGCAGACGCTTCCCGACTGGCGCAACGAGCC	1195
Qy	601	GCCGACAAACCGCAGCTTGGATGACCGGAGCA-----	631
Db	1196	GCCGACAAACCGCAGCTTGGATGACCGGAGCAGGTA-----	1255
Qy	632	-----GGATATTCAGCTATCTGCATAGGTGTGTTCACTGCCAGTGCATCGTGGGTTTC	687
Db	1256	TCCGGGATAATTGAAGCTATCTGCATAGGTGTGTTCACTGCCAGTGCATCGTGGGTTTC	1315

QY 688 ATTGCTCAAAAACAAGTGTGAGTTTCTCAAGAGACCCCTGACATCATTTGATTACTG 747
Db 1316 ATTGCTCAAAAACAAGTGTGAGTTTCTCAAGAGACCCCTGACATCATTTGATTACTG 1375
QY 748 GCAATCAGCCGCTATTACATCTCTGTTGTATGACAGTGTTTACAGGCGAGAACTCTCAA 807
Db 1376 GCAATCAGCCGCTATTACATCTCTGTTGTATGACAGTGTTTACAGGCGAGAACTCTCAA 1435
QY 808 CTCAGAGGCTGGAGTACCTTGGAGTCTTGAAGATGATGAGGATTTTGGTGAAT 867
Db 1436 CTCAGAGGCTGGAGTACCTTGGAGTCTTGAAGATGATGAGGATTTTGGTGAAT 1495
QY 868 AAGCTTGCCCGTCACTTCATTTGCTTTCAGACATCTGTTGACCTCAAAAGTGTCTAC 927
Db 1496 AAGCTTGCCCGTCACTTCATTTGCTTTCAGACATCTGTTGACCTCAAAAGTGTCTAC 1555
QY 928 CGAGAGATGTTATGTTATCTTCTTCAATTTGTTGCACTGGCAATCTTTAGTGCACTT 987
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QY 1168 TTGGATTAACCTATACATTTTATCTACCATAGCTTTTGGAGTGTATCATGAGCTCAAG 1227
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QY 1228 TTTAGATCTGATGATAGTATAGTATAGGAGCTCTCCACTGAATTCCTGAATTA 1278
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RESULT 7
AF454548 3703 bp mRNA linear PRI 09-AUG-2002
LOCUS Homo sapiens voltage-gated potassium channel subunit Kv10.1b mRNA,
DEFINITION complete cds, alternatively spliced.
ACCESSION AF454548
VERSION AF454548.1 GI:22164083
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3703)
AUTHORS Vega-Saenz de Miera, E.C. and Rudy, B.
TITLE Kv10.1a and Kv10.1b: Two novel alternatively spliced potassium channel subunits
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3703)
AUTHORS Vega-Saenz de Miera, E.C. and Rudy, B.
TITLE Direct Submission
JOURNAL Submitted (04-DEC-2001) Physiology and Neuroscience, New York University School of Medicine, 550 First Avenue, New York, NY 10016, USA
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polya_site
ORIGIN
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Best Local Similarity 97.5%; Pred. No. 7.3e-164;
Matches 1278; Conservative 0; Mismatches 0; Indels 33; Gaps 1;
QY 1 ATGACCTTCGGGGCGAGCGGGCGCTCGTGGTGTGTGAACGTGGCGCGCGCGGTAT 60
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QY 121 TGGCGCTCCGAGCGCGAGCTGTGAGGTGTGCGAGCTACGACCGCGAGCGCAACGAG 180
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QY 241 GGCAGCTGGCTTCGCGCGCGGATGTGCGAGCTCTCTTCTTACACAGAGATCATCTAC 300
Db 718 GGCAGCTGGCTTCGCGCGCGGATGTGCGAGCTCTCTTCTTACACAGAGATCATCTAC 777
QY 301 TGGGCGCTGGAGGGCGCGCACCTCGAGTACTGTGTCCAGCGCGCGCTCGACGCGCATG 360
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QY 361 TCCGACACTTACCTTCTACTCGCGCGAGCGCGGCGTGTGGCGCGCGAGCGGCG 420
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QY 632 ----GGATAATTGAAGCTATCTGCATAGTGTGGTTCATCTCGGAGTGCATCGTGGTTC 687
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QY 688 ATTGTCTCCAAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGAAACATCATTTACTG 747
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RESULT 9
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 LOCUS Mus musculus voltage-gated potassium channel subunit Kv10.1a mRNA,
 DEFINITION complete cds, alternatively spliced.
 ACCESSION AF454551
 VERSION AF454551.1
 KEYWORDS GI:22164089
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 3323)
 VEGA-Saenz de Miera, B.C. and Rudy, B.
 Kv10.1a and Kv10.1b: Two novel alternatively spliced potassium
 channel subunits
 Unpublished
 2 (bases 1 to 3323)
 VEGA-Saenz de Miera, B.C. and Rudy, B.
 Direct Submission
 TITLE Submitted (04-DEC-2001) Physiology and Neuroscience, New York
 JOURNAL University School of Medicine, 550 First Avenue, New York, NY
 10016, USA

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KEYWORDS
SOURCE
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AUTHORS
TITLE
JOURNAL
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CDS
polyA_signal
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Qy	688	ATTGTCTCCAAAAACAAGTGTGATTTTCAAGAGACCCCTGAAACATCATTTGATTTACTG	747
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Qy	1048	CTGCTGCTGCTGCTGGTGGTGAATCTCTATGACTACAGTTGGCTATGGAGATATG	1107
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AF450110 Homo sapiens voltage-gated potassium channel subunit Kv6.4 mRNA, complete cds.			
ACCESSION			
AF450110			
VERSION			
AF450110.1 GI:31295623			
KEYWORDS			
SOURCE			
ORGANISM			
Homo sapiens (human)			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE			
1 (bases 1 to 1302)			
AUTHORS			
Preisig-Muller, R., Derst, C., Mederos Y Schnitzler, M. and Daut, J.			
TITLE			
Cloning and characterization of two novel gamma Kv subunits			
JOURNAL			
Unpublished			
REFERENCE			
2 (bases 1 to 1302)			
AUTHORS			
Preisig-Muller, R., Derst, C., Mederos Y Schnitzler, M. and Daut, J.			
TITLE			
Direct Submission			
JOURNAL			
Submitted (23-NOV-2001) University of Marburg, Institute of Physiology, Deutschhausstrasse 1-2, Marburg 35037, Germany			
FEATURES			
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Best Local Similarity 89.6%; Pred. No. 8.9e-139;			

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 LOCUS AX392945 2312 bp DNA linear PAT 23-MAR-2002
 DEFINITION Sequence 47 from Patent WO0212340.
 ACCESSION AX392945
 VERSION AX392945.1 GI:19700992
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Yue, H., Thornton, M., Ramkumar, J., Tang, Y.T., Azimzai, Y.,
 Baughn, M.R., Yang, J., Yao, M.G., Lal, P., Wallia, N.K., Gandhi, A.R.,
 Hafalia, A.J., Nguyen, D.B., Patterson, C., Elliott, V.S.,
 Tribouley, C.M., Lu, D.A., Xu, Y., Reddy, R., Hernandez, R.,
 Borowsky, M.L., Lo, T.P., Lu, Y., Policky, J.L., Greene, B.D.,
 Sanjanwalla, M.S., Raumann, B.E., Burford, N., Ison, C.H., Lee, E.A.,
 Ding, L., Das, D., Kallick, D.A., Khan, F.A. and Seilhamer, J.J.
 JOURNALS Patent: WO 0212340-A 47 14-FEB-2002;
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Job time : 5127 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 6, 2004, 16:14:11 ; Search time 577 Seconds

(without alignments)

9409.354 Million cell updates/sec

Title: US-10-016-647-1

Perfect score: 1278

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Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002s:*

7: Geneseqn2003as:*

8: Geneseqn2003bs:*

9: Geneseqn2003cs:*

10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1235	96.6	1947	7 ABZ24711	ABZ24711 Human pot
4	1235	96.6	5174	9 ADD01447	ADD01447 Human TCH
5	1232	96.4	1308	9 ADD01427	ADD01427 Human TCH
6	1178.4	92.2	2235	6 ABK83228	ABK83228 Human tra
7	1099.4	86.0	1651	7 ABX72192	ABX72192 Human NOV
8	1070	83.7	5775	7 ABZ24716	ABZ24716 Murine po
9	846.6	66.2	2312	6 AD33662	AD33662 Human TBI
10	729.8	57.1	950	9 ADD01469	ADD01469 Mouse TCH
11	406.6	31.8	1634	6 ABQ49122	ABQ49122 Oligonuc
12	406.6	31.8	1634	6 ABQ49123	ABQ49123 Oligonuc
13	395.4	30.9	1634	6 ABQ49124	ABQ49124 Oligonuc
14	395.4	30.9	1634	6 ABQ49125	ABQ49125 Oligonuc
15	383	30.0	461	6 ABK27494	ABK27494 DNA encod
16	348.4	27.3	777	6 ABX91965	ABX91965 Lung spec
17	336.4	26.3	911	6 ABX91966	ABX91966 Lung spec
18	283.8	22.2	1401	2 AAZ23803	AAZ23803 Human Kv6
19	283.8	22.2	1401	5 AAS75631	AAS75631 DNA encod
20	280	21.9	2370	9 ADB47439	ADB47439 Human cDN
21	277.4	21.7	2127	2 AAT12461	AAT12461 Human K+
22	277.4	21.7	2127	2 AAV04873	AAV04873 cDNA sequ
23	277.4	21.7	2127	9 ADC99152	ADC99152 Human mat

24	262	20.5	1560	7 ABZ24710	ABZ24710 Human pot
25	260.6	20.4	2577	6 AAL45289	AAL45289 Human KCN
26	260.2	20.4	2565	3 ABZ36415	ABZ36415 cDNA enco
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29	257.6	20.2	2499	6 ABZ35517	ABZ35517 Human gen
30	251	19.6	1518	3 AAZ49454	AZ49454 Mouse Vol
31	226	17.7	3339	4 ABZ35517	ABZ35517 Human gen
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34	201.4	15.8	1488	2 AAZ06653	AZ06653 hkv5.1 hu
35	201.4	15.8	1880	2 AAZ06652	AZ06652 hkv5.1 hu
36	198.2	15.5	1485	7 ABZ24715	ABZ24715 Human pot
37	198.2	15.5	2483	2 AAT12462	AAT12462 Human K+
38	198.2	15.5	2483	2 AAV04874	AAV04874 cDNA sequ
39	198.2	15.5	2483	9 ADC99154	ADC99154 Human mat
40	197.8	15.5	3102	2 AAZ11905	AZ11905 Human pot
41	197.8	15.5	5027	6 ABZ35328	ABZ35328 Human gen
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ALIGNMENTS

RESULT 1
ABN83930
ID ABN83930 standard; cDNA; 1278 BP.
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AC ABN83930;
XX
DT 06-SEP-2002 (first entry)
XX
DE Human voltage-gated potassium channel-like protein encoding cDNA.
XX
KW Human; voltage-gated potassium channel; ion channel; neuroprotective;
KW therapeutic; diagnostic; pharmacogenomic; gene therapy; SNP;
KW single nucleotide polymorphism; foetal brain; brain; cerebellum;
KW pituitary; prostate; thymus; lymph node; bone marrow; trachea;
KW foetal liver; liver; testis; thyroid; salivary gland; stomach;
KW skeletal muscle; heart; uterus; adipose; hypothalamus; ovary; aorta;
KW 12 week old embryo; adenocarcinoma; osteosarcoma; gene; ss.
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OS Homo sapiens.
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XX
PD 27-JUN-2002.
XX
PF 10-DEC-2001; 2001WO-US048050.
XX
XX 20-DEC-2000; 2000US-0257932P.
XX
XX (LEXI-) LEXICON GENETICS INC.
XX
XX Fiddle CJ, Hilbun E, Turner CA;
XX
XX WPI; 2002-508799/54.
XX
XX P-PSDB; ABB83073.
XX
XX Human ion channel polynucleotide useful in therapeutic, diagnostic and
XX
XX pharmacogenomic applications.

Claim 1; Page 34; 36pp; English.

PS The invention relates to a novel human ion channel polynucleotide that
 CC shares structural similarity with voltage-gated potassium channel
 CC proteins. The activity of the protein of the invention may be described
 CC as neuroprotective. The protein of the invention is useful in
 CC therapeutic, diagnostic and pharmacogenomic applications, for example to
 CC identify mutations associated with a particular disease, as a diagnostic
 CC or prognostic assay, or in gene therapy. The protein of the invention has
 CC been found to be expressed in human foetal brain, brain, cerebellum,
 CC pituitary, prostate, thymus, lymph node, bone marrow, trachea, foetal
 CC liver, liver, testis, thyroid, salivary gland, stomach, skeletal muscle,
 CC heart, uterus, adipose, hypothalamus, ovary, aorta, 12 week old embryo,
 CC adenocarcinoma and osteosarcoma cells. The current sequence represents
 CC the human voltage-gated potassium channel-like protein encoding CDNA
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SQ Sequence 1278 BP; 237 A; 349 C; 376 G; 316 T; 0 U; 0 Other;

Query Match 100.0%; Score 1278; DB 6; Length 1278;
 Best Local Similarity 100.0%; Pred. No. 3e-260;
 Matches 1278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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 ID ASN83931 standard; DNA; 1844 BP.
 XX AC ASN83931;
 XX XX
 DT 06-SEP-2002 (first entry)
 XX XX
 DE Human voltage-gated potassium channel-like protein encoding sequence.
 XX XX
 KW Human; voltage-gated potassium channel; ion channel; neuroprotective;
 KW therapeutic; diagnostic; pharmacogenomic; gene therapy; SNP;
 KW single nucleotide polymorphism; foetal brain; brain; cerebellum;
 KW pituitary; prostate; thymus; lymph node; bone marrow; trachea;
 KW foetal liver; liver; testis; thyroid; salivary gland; stomach;
 KW skeletal muscle; heart; uterus; adipose; hypothalamus; ovary; aorta;
 KW 12 week old embryo; adenocarcinoma; osteosarcoma; gene; ds.
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 XX 27-JUN-2002.
 PD

FT FT /*tag= a
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XX WO200296944-A2.
XX 05-DEC-2002.
XX 31-MAY-2002; 2002WO-EP006082.
XX 31-MAY-2001; 2001EP-00202060.
XX (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX Snyders DJ, Ottschytch N, Raes A, Van Hoorick D;
XX WPI; 2003-140443/13.
XX P-PSDB; ABP58352.
XX Novel voltage-gated heterotetrameric potassium channel useful for
XX diagnosing, preventing and/or treating excitability disorders, comprises
XX Kv2.1, Kv3.1, Kv5.1, Kv6.3, Kv10.1 or Kv11.1 potassium channel subunits.
XX
XX Claim 3; Page 50-53; 93pp; English.
XX
XX The present sequence is that of cDNA encoding human potassium channel
XX subunit Kv10.1. The cDNA was obtained by PCR from a brain library. The
XX invention relates to the cloning and characterisation of 3 novel voltage-
XX gated potassium channel subunits that were identified in the human
XX genome: Kv6.3 (located at 16q24.1), Kv10.1 (2p21) and Kv11.1 (9p24.2).
XX yeast two-hybrid and co-immunoprecipitation experiments showed that these
XX heterotetrameric channels with Kv2.1, Kv3.1 and/or Kv5.1. Co-expression
XX of each of the diver subunits with Kv2.1, Kv3.1 and/or Kv5.1 results in
XX currents that differ from typical Kv2.1 currents. Kv6.3, Kv10.1 and
XX Kv11.1 alone do not reach the plasma membrane but are retained in the
XX endoplasmic reticulum. Co-expression with Kv2.1 results in transport to
XX the plasma membrane. The invention provides novel, voltage-gated
XX heterotetrameric potassium channels comprising Kv2.1, Kv3.1, Kv5.1,
XX Kv6.3, Kv10.1 or Kv11.1. These are useful for identifying a molecule that
XX increases or decreases ion flux through the potassium channel. Nucleic
XX acids encoding the heterotetrameric potassium channels are used in gene
XX therapy to prevent or treat congenital or acquired excitability disorders
XX including epilepsy, long QT syndrome, muscular ataxia, arrhythmia (all
XX claimed), as well as hyperactivity disorders, mental disorders, mood
XX disorders, behavioural disorders, anxiety disorders, hypokalaemic
XX periodic paralysis, spasticity disorders, myotonia and paramyotonia. The
XX nucleic acids can be used to transfect cells. For example, stem cells are
XX used in ex vivo procedures for cell transfection and gene therapy. The
XX nucleic acids are also useful in diagnosis, and in the creation of
XX transgenic or knockout animals
XX
SQ Sequence 1947 BP; 324 A; 596 C; 644 G; 383 T; 0 U; 0 Other;
Query Match 96.6%; Score 1235; DB 7; Length 1947;
Best Local Similarity 97.5%; Pred. No. 3.9e-251;
Matches 1278; Conservative 0; Mismatches 0; Indels 33; Gaps 1;
QY 1 ATGACCTTCGGGCGACGGGGCGGCTCGTGGTGTCTGAACGTGGGGCGGCGCGGAT 60
DB 596 ATGACCTTCGGGCGACGGGGCGGCTCGTGGTGTCTGAACGTGGGGCGGCGGAT 655
QY 61 TCGCTGTCGGGAGCTGCTGAAGGACTCCGCTGCGCGCGGCTGAGCGCGGTGACGGC 120
DB 656 TCGCTGTCGGGAGCTGCTGAAGGACTCCGCTGCGCGCGGCTGAGCGCGGTGACGGC 715
QY 121 TCGCGCTCCGAGCGGACGTGCTCGAGGTGTCGCGAGACTACGACCGGAGCGCAACGAG 180
DB 716 TCGCGCTCCGAGCGGACGTGCTCGAGGTGTCGCGAGCTACGACCGGAGCGCAACGAG 775
QY 181 TACTTCTCGACGGGACCTCGGAGGCTTCGCGCTTCATCCTGCTAGTGGCGGCCAC 240
DB 776 TACTTCTCGACGGGACCTCGGAGGCTTCGCGCTTCATCCTGCTAGTGGCGGCCAC 835

QY 241 GGCAGAGCTGCGCTTCGGCGCGCGGATGTGCGAGCTCTCCTTCTACACGAGATGATCTAC 300
DB 836 GGCAGAGCTGCGCTTCGGCGCGCGGATGTGCGAGCTCTCCTTCTACACGAGATGATCTAC 895
QY 301 TGGGCGCTTGGAGGGCGGCGCACCTCGAGTACTGCTGCCAGCGCGCCCTCGACGACCGCATG 360
DB 896 TGGGCGCTTGGAGGGCGGCGCACCTCGAGTACTGCTGCCAGCGCGCCCTCGACGACCGCATG 955
QY 361 TCCGACACCTACACCTTCTACTCGGCCGAGAGCGGGCGGTGCTGGGCCCGGAGAGGCG 420
DB 956 TCCGACACCTACACCTTCTACTCGGCCGAGAGCGGGCGGTGCTGGGCCCGGAGAGGCG 1015
QY 421 CGCCCCGGCGGGCGGAGGGCGCTCCCTCCAGGGCGGTGGCTGGAGCGCATCCGCGCGACC 480
DB 1016 CGCCCCGGCGGGCGGAGGGCGCTCCCTCCAGGGCGGTGGCTGGAGCGCATCCGCGCGACC 1075
QY 481 TTCGAGGAGCGCACCTCGTCTGGCGCGCGAGATCCTGTAGCTAGCGTTCGGTGGTTC 540
DB 1076 TTCGAGGAGCGCACCTCGTCTGGCGCGCGAGATCCTGTAGCTAGCGTTCGGTGGTTC 1135
QY 541 GTGATCGTGTCCATGCTGTGCTGCGCGCGAGCATGTTGCCCGACTGGCGCGACGCGACC 600
DB 1136 GTGATCGTGTCCATGCTGTGCTGCGCGCGAGCATGTTGCCCGACTGGCGCGACGCGACC 1195
QY 601 GCCGACAAACCGGAGCGCTGGATGACCGGAGCA----- 631
DB 1196 GCCGACAAACCGGAGCGCTGGATGACCGGAGCGAGGTACTCCGCGCGCTGGGAGGAGCC 1255
QY 632 ----GGATTAATTGAAGCTATCTGCAATAGTGTGTTCTACTGCCAGATGCTAGTGGTTC 687
DB 1256 TCCGGGATAATTGAAGCTATCTGCAATAGTGTGTTCTACTGCCAGATGCTAGTGGTTC 1315
QY 688 ATTCTCTCCAAAACAAAGTGTGAGTTTGTCAAGAGAGCCCTGAAACATCATTTGATTTACTG 747
DB 1316 ATTCTCTCCAAAACAAAGTGTGAGTTTGTCAAGAGAGCCCTGAAACATCATTTGATTTACTG 1375
QY 748 GCAATCAAGCGGTATTAACATCTCTGTGTTGATGACAGTGTGTTACAGCGGAGAACTCTCAA 807
DB 1376 GCAATCAAGCGGTATTAACATCTCTGTGTTGATGACAGTGTGTTACAGCGGAGAACTCTCAA 1435
QY 808 CTCAGAGGGCTGAGTCACTTTGAGGTTACTTAGAATGATGAGGATTTTTTGGGTGATT 867
DB 1436 CTCAGAGGGCTGAGTCACTTTGAGGTTACTTAGAATGATGAGGATTTTTTGGGTGATT 1495
QY 868 AAGCTTCCCGCTCACTTCATTGCTTCAGACACTCGGTTGACTCTCAAACGTTGCTAC 927
DB 1496 AAGCTTCCCGCTCACTTCATTGCTTCAGACACTCGGTTGACTCTCAAACGTTGCTAC 1555
QY 928 CGAGAGATGTTATGTTACTTGTCTTCATTTGTTGGCATGGCAATCTTTAGTGACATT 987
DB 1556 CGAGAGATGTTATGTTACTTGTCTTCATTTGTTGGCATGGCAATCTTTAGTGACATT 1615
QY 988 TCTCAGCTTCTTGAACATGGGCTGGACCTGGAACACATCCAAAGGACTTTTACAGCAAT 1047
DB 1616 TCTCAGCTTCTTGAACATGGGCTGGACCTGGAACACATCCAAAGGACTTTTACAGCAAT 1675
QY 1048 CTTGCTGCTGCTGCTGGTGGTGGTATCTCTATGACTACAGTTGGCTATGGAGATATGAT 1107
DB 1676 CTTGCTGCTGCTGCTGGTGGTGGTATCTCTATGACTACAGTTGGCTATGGAGATATGAT 1735
QY 1108 CCTATACAGTGGCTGGAAGAAATTTGGAGGAGTTTGTGTTCTCAGTGGAAATGTTCTA 1167
DB 1736 CCTATACAGTGGCTGGAAGAAATTTGGAGGAGTTTGTGTTCTCAGTGGAAATGTTCTA 1795
QY 1168 TTGGCATATCATATCATTTTATCTACCATAGCTTTGTGCGAGTGTATCATGAGCTCAAG 1227
DB 1796 TTGGCATATCATATCATTTTATCTACCATAGCTTTGTGCGAGTGTATCATGAGCTCAAG 1855
QY 1228 TTTAGATCTGCTAGGTATAGTAGGAGCTCTCCACATGAATTCCTGAATTA 1278
DB 1856 TTTAGATCTGCTAGGTATAGTAGGAGCTCTCCACATGAATTCCTGAATTA 1906

Query Match 96.6%; Score 1235; DB 9; Length 5174;
Best Local Similarity 97.5%; Pred. No. 4.6e-251;
Matches 1278; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

1 ATGACCTTGGGCGCAGCGGCGCTCGGTGCTGCTGAACGTGGGGGGCGCGCGGTAT 60
485 ATGACCTTGGGCGCAGCGGCGCTCGGTGCTGCTGAACGTGGGGCGCGCGGTAT 544
61 TCCTGTCCCGGAGCTGTGAAGGACTTTCCTGCTGCGCGCGGTGAGCGCGGTGACCGC 120
545 TCCTGTTCCTCGGAGCTGTGAAGGACTTTCCTGCTGCGCGCGGTGAGCGCGGTGACCGC 604
121 TGGCGTCCGAGCGCGGAGCTGTGAGGCTGCGGAGCTGCGGAGCTGCGGAGCTGCGGAG 180
605 TGGCGTCCGAGCGCGGAGCTGTGAGGCTGCGGAGCTGCGGAGCTGCGGAGCTGCGGAG 664
181 TACTTCTTCGACCGGCACTCGGAGGCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
665 TACTTCTTCGACCGGCACTCGGAGGCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 724
241 GCGAAGCTGGCTTCGCGCGCGGAGTGTGCGAGCTCTCTCTTCAACAGAGATGATCTAC 300
725 GCGAAGCTGGCTTCGCGCGCGGAGTGTGCGAGCTCTCTCTTCAACAGAGATGATCTAC 784
301 TGGGGCTCGAGGCGCGGCACTTCGAGTACTGCTGCGGAGCGCGCTCGAGACCGCATG 360
785 TGGGGCTCGAGGCGCGGCACTTCGAGTACTGCTGCGGAGCGCGCTCGAGACCGCATG 844
361 TCGAAGCTGACCTTCTACTCGGCGGAGCGCGGAGTGTGCGGCGCGGAGTGTGCGGCGG 420
845 TCGAAGCTGACCTTCTACTCGGCGGAGCGCGGAGTGTGCGGCGCGGAGTGTGCGGCGG 904
421 CGCGCGCGGCGCGGAGCGGCTTCCTCGGCGGCTGCTGCGGAGCGCGCTGCGGCGGAGC 480
905 CGCGCGCGGCGCGGAGCGGCTTCCTCGGCGGCTGCTGCGGAGCGCGCTGCGGCGGAGC 964
481 TCGAGAGCGCGAGCTGCTGCTGCGGCGGAGTGTGCGGAGCTGCTGCGGAGCTGCTGCGG 540
965 TCGAGAGCGCGAGCTGCTGCTGCGGCGGAGTGTGCGGAGCTGCTGCGGAGCTGCTGCGG 1024
541 GTGATCGTGTCCATGTTGTTGCTGCGGCGGAGTGTGCGGCGGAGTGTGCGGCGGAGC 600
1025 GTGATCGTGTCCATGTTGTTGCTGCGGCGGAGTGTGCGGCGGAGTGTGCGGCGGAGC 1084
601 GCGGACAAACCGGAGCTGAGTACCGGAGCA----- 631
1085 GCGGACAAACCGGAGCTGAGTACCGGAGCACTCTCGCGCGGCGCTGCGGAGGAGCGCC 1144
632 ----GGATAATGAAGCTATCTGATAGTGTGTTGCTGCTGCGGAGTGTGCTGAGGTTTC 687
1145 TCGGGGATAATGAAGCTATCTGATAGTGTGTTGCTGCTGCGGAGTGTGCTGAGGTTTC 1204
688 ATTGTCTCCAAAAACAAAGTGTGAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 747
1205 ATTGTCTCCAAAAACAAAGTGTGAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1264
748 GCAATACGCGGTATTACATCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 807
1265 GCAATACGCGGTATTACATCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1324
808 CTCAGAGGCTCGAGTACCTTTCAGGCTTCTAGATGATGAGGATTTTTCGTTGTTGTTGTTG 867
1325 CTCAGAGGCTCGAGTACCTTTCAGGCTTCTAGATGATGAGGATTTTTCGTTGTTGTTGTTG 1384
868 AAGTTTCGCGTCACTTCACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 927
1385 AAGTTTCGCGTCACTTCACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1444
928 CGAGAGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 987
1445 CGAGAGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1504

ds; gene; antidiabetic; antilipemic; antiarteriosclerotic; neurotropic;
neuroprotective; anabolic; antiinflammatory; immunosuppressive;
cytostatic; antiasthmatic; antiarthritic; cerebroprotective;
antiallergic; dermatological; cardiatic; antiparkinsonian; neuroleptic;
glucose transporter; potassium ion channel protein; diabetes;
hyperlipemia; arteriosclerosis; digestive disorder; Crohn's disease;
colitis; gastritis; ileitis; rectal inflammation; inflammatory disease;
sepsis; prostatic hypertrophy; reproductive disorder; pneumonia;
meningitis; hepatitis; myocarditis; asthma; immune disorder;
multiple sclerosis; rheumatoid arthritis; Sjogren's disease; lupus;
allergy; hay fever; allergic rhinitis; anaphylactic shock;
atopic dermatitis; circulatory disorder; heart failure; cancer;
Alzheimer's disease; Parkinson's disease; schizophrenia;
hyperprolactinemia; Cushing's disease; vesicular glutamate transporter.
Homo sapiens.
WO2003054190-A1.
03-JUL-2003.
19-DEC-2002; 2002WO-JP013290.
21-DEC-2001; 2001JP-00389361.
25-DEC-2001; 2001JP-00392577.
26-DEC-2001; 2001JP-00394947.
26-DEC-2001; 2001JP-00395467.
06-FEB-2002; 2002JP-00030010.
08-FEB-2002; 2002JP-00033095.
06-JUN-2002; 2002JP-00165336.
(TAKE) TAKEDA CHEM IND LTD.
Nakanishi A, Sagiya Y, Uno Y;
WPI; 2003-541817/51.
Glucose transporter TCH099, vesicular glutamate transporter TCH177 and
potassium channel protein TCH136 and DNA encoding them for diagnosis, and
treatment and prevention of diabetes, hyperlipemia, arteriosclerosis, and
digestive disorders.
Claim 62; SEQ ID NO 83; 221pp; Japanese.
The invention relates to a novel glucose transporter TCH099, vesicular
glutamate transporter TCH177 and voltage-dependent potassium ion channel
protein TCH136. The sequences are useful in the treatment, prevention and
diagnosis of a broad range of diseases including diabetes, hyperlipemia,
arteriosclerosis, digestive disorders (such as Crohn's disease, colitis,
gastritis, ileitis and rectal inflammation), inflammatory diseases,
sepsis, prostatic hypertrophy, reproductive disorders, pneumonia,
meningitis, hepatitis, myocarditis, asthma, immune disorders (such as
multiple sclerosis, rheumatoid arthritis, Sjogren's disease and lupus),
allergies (such as hay fever, allergic rhinitis, anaphylactic shock and
atopic dermatitis), circulatory disorders (such as heart failure), cancer
(such as cancer of the lung, kidney, liver, ovary, prostate, stomach,
pancreas, bladder, breast, fallopian tubes or colon), central nervous
system diseases (such as Alzheimer's, Parkinson's and schizophrenia) and
secretory disorders (such as hyperprolactinemia and Cushing's disease). This
sequence represents the cDNA sequence for the novel human voltage-gated
potassium ion channel protein TCH136.
Sequence 5174 BP; 1335 A; 1139 C; 1257 G; 1443 T; 0 U; 0 Other;
SQ

QY 988 TCTCAGCTTCTTGAACATGGCTGGACCTGGAAACATCCAAAGGACTTTACCAGCAT 1047
 Db 1505 TCTCAGCTTCTTGAACATGGCTGGACCTGGAAACATCCAAAGGACTTTACCAGCAT 1564
 QY 1048 CTGCTGCTGCTGGTGGTGAATATCTCTATGACTACAGTGGCTATGAGATATGAT 1107
 Db 1565 CTGCTGCTGCTGGTGGTGAATATCTCTATGACTACAGTGGCTATGAGATATGAT 1624
 QY 1108 CCTATCAGCTGCTGGAGAGATCTTGGAGAGTTGTGTCAGTGGATTTCTTA 1167
 Db 1625 CCTATCAGCTGCTGGAGAGATCTTGGAGAGTTGTGTCAGTGGATTTCTTA 1684
 QY 1168 TTGGCTATTACCTATCACTTTTATCTACCATAGCTTTGTGCAGTGTATCATGAGCTCAAG 1227
 Db 1685 TTGGCTATTACCTATCACTTTTATCTACCATAGCTTTGTGCAGTGTATCATGAGCTCAAG 1744
 QY 1228 TTATGATCTGCTAGGTATAGTAGGAGCCTCTCCACTGAATTTCTGAATTA 1278
 Db 1745 TTATGATCTGCTAGGTATAGTAGGAGCCTCTCCACTGAATTTCTGAATTA 1795

RESULT 5

ADD01427
 ID ADD01427 standard; DNA; 1308 BP.

XX AC ADD01427;

XX DT 01-JAN-2004 (first entry);

XX DE Human TCH136 coding sequence.

XX db; gene; antidiabetic; antilipemic; antiarteriosclerotic; nootropic;
 neuroprotective; anabolic; antiinflammatory; immunosuppressive;
 cytoskeletal; antiaesthetic; antiarthritic; cerebroprotective;
 antiallergic; dermatologic; cardiac; antiParkinsonian; neuroleptic;
 glucose transporter; potassium ion channel protein; diabetes;
 hyperlipemia; arteriosclerosis; digestive disorder; Crohn's disease;
 colitis; gastritis; ileitis; rectal inflammation; inflammatory disease;
 sepsis; prostatic hypertrophy; reproductive disorder; pneumonia;
 meningitis; hepatitis; myocarditis; asthma; immune disorder;
 multiple sclerosis; rheumatoid arthritis; Sjogren's disease; lupus;
 allergy; hay fever; allergic rhinitis; anaphylactic shock;
 atopic dermatitis; circulatory disorder; heart failure; cancer;
 Alzheimer's disease; Parkinson's disease; schizophrenia;
 hyperprolactinemia; Cushing's disease; vesicular glutamate transporter.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX CDS 1..1308

FT /*tag= a

FT /product= "human TCH136 protein"

FT /function= "voltage-dependent potassium ion channel"

XX PN WO2003054190-A1.

XX PD 03-JUL-2003.

XX PF 19-DEC-2002; 2002WO-JP013290.

XX PR 21-DEC-2001; 2001JP-00389361.

XX PR 25-DEC-2001; 2001JP-00392577.

XX PR 26-DEC-2001; 2001JP-00394947.

XX PR 26-DEC-2001; 2001JP-00395467.

XX PR 06-FEB-2002; 2002JP-00030010.

XX PR 08-FEB-2002; 2002JP-00033095.

XX PR 06-JUN-2002; 2002JP-00165336.

XX PA (TAKE) TAKEDA CHEM IND LTD.

XX PI Nakanishi A, Sagiya Y, Uno Y;

XX PI WPI; 2003-541817/51.

XX DR

DR P-PSDB; ADD01426.
 XX Glucose transporter TCH099, vesicular glutamate transporter TCH177 and
 PT potassium channel protein TCH136 and DNA encoding them for diagnosis,
 PT treatment and prevention of diabetes, hyperlipemia, arteriosclerosis and
 PT digestive disorders.
 XX Claim 62; SEQ ID NO 63; 221pp; Japanese.
 PS The invention relates to a novel glucose transporter TCH099, vesicular
 CC glutamate transporter TCH177 and voltage-dependent potassium ion channel
 CC protein TCH136. The sequences are useful in the treatment, prevention and
 CC diagnosis of a broad range of diseases including diabetes, hyperlipemia,
 CC arteriosclerosis, digestive disorders (such as Crohn's disease, colitis,
 CC gastritis, ileitis and rectal inflammation), inflammatory diseases,
 CC sepsis, prostatic hypertrophy, reproductive disorders, pneumonia,
 CC meningitis, hepatitis, myocarditis, asthma, immune disorders (such as
 CC multiple sclerosis, rheumatoid arthritis, Sjogren's disease and lupus),
 CC allergies (such as hay fever, allergic rhinitis, anaphylactic shock and
 CC atopic dermatitis), circulatory disorders (such as heart failure), cancer
 CC (such as cancer of the lung, kidney, liver, ovary, prostate, stomach,
 CC pancreas, bladder, breast, fallopian tubes or colon), central nervous
 CC system diseases (such as Alzheimer's, Parkinson's and schizophrenia) and
 CC secretory disorders (such as hyperprolactinemia and Cushing's disease). This
 CC sequence represents the coding sequence for the novel human voltage-gated
 CC potassium ion channel protein TCH136.
 XX SQ Sequence 1308 BP; 238 A; 362 C; 389 G; 319 T; 0 U; 0 Other;

Query Match 96.4%; Score 1232; DB 9; Length 1308;

Best Local Similarity 97.5%; Pred. No. 1.5e-250;

Matches 1275; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

QY 1 ATGACCTTCGCGGGGCGAGCGGGCGGCTCGGTGCTGAACCTGGCGGCGCGCGGTAT 60

Db 1 ATGACCTTCGCGGGGCGAGCGGGCGGCTCGGTGCTGAACCTGGCGGCGCGCGGTAT 60

QY 61 TCGTGTCCGGGAGCTGTGAAGGACTTCCGCTGCGCGCGCGCTGACCGGCTGACCGC 120

Db 61 TCGTGTCCGGGAGCTGTGAAGGACTTCCGCTGCGCGCGCGCTGACCGGCTGACCGC 120

QY 121 TGCCGCTCCGAGCGCGACGCTCGAGGTGTGCGAGCTACACCGCGAGCGCAACGAG 180

Db 121 TGCCGCTCCGAGCGCGACGCTCGAGGTGTGCGAGCTACACCGCGAGCGCAACGAG 180

QY 181 TACTTCTTCGACCGGCACTCGAGGCGCTTCGCTTATCTGCTCTACGTCGCGCGCAC 240

Db 181 TACTTCTTCGACCGGCACTCGAGGCGCTTCGCTTATCTGCTCTACGTCGCGCGCAC 240

QY 241 GGCAAGCTGCGCTTCGCGCGCGGATGTGGAGCTCTCTTCTACACGAGATGATCTAC 300

Db 241 GGCAAGCTGCGCTTCGCGCGCGGATGTGGAGCTCTCTTCTACACGAGATGATCTAC 300

QY 301 TGGGGCTTGAGGCGCGCACCTCGAGTACTGTGCGAGCGCGCTTCGACGACCGCATG 360

Db 301 TGGGGCTTGAGGCGCGCACCTCGAGTACTGTGCGAGCGCGCTTCGACGACCGCATG 360

QY 361 TCCGACACCTACACCTTCTACTCGCGCGAGCGCGGCTGCTGGCGCGCGAGGGCG 420

Db 361 TCCGACACCTACACCTTCTACTCGCGCGAGCGCGGCTGCTGGCGCGCGAGGGCG 420

QY 421 CGCCCCCGCGGGCGCGAGGCGGCTCCCTCCAGCGCTGGCTGGAGCGCATGCGCGGACC 480

Db 421 CGCCCCCGCGGGCGCGAGGCGGCTCCCTCCAGCGCTGGCTGGAGCGCATGCGCGGACC 480

QY 481 TTGAGAGAGCCACGCTGCTGCGCGCGCGACATCTGGCTAGCGTTCGGTGGTTC 540

Db 481 TTGAGAGAGCCACGCTGCTGCGCGCGCGACATCTGGCTAGCGTTCGGTGGTTC 540

QY 541 GTGATCGTGTCCATGTGTGCTGTGCGCGCGAGCAGCTTGCCTGCGGCGCAACGAGCC 600

Db 541 GTGATCGTGTCCATGTGTGCTGTGCGCGCGAGCAGCTTGCCTGCGGCGCAACGAGCC 600

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QY 601 GCCGACACCGCAGCCTGTGATGACCGGAGCA----- 631
DB 601 GCCGACACCGCAGCCTGTGATGACCGGAGCAAGTACTCCGCGGCCCTCGGAGGAGGCC 660
QY 632 ----GGAATAATTGAAGCTATCTGCTAGTGGTGGTTCCTCCGAGTGCATCGTGGGTTTC 697
DB 661 TCCGGGATTAATTGAAGCTATCTGCTAGTGGTGGTTCCTCCGAGTGCATCGTGGGTTTC 720
QY 688 ATTGTCTCAAAAACAAGTGAGTTTGTCAAGAGACCCCTGAACATCATTTACTG 747
DB 721 ATTGTCTCAAAAACAAGTGAGTTTGTCAAGAGACCCCTGAACATCATTTACTG 780
QY 748 GCAATCAGCGGTATATACATCTCTGTTGTATGACAGTGTTCACAGCGGAATCTCAA 807
DB 781 GCAATCAGCGGTATATACATCTCTGTTGTATGACAGTGTTCACAGCGGAATCTCAA 840
QY 808 CTCACAGAGGCTGGAGTCACTTGGAGTACTTGAATGATGAGATTTTGGGTGATT 867
DB 841 CTCACAGAGGCTGGAGTCACTTGGAGTACTTGAATGATGAGATTTTGGGTGATT 900
QY 868 AGCTTGGCGGTCACTTCAATGGTCTTCAGACACTCGGTTTGACTCTCAAACTGTCTAC 927
DB 901 AGCTTGGCGGTCACTTCAATGGTCTTCAGACACTCGGTTTGACTCTCAAACTGTCTAC 960
QY 928 CAAGAGATGGTTATCTTACTTGTCTTCTTCTTGTGTCATGGCAATCTTTAGTGCACTT 987
DB 961 CAAGAGATGGTTATCTTACTTGTCTTCTTCTTGTGTCATGGCAATCTTTAGTGCACTT 1020
QY 988 TCTCAGCTTCTTGAACATGGGCTGGACCTGGAACATCCAAACAGGACTTTACGAGCAAT 1047
DB 1021 TCTCAGCTTCTTGAACATGGGCTGGACCTGGAACATCCAAACAGGACTTTACGAGCAAT 1080
QY 1048 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1107
DB 1081 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1108 CTTATCACAGTGCCTGGAGAAATCTTGGAGAGTTTGTGTCAGTGAATTTGTTCTA 1167
DB 1141 CTTATCACAGTGCCTGGAGAAATCTTGGAGAGTTTGTGTCAGTGAATTTGTTCTA 1200
QY 1168 TTGGATTAACCTATCACTTTATCTACCATAGCTTTGCTAGTGTATCATGACCTCAAG 1227
DB 1201 TTGGATTAACCTATCACTTTATCTACCATAGCTTTGCTAGTGTATCATGACCTCAAG 1260
QY 1228 TTTAGATCTGCTAGGTATAGTAGGAGCCTCTCCACTGAATTCCTGAAT 1275
DB 1261 TTTAGATCTGCTAGGTATAGTAGGAGCCTCTCCACTGAATTCCTGAAT 1308

RESULT 6
ID ABK83228
XX ABK83228 standard; cDNA; 2235 BP.
AC ABK83228;
XX
XX
DT 27-AUG-2002 (first entry)
DE Human transporter and ion channel, TRICH19, Incyte ID 7482060CB1, cDNA.
XX
XX Human; ss: gene; transporter and ion channel; TRICH; transport disorder;
XX neurological disorder; muscle disorder; immunological disorder; cancer;
XX scleroderma; systemic lupus erythematosus; allergy; leukaemia;
XX cell proliferative disorder; cervical cancer; breast cancer;
XX neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;
XX myotonic dystrophy; catatonia; endocrine disorder; diabetes;
XX Grave's disease; gastrointestinal disorder; Crohn's disease;
XX renal disorder; Good pasture's syndrome; viral infection; cirrhosis;
XX bacterial infection; fungal infection; parasitic infection;
XX protozoal infection; helminthic infection; cardiovascular disorder;
XX atherosclerosis; hepatic disease.
OS Homo sapiens.
XX
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PN WO200240541-A2.
XX 23-MAY-2002.
XX
XX 25-OCT-2001; 2001WC-US046055.
XX
XX 27-OCT-2000; 2000US-0243989P.
XX 03-NOV-2000; 2000US-0245904P.
XX 09-NOV-2000; 2000US-0247673P.
XX 17-NOV-2000; 2000US-0249661P.
XX 20-NOV-2000; 2000US-0252323P.
XX 01-DEC-2000; 2000US-0250790P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Tang YT, Yue H, Nguyen DB, Hafalia AJA, Elliott VS, Lu Y;
XX Walia NK, Yao MG, Baughn MR, Gandhi AR, Ding L, Sanjanwala M;
XX Ramkumar J, Arvizu C, Gietzen KJ, Lal BG, Azimzai Y, Khan FA;
XX Tiangavelu K, Thornton M, Lu DAM, Tribouley CM, Warren BA, Ison CH;
XX Das D, Raumann BE, Policky JL, Kearney L;
XX WPI; 2002-463570/49.
XX P-PSDB; ABG61549.
XX
XX New transporters and ion channels (TRICH) polypeptides, useful for
XX diagnosing, preventing, and treating disorders associated with an
XX abnormal expression or activity of TRICH, e.g. immunological, muscular or
XX renal disorders.
XX
XX Claim 5; Page 176-177; 178pp; English.
XX
XX The invention relates to human transporters and ion channels (TRICH)
XX polypeptides, a naturally occurring amino acid sequence 90 % identical to
XX TRICH, a biologically active fragment of TRICH or an immunogenic fragment
XX of TRICH. Also included are an isolated polynucleotide encoding TRICH, a
XX recombinant polynucleotide comprising a promoter sequence operably linked
XX to the TRICH polynucleotide, a cell transformed with the recombinant
XX polynucleotide, a transgenic organism comprising the recombinant
XX polynucleotide, an isolated antibody that binds specifically to TRICH,
XX and screening for compounds which bind to TRICH. The polypeptides are
XX TRICH expression or are antagonists of TRICH. The polypeptides are
XX useful for diagnosing, treating, and preventing transport, neurological,
XX muscle, immunological disorders (e.g. scleroderma, systemic lupus
XX erythematosus, allergies), cell proliferative disorders such as cancers
XX (e.g. leukaemia, cervical or breast cancers), neurodegenerative disorders
XX (e.g. Parkinson's disease, Alzheimer's disease), muscular disorders (e.g.
XX myotonic dystrophy, catatonia), endocrine disorders (e.g. diabetes,
XX Grave's disease), gastrointestinal disorders (e.g. Crohn's disease),
XX renal disorders (e.g. Good pasture's syndrome), viral, bacterial, fungal,
XX parasitic, protozoal and helminthic infections, cardiovascular disorders
XX (e.g. atherosclerosis), or hepatic diseases (e.g. cirrhosis) and many
XX other diseases and disorders detailed in the specification. They can also
XX be used in assessing the effects of exogenous compounds on the expression
XX of nucleic acid and amino acid sequences of transporters and ion
XX channels. TRICH or its fragments may also be used in screening for
XX compounds that specifically bind to and modulate the activity of TRICH.
XX The polynucleotides can be used to create knock-in humanised animals or
XX transgenic animals to model human disease. The present sequence encodes a
XX TRICH protein
XX
XX Sequence 2235 BP; 395 A; 657 C; 715 G; 468 T; 0 U; 0 Other;
```

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Query Match 92.2%; Score 1178.4; DB 6; Length 2235;
Best Local Similarity 97.8%; Pred. No. 3.5e-239;
Matches 1223; Conservative 0; Mismatches 6; Indels 21; Gaps 2;

QY 1 ATGACCTTCGGGCGGAGCGGGCGGCGCTCGGTGGTCTGCTGAACGTGGCGGCGCCCGGTAT 60
DB 428 ATGACCTTCGGGCGGAGCGGGCGGCGCTCGGTGGTCTGCTGAACGTGGCGGCGCCCGGTAT 487
QY 61 TCGCTGTCCCGGAGCGTGTCTGAAGGACTTCCCGCTCGCGCGGTGTGAGCGCGGTGACGGC 120
DB 488 TCGCTGTCCCGGAGCGTGTCTGAAGGACTTCCCGCTCGCGCGGTGTGAGCGCGGTGACGGC 547
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PI Patturajan M, Liu X, Gusev VA, Li L, Vernet CAM, Zerhusen BD;
PI Gorman L, Shenoy SG, Pena CE, Smithson G, Burgess CE, Gerlach V;
PI Padigaru M, Shimkets RA, Gastelli EA, Tappier RJ, Casman SJ, Ji W;
PI Anderson DW, Leite KW, Rastelli L, Edinger SR, Stone DJ;
PI Macdougall JR, Rothenberg ME, Mazur A, Millet I, Feyman JA;
PI Ellemann K;
XX
DR WPI; 2003-046858/04.
DR P-P8DB; ABU54564.
XX
XX New isolated NOVX polypeptide useful for treating atherosclerosis,
PT metabolic disorders, diabetes, obesity, infectious disease, anorexia,
PT neurodegenerative disorders, Alzheimer's disease and cancer.
XX
PS Claim 17; Page 136; 666pp; English.
XX
CC The invention relates to human polypeptides, termed NOVX, and the
CC polynucleotides encoding them. The polypeptides and polynucleotides are
CC useful for diagnosing disease, and screening for potential therapeutic
CC agents. The sequences are useful for treating metabolic disorders,
CC cardiomyopathy, diabetes, hypertension, congenital heart defects, aortic
CC stenosis, atrial septal defect (ASD), atrioventricular canal defect,
CC ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular
CC septal defect (VSD), valve diseases, tuberculous sclerosis, scleroderma,
CC atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative
CC disorders, Alzheimer's disease, Parkinson's disease, immune disorders,
CC haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease
CC and cancer. Sequences ABX72170-ABX72275 represent human NOVX
CC polynucleotides of the invention
XX
SQ Sequence 1651 BP; 292 A; 476 C; 510 G; 373 T; 0 U; 0 Other;

Query Match 86.0%; Score 1099.4; DB 7; Length 1651;
Best Local Similarity 91.4%; Pred. No. 1.6e-222;
Matches 1231; Conservative 0; Mismatches 11; Indels 105; Gaps 2;

QY 1 ATGACCTTCGGGCGCAGCGGGCGCGCTCGGTGGTCTGAACGTGGGGCGCGCGGTAT 60
DB 58 ATGACCTTCGGGCGCAGCGGGCGCGCTCGGTGGTCTGAACGTGGGGCGCGCGGTAT 117
QY 61 TCGCTGTCCCGGAGCTGCTGAAGACCTTCGCGCTGCGCGCGGTGAGCGCGCTGACCGC 120
DB 118 TCGCTGTCCCGGAGCTGCTGAAGACCTTCGCGCTGCGCGCGGTGAGCGCGCTGACCGC 177
QY 121 TCGCGCTCGGAGCGAGCTGCTCGAGGTGTCGAGGACTAGCAGCGGCGGCGAGCAG 180
DB 178 TCGCGCTCGGAGCGAGCTGCTCGAGGTGTCGAGGACTAGCAGCGGCGGCGAGCAG 237
QY 181 TACTTCTTCGACCGGCACTCGAGGCGCTTCGCGCTTCATCTGCTACGTCGGGGCGCAC 240
DB 238 TACTTCTTCGACCGGCACTCGAGGCGCTTCGCGCTTCATCTGCTACGTCGGGGCGCAC 297
QY 241 GCGAGCTGCGCTTCGCGCGCGGATGTGCGAGCTCTCTTCTACAGAGATGATCTAC 300
DB 298 GCGAGCTGCGCTTCGCGCGCGGATGTGCGAGCTCTCTTCTACAGAGATGATCTAC 357
QY 301 TGGGCGCTTGGAGGCGCGCCTCGAGTACTGCTCCAGCGCGCGCTCGAGCGCGCATG 360
DB 358 TGGGCGCTTGGAGGCGCGCCTCGAGTACTGCTCCAGCGCGCGCTCGAGCGCGCATG 417
QY 361 TCGCACCTACCTTCTACCTGCGCGAGCGCGCGCTGCTGGCGCGCGAGCGCG 420
DB 418 TCGCACCTACCTTCTACCTGCGCGAGCGCGCGCTGCTGGCGCGCGAGCGCG 477
QY 421 CGCCCGCGCGGCGC----- 434
DB 478 CGCCCGCGCGGCGGCGCTCCCTCCAGGCGCTGGCTGGAGCGCATGCGCGGACCTT 537
QY 435 -----CGAGCGCGCTCCCTCCAGGCGCTGGCTGGAGCGCATGCGCGGACCTT 483
DB 538 CGAGGAGCGCGCTGCTGCTGGCGCGGCGCTGGCTGGAGCGCATGCGCGGACCTT 597
QY 484 GAGGAGCGCGCTGCTGCTGGCGCGGCGCATGCTGGCTAGCGTGGCTGGTTCGTG 543

DB 598 GAGGAGCGCGCTGCTGCTGGCGCGCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTG 657
QY 544 ATCGTGTCCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 603
DB 658 ATCGTGTCCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 717
QY 604 GACAAACCGCAGCGCTGATGACCGGAG----- 629
DB 718 GACAAACCGCAGCGCTGATGACCGGAGCGAGTACTCCGCGCGCGCTGGGAGGAGCGCTCC 777
QY 630 -----CAGGATAATGAAGCTATCTGATGATGATGATGATGATGATGATGATGATG 675
DB 778 GGGTGTTCCTCTTGACAGGATAATGAAGCTATCTGATAGTGTGTGTGTGTGTGTGTGTGT 837
QY 676 ATCGTGTGAGTTCATGCTCCAAACCAAGTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 735
DB 838 ATCGTGTGAGTTCATGCTCCAAACCAAGTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 897
QY 736 ATTGAATTTACTGCAATACGCGCTATTAATCATCTCTGTGTGTGTGTGTGTGTGTGTGTGT 795
DB 898 ATTGAATTTACTGCAATACGCGCTATTAATCATCTCTGTGTGTGTGTGTGTGTGTGTGTGT 957
QY 796 GAGNACTCTCAACTCCAGAGCGGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 855
DB 958 GAGNACTCTCAACTCCAGAGCGGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1017
QY 856 TTTTGGGTGATTAAAGCTTGGCGGTCACTTCATTTGGTCTTCAGACACTTCGCTTTGACCTCTC 915
DB 1018 TTTTGGGTGATTAAAGCTTGGCGGTCACTTCATTTGGTCTTCAGACACTTCGCTTTGACCTCTC 1077
QY 916 AAACGTTGCTACCGAGAGATGTTATGTTACTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 975
DB 1078 AAACGTTGCTACCGAGAGATGTTATGTTACTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1137
QY 976 TTTAGTGCATCTTCTCAGCTTCTTGAACCTGCGCTGGACCTGGAACATCCAAACAGGAC 1035
DB 1138 TTTAGTGCATCTTCTCAGCTTCTTGAACCTGCGCTGGACCTGGAACATCCAAACAGGAC 1197
QY 1036 TTTACAGCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTAT 1095
DB 1198 TTTACAGCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTAT 1257
QY 1096 GGAGATATGATCTATCAGTGTGCTGAGTGTGCTGAGGAAATCTTGGAGAGTGTGTGTGTGTGT 1155
DB 1258 GGAGATATGATCTATCAGTGTGCTGAGTGTGCTGAGGAAATCTTGGAGAGTGTGTGTGTGTGT 1317
QY 1156 GGAATTTCTTATTGGCAATACCTATCCTTTTATCTTACCATAGCTTTGTGCAAGTGTAT 1215
DB 1318 GGAATTTCTTATTGGCAATACCTATCCTTTTATCTTACCATAGCTTTGTGCAAGTGTAT 1377
QY 1216 CATGAGCTCAAGTTTATGATCTGCTAGG 1242
DB 1378 CATGAGCTCAAGTTTATGATCTGCTAGG 1404

RESULT 8
ABZ24716
ID ABZ24716 standard; cDNA; 5775 BP.
XX
AC ABZ24716;
XX
DT 07-APR-2003 (first entry)
XX
DE Murine potassium channel subunit Kv10.1 - flag sequence.
XX
KW Potassium channel; Kv10.1; mouse; transgenic mouse; gene; ss.
XX
OS Mus musculus.
XX
PH Key Location/Qualifiers
PT misc_feature 3424..4749
FT /*tag= a

FT XX /note= "flag"

PN WO200296944-A2.

XX 05-DEC-2002.

PD 31-MAY-2002; 2002WO-BP006082.

XX 31-MAY-2001; 2001EP-00202060.

XX (VLA-) VLAMS INTERUNIVERSITAIR INST BIOTECHNOG.

XX Snyder DJ, Otschysch N, Raes A, Van Hoorick D;

PI MPI; 2003-140443/13.

XX Novel voltage-gated heterotetrameric potassium channel useful for

PT diagnosing, preventing and/or treating excitability disorders, comprises

PT Kv2.1, Kv3.1, Kv5.1, Kv6.3, Kv10.1 or Kv11.1 potassium channel subunits.

XX Example; Page 80-82; 93pp; English.

XX The present sequence is that of a construct used in the creation of a

CC potassium channel subunit Kv10.1 transgenic mouse. In an example from the

CC invention, the construct was microinjected into the pronucleus of a one-

CC cell embryo, and then incubated in a foster mother of the FVB/Nlco mouse

CC strain. The invention provides novel, voltage-gated heterotetrameric

CC potassium channels comprising Kv2.1, Kv3.1, Kv5.1, Kv6.3, Kv10.1 or

CC Kv11.1. These are useful for identifying a molecule that increases or

CC decreases ion flux through the potassium channel (claimed). Nucleic acids

CC encoding the heterotetrameric potassium channels are used in gene therapy

CC to prevent or treat congenital or acquired excitability disorders

CC including epilepsy, long QT syndrome, muscular ataxia, and arrhythmia

CC (all claimed).

XX SQ Sequence 5775 BP; 1327 A; 1530 C; 1532 G; 1386 T; 0 U; 0 Other;

Query Match 83.7%; Score 1070; DB 7; Length 5775;

Best Local Similarity 90.3%; Pred. No. 3.2e-216;

Matches 1183; Conservative 0; Mismatches 85; Indels 42; Gaps 2;

QY 1 ATGACCTTCGGCGCGAGCGGGCGGCTCGGTGCTGCTGAACTGGCGCGCGCGGTAT 60

DB 3424 ATGACCTTCGGCGCGCGGGCGGCTCGGTGCTGCTGAACTGGCGCGCGCGGTAT 3483

QY 61 TCCTCTCCCGGAGCTGCTGAGGACTTCCGCTCGCGCGGCTGAGCGCGGTGCACGCG 120

DB 3484 TCCTCTCCCGGAGCTGCTCAAGGACTTCCGCTCGCGCGGCTGAGCGCGGTGCACGCG 3543

QY 121 TGCCGCTTCGAGCGCGACGCTGCTCGAGGTGTGCGAGCTACGACCGGAGCGCAACGAG 180

DB 3544 TGCCGCTTCGAGCGCGACGCTGCTCGAAGTGTGCGAGCTACGACCGGAGCGCAACGAG 3603

QY 181 TACTTCTTGACCGGCGACTCGGAGGCTTCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 240

DB 3604 TACTTCTTGACCGGCGACTCGGAGGCTTCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 3663

QY 241 GGCAAGCTGGCTTCGCGCGCGGAGTGTGCGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300

DB 3664 GGCAAGCTGGCTTCGCGCGCGGAGTGTGCGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3723

QY 301 TGGGGCTTGAGGGCGCGACCTCTGAGTACTGTGCTGCGAGCGCGGCTCTGACACCGCATG 360

DB 3724 TGGGGCTTGAGGGCTGCGACCTCTGAGTACTGTGCTGCGAGCGCGGCTCTGACACCGCATG 3783

QY 361 TCGGACACCTTACACCTTCTACTCGGCGGAGCGCGGCGGCTGTGCGCGCGCGACGAGCGG 420

DB 3784 TCGGACACCTTACACCTTCTACTCGGCGGAGCGCGGCGGCTGTGCGCGCGCGACGAGCGG 3834

QY 421 CGCCCGCGGCGCGAGCGGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480

DB 3835 CGTCCGCGCGGAGCGCGGCGGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3894

QY 481 TTCGAGAGCCACGCTGCTGCTGCGCGCGCAGATCCTGGCTAGCTGCGGTGGTTC 540

DB 3895 TTCGAGAGCCACGCTGCTGCTGCGCGCGCAGATCCTGGCTAGCTGCGGTGGTTC 3954

QY 541 GTGATCGTGTCCATGCTGCTGCTGCGCGCAGCAGCTTGGCCGCTGCGGCAACGAGCC 600

DB 3955 GTGATCGTGTCCATGCTGCTGCGCGCAGCAGCTTGGCCGCTGCGGCGGTT 4014

QY 601 GCCGACAAACCGAGCTGCTGCTGCGCGGCAACGAGCC 631

DB 4015 GCTGACAAACCGAGCTGCTGCTGCGCGGCAACGAGCC 4074

QY 632 ----GGATAATTGAAGCTATCTGCATAGGTTGGTTTCACTTGGCCGCTGCGGAGGAAACC 687

DB 4075 TCCGGGATAATTGAAGCTATCTGCATAGGTTGGTTTCACTTGGCCGCTGCGGAGGAAACC 4134

QY 688 ATTGTCTCCAAAACCAAGTGTGCTGCTGCGCGCAGCAGCTTGAACATCATTTGATTTACTG 747

DB 4135 ATGCTCTCCAAAACCAAGTGTGCTGCTGCGCGCAGCAGCTTGAACATCATTTGATTTACTG 4194

QY 748 GCAATCAGCGCGTATTACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 807

DB 4195 GCAATCAGCGCGTATTACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4254

QY 808 CTCGAGAGGGCTGAGTCACTTGGAGGTACTTAGAATGATGAGGATTTTGGGGTATT 867

DB 4255 CTCGAGAGGGCTGAGTCACTTGGAGGTACTTAGAATGATGAGGATTTTGGGGTATT 4314

QY 868 AGCTTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 927

DB 4315 AGCTTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4374

QY 928 CGAGAGTGGTATTGTTTACTTGTCTTCACTTGTGTTGCCATGGCAATCTTTAGTGCACTT 987

DB 4375 CGAGAGTGGTATTGTTTACTTGTCTTCACTTGTGTTGCCATGGCAATCTTTAGTGCACTT 4434

QY 988 TCTCAGTCTTCTGAAACATGGGCTGGACCTGGAACATCCAAAGGACCTTACAGCAAT 1047

DB 4435 TCTCAGTCTTCTGAAACATGGGCTGGACCTGGAACATCCAAAGGACCTTACAGCAAT 4494

QY 1048 CCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1107

DB 4495 CCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4554

QY 1108 CCTATCAGTGGCTGGAAGAAATCTTGGAGGAGTGTGTTGCTCAGTGGAAATGTTCTA 1167

DB 4555 CCTATCAGTGGCTGGAAGAAATCTTGGAGGAGTGTGTTGCTCAGTGGAAATGTTCTG 4614

QY 1168 TTGGCATTTACCTATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1227

DB 4615 TTGGCATTTACCTATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 4674

QY 1228 TTTAGATCTGCTAGGTATAGTAGAGCTCTCCAGTGAATTCCTGAATTA 1277

DB 4675 TTTAGATCTGCTAGGTATAGTAGAGCTCTCCAGTGAATTCCTGAATTA 4724

RESULT 9

AAD33662

ID AAD33662 standard; cDNA; 2312 BP.

XX

XX AAD33662;

XX

XX 01-JUL-2002 (first entry)

XX

XX Human TRICH-17 cDNA.

XX

XX Human; transporter and ion channel; TRICH-17; transport disorder; angina;

XX

XX amyotrophic lateral sclerosis; cystic fibrosis; neuromuscular disorder;

XX

XX cardiac disorder; polymyositis; diabetes; neurological disorder; cancer;

XX

XX depression; schizophrenia; anaemia; Wilson's disease; Cushing's disease;

XX

XX cell proliferated disorder; infertility; arteriosclerosis; gene therapy;

XX

XX Alzheimer's disease; Parkinson's disease; Huntington's disease; allergy;

KW myasthenia gravis; multiple sclerosis; metabolic disorder; hypertension;
 KW acquired immune deficiency syndrome; immunological disorder; scleroderma;
 KW endocrine disorder; autoimmune thyroiditis; rheumatoid arthritis; goitre;
 KW cardiac myopathy; amnesia; toxic myopathy; Addison's disease; infection;
 KW epilepsy; mental disorder; myocarditis; Crohn's disease; Grave's disease;
 KW muscle disorder; stroke; dementia; anxiety; AIDS; asthma; cirrhosis;
 KW gene, ss.
 XX Homo sapiens.
 OS

XX Key Location/Qualifiers
 FH 325..1845
 FT CDS /*tag= a
 FT /*product= "Human TRICH-17 protein"
 XX W0200212340-A2.
 XX 14-FEB-2002.
 XX 01-AUG-2001; 2001WO-US024217.
 XX 03-AUG-2000; 2000US-0223269P.
 XX 10-AUG-2000; 2000US-0224456P.
 XX 18-AUG-2000; 2000US-0226410P.
 XX 25-AUG-2000; 2000US-0228140P.
 XX 31-AUG-2000; 2000US-0230067P.
 XX 08-SEP-2000; 2000US-0231434P.
 XX (INCY-) INCYTE GENOMICS INC.
 XX Yue H, Thornton M, Ramkumar J, Tang Y, Azimzai Y, Baughn MR;
 PI Yang J, Yao MG, Lal P, Wallia NK, Gandhi AR, Hafalia AJA, Nguyen DB;
 PI Patterson C, Elliott VS, Tribouley CM, Lu DAM, Xu Y, Reddy R;
 PI Hernandez R, Borowsky ML, Lo TP, Lu Y, Policky JL, Greene BD;
 PI Sanjanwala MS, Raumann BE, Burford N, Ison CH, Lee EA, Ding L;
 PI Das D, Kallick DA, Khan FA, Seilhamer JJ;
 XX WPI; 2002-206330/26.
 DR P-PSDB; AAE21173.
 DR

XX New human transporters and ion channels polypeptides and polynucleotides
 PT for diagnosing, preventing or treating transport, neurological, muscle,
 PT immunological and cell proliferative disorders.
 XX Claim 91; Page 217; 230pp; English.
 PS
 XX The invention relates to human transporter and ion channel polypeptides
 CC designated TRICH and nucleic acid molecules encoding such polypeptides.
 CC TRICH sequences are useful for diagnosis, treatment and prevention of
 CC transport, muscle, neurological, immunological and cell proliferative
 CC disorders. Transport disorders include akinesia, amyotrophic lateral
 CC sclerosis, ataxia telangiectasia, cystic fibrosis, Becker's muscular
 CC dystrophy, diabetes mellitus, diabetes insipidus, myasthenia gravis,
 CC myocarditis, prostate cancer, cardiac disorders associated with transport
 CC e.g. polymyositis, bradyarrhythmia, dermatomyositis, angina, neurological
 CC disorders associated with transport e.g. amnesia, bipolar disorder,
 CC depression, Tourette's disorder, schizophrenia, other disorders
 CC associated with transport e.g. neurofibromatosis, sickle cell anaemia,
 CC Wilson's disease, cataracts, infertility, hyperglycaemia, hypoglycaemia,
 CC goitre, Cushing's disease, hypercholesterolaemia and cystinuria. Cell
 CC proliferated disorders include cancer, actinic keratosis, cirrhosis,
 CC arteriosclerosis, atherosclerosis, bursitis, hepatitis and psoriasis.
 CC Neurological disorders include Alzheimer's, Pick's and Parkinson's
 CC disease, amyotrophic lateral sclerosis, epilepsy, stroke, Huntington's
 CC disease, multiple sclerosis, dementia and other extrapyramidal disorder,
 CC motor neuron disorder, prion disease, metabolic disease of the nervous
 CC system and other developmental disorders of the central nervous system,
 CC neuromuscular disorders, metabolic, endocrine and toxic myopathies,
 CC periodic paralysis, mental disorders including mood, anxiety; and
 CC immunological disorders include acquired immune deficiency syndrome
 CC (AIDS), adult respiratory distress syndrome, Addison's disease,
 CC allergies, asthma, atherosclerosis, osteoporosis, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, Crohn's disease, atopic dermatitis,

CC Grave's disease, glomerulonephritis, rheumatoid arthritis, scleroderma,
 CC systemic lupus erythematosus, systemic sclerosis, ulcerative colitis,
 CC haemodialysis, uveitis; viral, bacterial, fungal, parasitic, protozoal,
 CC helminthic infections and trauma; and muscle disorders include cardiac
 CC myopathy, myocarditis, polymyositis, arrhythmias and hypertension. The
 CC TRICH polynucleotides are used in gene therapy. The present sequence is
 CC human TRICH-17 cDNA
 XX
 XX Sequence 2312 BP; 475 A; 607 C; 674 G; 556 T; 0 U; 0 Other;

Query Match Similarity 66.2%; Score 846.6; DB 6; Length 2312;
 Best Local Similarity 93.3%; Pred. No. 4e-169;
 Matches 885; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 330 CTGCTGCCAGCGCGCCCTCGACGACCGCATGTCCGACACCTTACTCTACCTCGGCGGA 389
 DB 897 CTGCGCTCGAGCGCGACGCTGCTCGAGGTGTGCGACGACTACGCCGCGACGCA 956
 QY 390 CGAGCGGGGGTGTGGGCGCGGACGAGGCGCGCCCGGGGGCCGAGGCGGCTCCCTC 449
 DB 957 GTACTTCTTCACCGGCACCTCGAGGGCTTCGGGCTTCATCTGCTACGCGGCTCCCTC 1016
 QY 450 CAGGCGCTGGCTGGAGCGCATGCGCGGACCTTCGAGGAGCCACGCTGCTGCGTGGCGGC 509
 DB 1017 CAGGCGCTGCTGGAGCGCATGCGCGGACCTTCGAGGAGCCACGCTGCTGCGTGGCGGC 1076
 QY 510 GCAGATCCTGCTAGCTGTGCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 569
 DB 1077 GCAGATCCTGCTAGCTGTGCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1136
 QY 570 CAGCACCTTCCCGACTGCGGCGGACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGAG 629
 DB 1137 CAGCACCTTCCCGACTGCGGCGGACCGCGGCGGCGGCGGCGGCGGCGGCGGAG 1196
 QY 630 CAGGATAATGAAGCTATCTGCTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 689
 DB 1197 CAGGATAATGAAGCTATCTGCTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1256
 QY 690 TGCTCCAAAAACAAGTGTGAGTTTGTCAAGACCCCTGAAACATCATTTACTTCTGCTG 749
 DB 1257 TGCTCCAAAAACAAGTGTGAGTTTGTCAAGACCCCTGAAACATCATTTACTTCTGCTG 1316
 QY 750 AATCACCCCTTATATACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 809
 DB 1317 AATCACCCCTTATATACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1376
 QY 810 CCAGAGGCTGGAGTCACTTGGAGGTTACTTGAATGATGAGGATTTTGGGTGATTA 869
 DB 1377 CCAGAGGCTGGAGTCACTTGGAGGTTACTTGAATGATGAGGATTTTGGGTGATTA 1436
 QY 870 GCTTGCCCGTCACTTCACTTGGTCTTCAGACACTCGGTTTGAATCTCAAAAGTTGCTACCG 929
 DB 1437 GCTTGCCCGTCACTTCACTTGGTCTTCAGACACTCGGTTTGAATCTCAAAAGTTGCTACCG 1496
 QY 930 AGAGATGGTTATGTTACTTGTCTTCAATTTGTGTTGCCATGGCAATCTTTAGTGCATTTTC 989
 DB 1497 AGAGATGGTTATGTTACTTGTCTTCAATTTGTGTTGCCATGGCAATCTTTAGTGCATTTTC 1556
 QY 990 TCAGCTCTTGACATGGCTGACCTGGAACATCCAAAGGATTTTACGAGGATTC 1049
 DB 1557 TCAGCTCTTGACATGGCTGACCTGGAACATCCAAAGGATTTTACGAGGATTC 1616
 QY 1050 TGCTGCTGCTGGTGGTGAATATCTCTATGACTAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 1109
 DB 1617 TGCTGCTGCTGGTGGTGAATATCTCTATGACTAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 1576
 QY 1110 TATCAGAGTCCCTGGGAAGAAATCTTGGAGAGTTTGTGTTGTCAGTGGAAATTTCTTCTATT 1169
 DB 1677 TATCAGAGTCCCTGGGAAGAAATCTTGGAGAGTTTGTGTTGTCAGTGGAAATTTCTTCTATT 1736
 QY 1170 GGCATTACCTATCATTCTTTTATCTACCATAGCTTTGTCAGTGTATCATGAGCTCAAGTT 1229
 DB 1737 GGCATTACCTATCATTCTTTTATCTACCATAGCTTTGTCAGTGTATCATGAGCTCAAGTT 1796

QY 1230 TAGATCTGCTAGTATAGTAGGAGCTCTCCACTGAAATTCCTGAATTA 1278
 Db 1797 TAGATCTGCTAGTATAGTAGGAGCTCTCCACTGAAATTCCTGAATTA 1845

RESULT 10

ADD01469
 ID ADD01469 standard; cDNA; 950 BP.
 XX
 AC ADD01469;
 XX
 XX 01-JAN-2004 (first entry)
 XX
 DE Mouse TCH136 cDNA sequence fragment.
 XX
 KW ds; antidiabetic; antilipemic; antiarteriosclerotic; nootropic;
 KW neuroprotective; anabolic; antiinflammatory; immunosuppressive;
 KW cytoskeletal; antiasthmatic; antiarthritic; cerebroprotective;
 KW antiallergic; dermatological; cardiant; antiParkinsonian; neuroleptic;
 KW glucose transporter; potassium ion channel protein; diabetes;
 KW hyperlipemia; arteriosclerosis; digestive disorder; Crohn's disease;
 KW colitis; gastritis; ileitis; rectal inflammation; inflammatory disease;
 KW sepsis; prostatic hypertrophy; reproductive disorder; pneumonia;
 KW meningitis; hepatitis; myocarditis; asthma; immune disorder;
 KW multiple sclerosis; rheumatoid arthritis; Sjogren's disease; lupus;
 KW allergy; hay fever; allergic rhinitis; anaphylactic shock;
 KW atopic dermatitis; circulatory disorder; heart failure; cancer;
 KW Alzheimer's disease; Parkinson's disease; schizophrenia;
 KW hyperprolactinemia; Cushing's disease; vesicular glutamate transporter.

XX Mus sp.

XX WO2003054190-A1.

XX 03-JUL-2003.

XX 19-DEC-2002; 2002WO-JP013290.

XX 21-DEC-2001; 2001JP-00389361.

XX 25-DEC-2001; 2001JP-00392577.

XX 26-DEC-2001; 2001JP-00394947.

XX 26-DEC-2001; 2001JP-00395467.

XX 08-FEB-2002; 2002JP-00030010.

XX 08-FEB-2002; 2002JP-00033095.

XX 06-JUN-2002; 2002JP-00165336.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Nakanishi A, Sagiya Y, Uno Y;

XX WPI; 2003-541817/51.

XX Glucose transporter TCH099, vesicular glutamate transporter TCH177 and potassium channel protein TCH136 and DNA encoding them for diagnosis, treatment and prevention of diabetes, hyperlipemia, arteriosclerosis and digestive disorders.

XX Example 21; SEQ ID NO 105; 211pp; Japanese.

XX The invention relates to a novel glucose transporter TCH099, vesicular glutamate transporter TCH177 and voltage-dependent potassium ion channel protein TCH136. The sequences are useful in the treatment, prevention and diagnosis of a broad range of diseases including diabetes, hyperlipemia, arteriosclerosis, digestive disorders (such as Crohn's disease, colitis, gastritis, ileitis and rectal inflammation), inflammatory diseases, sepsis, prostatic hypertrophy, reproductive disorders, pneumonia, meningitis, hepatitis, myocarditis, asthma, immune disorders (such as multiple sclerosis, rheumatoid arthritis, Sjogren's disease and lupus), allergies (such as hay fever, allergic rhinitis, anaphylactic shock and atopic dermatitis), circulatory disorders (such as heart failure), cancer (such as cancer of the lung, kidney, liver, ovary, prostate, stomach, pancreas, bladder, breast, fallopian tubes or colon), central nervous

CC system diseases (such as Alzheimer's, Parkinson's and schizophrenia) and
 CC secretory disorders (such hyperprolactinemia and Cushing's disease). This
 CC sequence represents a fragment of the cDNA sequence for the novel mouse
 CC voltage-dependent potassium ion channel protein TCH136.
 XX
 SQ Sequence 950 BP; 182 A; 263 C; 269 G; 230 T; 0 U; 6 Other;

Query Match 57.1%; Score 729.8; DB 9; Length 950;
 Best Local Similarity 88.9%; Pred. No. 1.6e-144;
 Matches 848; Conservative 0; Mismatches 87; Indels 19; Gaps 5;

QY 294 GATCTACTGGGGCTGGAGGGCGGCGACCTCGAGTACTGTCCAGCGCGCGCTCCACGA 353
 Db 1 GATCTACTGGGGCTGGAGGGTGGCGACCTCGAGTACTGTCCAGCGCGCGCTCCACGA 60
 QY 354 CCGCATGTCGACACACCTTACTCGGGCGAGCGCGGGCGTGTGGCGCGCGA 413
 Db 61 CCGCATGTCGACACACCTTACTCGGGCGAGCGA-----GCTGGCGCGCGA 111
 QY 414 CGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 473
 Db 112 GCAGCCTCGTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 171
 QY 474 GCGACCTTCGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 533
 Db 172 GCGACCTTCGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 231
 QY 534 GGTCTTCGATCGTCCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 593
 Db 232 GGTCTTCGATCGTCCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 291
 QY 594 CGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 653
 Db 292 GCGCGTTCGATCGTCCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 351
 QY 654 AGGTTCGTTTCACTCGCGAGTGCATCGTGGTTCATTTGTTCCAAACAAAGTGTGAGTT 713
 Db 352 AGGTTCGTTTCACTCGCGAGTGCATCGTGGTTCATTTGTTCCAAACAAAGTGTGAGTT 411
 QY 714 TGTCAAGAGACCCCTGACATCATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 773
 Db 412 TGTCAAGAGACCCCTGACATCATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 471
 QY 774 GTTTCATGACAGTGTTCAGCGCGAGAACTCTCAACTCCAGAGGGCTGGAGTCACTTTGAG 833
 Db 472 GCTAATGACAGTGTTCAGCGCGAGAACTCTCAACTCCAGAGGGCTGGAGTCACTTTGAG 531
 QY 834 GGTACTTGAATGATGAGGATTTTTCGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 893
 Db 532 GGTCTCCGAATGATGCGGATCTTCTGGGTGATCAAGCTTGCCTGGCGCTTTCATTTGTT 591
 QY 894 TCAGACACTCGTTTGTACTCTCAACGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 953
 Db 592 GCAGACACTCGTTTGTACTCTCAACGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 651
 QY 954 CATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1013
 Db 652 CATCTGTTGCCATGCGCAATCTTTAGTGCACTCTCTCAGCTCCTTGAACATGCGCTGGA 711
 QY 1014 CCTGGAACATCCCAAGAGACTTTTACAGCATTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1073
 Db 712 CCTGGAACATCCCAAGAGACTTTTACAGCATTTCTGCTGCTGCTGCTGCTGCTGCTGCT 771
 QY 1074 CTCTATGACTACAGTGGCTATGAGATATGATCTTATCTTATCTTATCTTATCTTATCTT 1133
 Db 772 CTCTATAACTACAGTGGCTATGAGATATGATCTTATCTTATCTTATCTTATCTTATCTT 831
 QY 1134 TGG---AGAGTTCGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1186
 Db 832 TTGNAGAGAGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 891
 QY 1187 TTAT-CTACCATAGCTTTGTGCTGCTGTTTATCATGA--GCTCAAGTTTATGATCTG 1237

Db 892 TCATCCTACCATAGCTTTGTGAGTGTCTACACGAGGCTCAAGTTTAGATCGG 945

RESULT 11

ABQ49122

ID ABQ49122 standard; DNA; 1634 BP.

XX AC ABQ49122;

XX DT 12-JUL-2002 (first entry)

XX OLigonucleotide for detecting cytosine methylation SEQ ID NO 35713.

DE Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;

XX KW drug; side effect; cancer; central nervous system; cardiovascular;

XX KW gastrointestinal; respiratory system; single nucleotide polymorphism;

XX KW SNP; cell differentiation; ds.

XX OS Homo sapiens.

XX WO200218632-A2.

XX PD 07-MAR-2002.

XX 01-SEP-2001; 2001WO-EP010074.

XX 01-SEP-2000; 2000DE-01043826.

XX 05-SEP-2000; 2000DE-01044543.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K, Guetig D;

PI WPI; 2002-371829/40.

XX Determining the degree of cytosine methylation in genomic DNA, useful for

PT diagnosis and prognosis, comprises selective hybridization of amplicons

PT from chemically treated DNA.

XX Claim 12; 56pp + Sequence Listing; 56pp; German.

XX This invention describes a novel method for determining the degree of

CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a

CC genomic sample of DNA. The sample is treated chemically to convert

CC cytosine (C) but not methylated C, to uracil, then part of the genomic

CC DNA that contains the target C is amplified to form a labeled amplicon.

CC The amplicon is hybridised to two classes, each with at least one member,

CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the

CC degree of hybridisation to both classes is determined from the label on

CC the amplicon. From the ratio of labels hybridised to the two classes of

CC oligomers, the degree of methylation is calculated. The method is used:

CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs

CC and of a wide range of diseases, e.g. cancer, disorders of the central

CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,

CC particularly by detecting mutations or single nucleotide polymorphisms

CC (SNPs); and (ii) for differentiation of cell or tissue types and for

CC investigating cell differentiation. The method allows the methylation

CC status of many C residues to be determined simultaneously. ABQ13410-

CC ABQ54121 represent genomic DNA sequences used to illustrate the method

CC for determining the degree of cytosine methylation described in the

CC disclosure of the invention

XX SQ Sequence 1634 BP; 212 A; 232 C; 624 G; 566 T; 0 U; 0 Other;

Query Match 31.8%; Score 406.6; DB 6; Length 1634;

Best Local Similarity 77.8%; Pred. No. 3e-76;

Matches 516; Conservative 0; Mismatches 144; Indels 3; Gaps 2;

QY 1 ATGACCTTCGGGGCAGCGGGCGGCTCGGTGGTCTGAACGTGGGGGGCCCGGTTAT 60

Db 726 ATGATTTTCGGGGTAGCGGGCGGTTTCGGTGGTTCGAACGTGGGGCGGCTTCGGTAT 785

QY 61 TCGCTCTCCGGAGCTGTGTAAGACTTCCCGCTCCGCGCTGAGCGGCTGACACGCG 120

Db 786 TCGTTGTTCCGGAGTTGTTGAAGATTTTCGTTGGTCCGCTGAGTCGGTTAGCGT 845

QY 121 TGCCECTCCGAGCCGAGCTGCTCGAGGTGTCGACGACTACGACCCGAGCGCAACGAG 180

Db 846 TGTGCTTTCGAGCGGACGCTGTTCCAGGTGTCGACGATTACGATCGCAGCGTAACGAG 905

QY 181 TACTTCTTCGACCGGCACTCGGAGCCTTCGGCTTCATCTGCTCTACGTCGCGGCCAC 240

Db 906 TATTTTTCGATCGGTATTCGAGGTTTCGTTTATTTTGTGTTTACGTCGCGGTTC 965

QY 241 GCGAAGCTCGCTTCGCGCCGCGGATGTCGAGTCTCTCTTCTACAACGAGATGATCTAC 300

Db 966 GGTAACTTCGCTTCGCGG-CGCGGATGTCGAGTTTTCGTTTATAACGAGATGATTAT 1024

QY 301 TGGGCGCTGAGGCGCGGCGACCTCGAGTACTGCTGCCAGCGCCGCTCGACGACGCGATG 360

Db 1025 TGGGCTTGGAGGCGCGGTATTCGAGTATTTGTTAGGCGTTCGTTTCGACGATCGTATG 1084

QY 361 TCCGACACCTACACCTTCTACTCCGCGGACGAGCGGCGCTGCTGGGCGCGACGAGCG 420

Db 1085 TTCGATATTTATATTTTTCGTTTCGAGTTCGAGTTCGCGGCTGTTGGTTCGCGACGAGCG 1144

QY 421 GCGCCGCGGCGGCGGAGGCGGCTCCCTCCAGGCGCTGGCTGGAGCGCATCGCGCGGACC 480

Db 1145 CGTTTCGCGCGG--CGAGGCGGTTTTTTTAGGCGTTGGTTGGAGCGTATCGCGCGGATT 1202

QY 481 TTCGAGAGCGCCACGTCGCTCGCTCGCGCGCGCAGATCTCGGCTAGCGTGTGGTGTTC 540

Db 1203 TTCGAGAGGTTTACGTCGTCGTTGGTTCGCGTAGATTTTGGTTAGCGTGTGGTGTTC 1262

QY 541 GTGATCGTGTCCATGGTGGTCTCTCGCGCAGCAGTTCGCGCGCTCGCGCGACGCGACCC 600

Db 1263 GTGATCGTGTTCGTTGGTGGTTCGCTAGTACGTTGTTTCGATTGCGCTAACGCTAGTC 1322

QY 601 GCCGACACCGCAGCTCGATGACCGGAGCAGGATAATTGAAGCTATCTGCATAGGTGG 660

Db 1323 GTCCATATCTAGTTTGGATGATCGGAGTAGGTATTCGTCGGTTTTGGAGGAGGTTT 1382

QY 661 TTC 663

Db 1383 TTC 1385

RESULT 12

ABQ49123/c

ID ABQ49123 standard; DNA; 1634 BP.

XX AC ABQ49123;

XX DT 12-JUL-2002 (first entry)

XX OLigonucleotide for detecting cytosine methylation SEQ ID NO 35714.

DE Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;

XX KW drug; side effect; cancer; central nervous system; cardiovascular;

XX KW gastrointestinal; respiratory system; single nucleotide polymorphism;

XX KW SNP; cell differentiation; ds.

XX OS Homo sapiens.

XX WO200218632-A2.

XX PD 07-MAR-2002.

XX 01-SEP-2001; 2001WO-EP010074.

XX 01-SEP-2000; 2000DE-01043826.

XX 05-SEP-2000; 2000DE-01044543.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K, Guetig D;

PI

Query Match	30.9%;	Score 395.4;	DB 6;	Length 1634;
Best Local Similarity	78.8%;	Pred. No. 7e-74;		
Matches 497;	Conservative	0;	Mismatches 131;	Indels 3; Gaps 2
QY	1	ATGACCTTCGGCGCAGCGGGCGGCGCTCGGTGCTGCTGAACGTGGCGCGCGCCGGGTAT	60	
Db	909	ATAACCTTCGAACGCAACGAAACGACCTCGATATATCTAAACGTAAACGACCCGATAT	850	
QY	61	TGCTGTCCGGAGACTGCTGAAGACATTCGCCGTGCGCGGTGAGCGGTGACACGGC	120	
Db	849	TGCTATCCCGAAAACTACTAAAAAATTCGCCGTAGCGCGGTAAACCGACTACACGAC	790	
QY	121	TGCCGTTCGACGCGGACGCTGCTCAGGTGTGCACGACTACGACCGCGAGGCGCAACGAG	180	
Db	789	TACCGCTCCGAACGCGAGTACTCGAATATACGACGACTACGACCGCGNAACGACGNA	730	
QY	181	TACTTTTCGACCGGACCTCGAGAGCCTTCGGCTTCACTCTGTCTACTCGTGCAGCGCCAC	240	
Db	729	TACTTTTCGACCGGACCTCGAAAAACCTTCGACTTCACTCTACTCTACGTACGCGACCAC	670	
QY	241	GGCAAGCTCGCTTCGCGCGCGGATGTGCAGACTCTCCCTTCTACACAGAGATGATCTAC	300	
Db	669	GACAACTAGCTTTCGCG - CGGNAATACGAATCTCCTTTCTAACGAAATAATCTAC	611	
QY	301	TGGGGCTTGGAGGGCGCACCTCGAGTACTGTGCCAGGCGCGCCTCGACGACCGCATG	360	
Db	610	TAAACCTTAAAAACCGGCACCTCGAATACTACTACCAACGCGCCTCGACGACCGCAT	551	
QY	361	TCGACACCTACACCTTCTACTCGGCCGACGAGCGGGGTGCTGGCGCGCGACGAGGGG	420	
Db	550	TCGACACCTACACCTTCTACTCGACCGCAACCGAACGTAATAACCGCGACGAAACG	491	
QY	421	CGCCCGCGGGCGGCGCGCTCCCTCCAGGGCTGGCTGAGAGGCGATCGGGGGACC	480	
Db	490	CGCCCGGACGG - CGAAACGACTCCCTCCAAAACGCTAACTAAAACGATACGACGAC	433	
QY	481	TTGAGGAGCCACGCTCGTTCGTTGCGCGCGAGATTCCTGGCTAGCGTGTGCGTGTGTC	540	
Db	432	TTCGAAAAACCCACGCTCGTTCGCTAACCGCGCAAAATCGTAACGATTCGATAATTC	373	
QY	541	GTGATCGTTCATGGTGGTGTGGCGCAGACGTTGCCGACTGGCGCGCAACGCGAC	600	
Db	372	GTAACTGATTCATTAATTAATCTATACGCCAACACGTTACCCGACTTAACGCAACGCA	313	
QY	601	GCGCAACCGCAGCTCGATGACCGGAGCA	631	
Db	312	GCGCAACCGCAACCTAAATAACCGAAACA	282	

RESULT 14	
ABQ49125	
ID	ABQ49125 standard; DNA; 1634 BP.
XX	
AC	ABQ49125;
XX	
XX	
DT	12-JUL-2002 (first entry)
XX	
DE	Oligonucleotide for detecting cytosine methylation SEQ ID NO 35716.
XX	
KW	Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW	drug; side effect; cancer; central nervous system; cardiovascular;
KW	gastrointestinal; respiratory system; single nucleotide polymorphism;
KW	SAP; cell differentiation; ds.
XX	
OS	Homo sapiens.
XX	
PN	WG200218632-A2.
XX	
PD	07-MAR-2002.
XX	
PF	01-SEP-2001; 2001WG-EF010074.
XX	
PR	01-SEP-2000; 2000DE-01043826.

```

05-SEP-2000; 2000DE-01044543.
(EPIG-) EPIGENOMICS AG.
Olek A, Pipenbrock C, Berlin K, Guetig D;
WPI; 2002-371829/40.
Determining the degree of cytosine methylation in genomic DNA, useful for
diagnosis and prognosis, comprises selective hybridization of amplicons
from chemically treated DNA.
Claim 12; 56pp + Sequence Listing; 56pp; German.
This invention describes a novel method for determining the degree of
methylation of a particular cytosine in a motif 5'-CpG-3', present in a
genomic sample of DNA. The sample is treated chemically to convert
cytosine (C) but not methylated C, to uracil, then part of the genomic
DNA that contains the target C is amplified to form a labeled amplicon.
The amplicon is hybridised to two classes, each with at least one member
of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
degree of hybridisation to both classes is determined from the label on
the amplicon. From the ratio of labels hybridised to the two classes of
oligomers, the degree of methylation is calculated. The method is used:
(i) for diagnosis and/or prognosis of side effects of therapeutic drugs
and of a wide range of diseases, e.g. cancer, disorders of the central
nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
particularly by detecting mutations or single nucleotide polymorphisms
(SNP's); and (ii) for differentiation of cell or tissue types and for
investigating cell differentiation. The method allows the methylation
status of many C residues to be determined simultaneously. ABQ13410-
ABQ54121 represent genomic DNA sequences used to illustrate the method
for determining the degree of cytosine methylation described in the
disclosure of the invention
Sequence 1634 Bp; 604 A; 588 C; 232 G; 210 T; 0 U; 0 Other;
Query March 30.98; Score 395.4; DB 6; Length 1634;
Best Local Similarity 78.8%; Pred. No. 7e-74;
Matches 497; Conservative 0; Mismatches 131; Indels 3; Gaps 2;
Qy 1 ATGACCTTCGGGGCGACGGGGGGCGCTCGGTGCTGTAACGTGGCGGGCGCCCGGTAT 60
Db 726 ATAACTTCGAAACGCAACGAAACGACCTCGATTAATCTAAACGTAAACGACGCCGATAT 785
Qy 61 TCGCTGTCCGGAGCTGCTGAAGGACTTCCCGTGGCGCGGTGAGCCGGCTGCACGGC 120
Db 786 TCGCTATCCCGAAACCTACTAAAAAACTTCCCGCTACGCCCGGTAAACCGACTACACGAC 845
Qy 121 TGGCGCTCCGAGCGCGACGTGCTCGAGGTGTGGACGACTACGACCGCGAGCGCAACGAG 180
Db 846 TACCGTCCGAAACGCGACGTACTCGAAATATACGACGACTACGACCGCAACGCAACGAA 905
Qy 181 TACTTCTTGACCGGACCTCGAGGCGCTTCGGGTTTATCTCGTCTCTACGTGGCGGCGCAC 240
Db 906 TACTTCTTGACCGGACCTCGAAACGCTTCGACTTCTATCTCTACTCTACGTACGCGACCC 965
Qy 241 GGCAAGTGGCGTTTCGGCGCGCGGATGTGGAGTCTCTCTTCTACACGAGATGATCTAC 300
Db 966 GACAACTAGCTTTGGCG-CGCGAATATACGAACCTCTCTTCTACACGAAATACTCTAC 1024
Qy 301 TGGGGCTTGAGGGCGGCGACCTTCGAGTACTGCTGCGACGCGCGCTTCGACGACCGCATG 360
Db 1025 TAAACCTTAAAAACGGCGACCTTCGAATACTACTACCAACGCGCGCTTCGACGACCGGATA 1084
Qy 361 TCGGACACCTTACCTTCTACTTCGGCGGACGACCGCGGCGTGTGGCGCCGCGACGAGCG 420
Db 1085 TCGGACACCTTACCTTCTACTTCGACCGGACCGACCGACTCTAAACCGCGACGAAACG 1144
Qy 421 CGCCCCGGCGGGCGCGAGCGGTTCCTCTCAGCGCGTGTGCTGAGCGCATGTCGGCGGAC 480
Db 1145 CGCCCCGACGCG--CGAAACGACTTCCTCTCAAAACGGTAACTAAAAACGATACGACGAC 1202

```

encodes a novel ion channel protein, ion-x (11). The nucleic acid, protein and antibody are useful for identifying a compound which binds a nucleic acid molecule encoding ion-x. These are useful for treatment of a neurological or psychiatric disorder which modulates ligand binding to ion-x in neurons of the mammal; in gene therapy to restore ion-x activity in certain disease states; for treating asthma, traumatic brain injury,

Search completed: October 6, 2004, 18:07:16
Job time : 590 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 6, 2004, 17:08:52 ; Search time 114 Seconds
(without alignments)
6221.292 Million cell updates/sec

Title: US-10-016-647-1
Perfect score: 1278
Sequence: 1 atgaccttcggcgagcg...ccactgaattcctgaataa 1278

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.NA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	277.4	21.7	2127	1 US-08-464-340A-1	Sequence 1, Appli
2	277.4	21.7	2127	5 PCT-US94-08449A-1	Sequence 1, Appli
3	258.8	20.3	2022	4 US-09-719-919A-18	Sequence 18, Appli
4	251	19.6	1518	4 US-09-719-919A-2	Sequence 2, Appli
5	198.2	15.5	2483	1 US-08-464-340A-3	Sequence 3, Appli
6	198.2	15.5	2483	5 PCT-US94-08449A-3	Sequence 3, Appli
7	197.8	15.5	3102	4 US-09-336-643A-17	Sequence 17, Appli
8	182.4	14.3	2494	4 US-09-181-339-6	Sequence 6, Appli
9	157.4	12.3	3080	4 US-09-336-643A-7	Sequence 7, Appli
10	146	11.4	2266	4 US-09-181-339-11	Sequence 11, Appli
11	146	11.4	2293	4 US-09-336-643A-5	Sequence 5, Appli
12	122	9.5	267	4 US-09-016-434-169	Sequence 169, App
13	115.4	9.0	1273	4 US-09-181-339-8	Sequence 8, Appli
14	113.4	8.9	1341	4 US-10-162-012-7	Sequence 7, Appli
15	107.8	8.4	2799	4 US-09-181-339-2	Sequence 2, Appli
16	100.6	7.9	1599	1 US-08-288-405A-9	Sequence 9, Appli
17	97.6	7.6	3424	4 US-09-336-643A-9	Sequence 9, Appli
18	95.4	7.5	696	1 US-07-955-916-5	Sequence 5, Appli
19	94.8	7.4	1994	1 US-08-527-152-1	Sequence 1, Appli
20	93.8	7.3	1805	1 US-07-955-916-6	Sequence 6, Appli
21	93	7.3	2064	4 US-09-178-109-3	Sequence 3, Appli
22	93	7.3	2072	4 US-09-142-791A-3	Sequence 3, Appli
23	93	7.3	2104	4 US-09-142-791A-1	Sequence 1, Appli
24	93	7.3	2121	4 US-09-178-109-1	Sequence 1, Appli
25	91.4	7.2	2104	4 US-09-142-791A-5	Sequence 5, Appli
26	88	6.9	774	4 US-09-181-339-4	Sequence 4, Appli
27	86.8	6.8	625	4 US-09-181-339-1	Sequence 1, Appli

28	80	6.3	1927	4	US-09-336-643A-3	Sequence 3, Appli
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30	65.4	5.1	2787	3	US-09-105-537-40	Sequence 40, Appl
31	65.4	5.1	5970	3	US-09-320-878-21	Sequence 21, Appl
32	65.4	5.1	5970	4	US-09-141-908-11	Sequence 11, Appl
33	65.4	5.1	5970	4	US-09-657-440-21	Sequence 21, Appl
34	61.6	4.8	1812	4	US-09-252-991A-16103	Sequence 16103, A
35	61.6	4.8	1938	4	US-09-352-991A-16208	Sequence 16208, A
36	61.6	4.8	3744	4	US-09-352-991A-16389	Sequence 16389, A
37	61.4	4.8	241	4	US-09-016-434-779	Sequence 779, App
38	61	4.8	1777	1	US-08-173-508-5	Sequence 5, Appli
39	61	4.8	1777	2	US-08-265-310-5	Sequence 5, Appli
40	58.4	4.6	3074	4	US-08-951-742-5	Sequence 5, Appli
41	58.4	4.6	3137	4	US-09-813-148-1	Sequence 1, Appli
42	57.2	4.5	1119	4	US-08-590-304-1	Sequence 1, Appli
43	57.2	4.5	2349	4	US-09-252-991A-13578	Sequence 13578, A
44	57.2	4.5	3081	4	US-09-252-991A-13765	Sequence 13765, A
45	57.2	4.5	3081	4	US-09-252-991A-13660	Sequence 13660, A

ALIGNMENTS

RESULT 1
US-08-464-340A-1
; Sequence 1, Application US/08464340A
; Patent No. 5710019
; GENERAL INFORMATION:

APPLICANT: LI, ET AL.
TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND

STATE: NEW JERSEY
COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/464,340A

FILING DATE: June 5, 1995

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: PCT/US94/08449

FILING DATE: 28 JUL 1994

ATTORNEY/AGENT INFORMATION:

NAME: FERRARO, GREGORY D.

REGISTRATION NUMBER: 36,134

REFERENCE/DOCKET NUMBER: 325800-415

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2127 BASE PAIRS

TYPE: NUCLEIC ACID

STRANDEDNESS: SINGLE

TOPOLOGY: LINEAR

MOLECULE TYPE: CDNA

US-08-464-340A-1

Query Match 21.7%; Score 277.4; DB 1; Length 2127;

Best Local Similarity 55.2%; Pred. No. 16-54;

Matches 676; Conservative 0; Mismatches 501; Indels 48; Gaps 5;

QY 38 TGAACGTGGCGCGCCCGGTATTCGCTGCCGAGCTCTGAAGAGATTCCCGCTGC 97

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Db 481 TCACAGTAGCGGCGCATCAAGTACTCGCTGCCCTGGACACAGCTGACAGAGTTCCCGCTGA 540
Qy 98 GCCCGTGAAGCGGCTGCAAGCTGCGCTCCGAGCGCGCAAGCTGCTGAGAGTGTGCGAGC 157
Db 541 CGCGCTGGGCGGAGCTCAAGGCGCTGACCAACTTCGACGACATCTCAACAGTGTGCGATG 600
Qy 158 ACTACAGCGGAGCGAGCGAGTACTCTTCCAGCGGCACTCGAGGCGCTTCGCGCTCA 217
Db 601 ACTACAGCGTCACTGCAAGAGTCTTCTTCCAGCGCAACCGGCGGCTTCGCGACTA 660
Qy 218 TCCTGTCTACGTGCGCGGCGCAAGCTGCGCTTCGCGCGCGGATGTCGAGCTCT 277
Db 661 TCCTGACCTTCCTGCGG--CGGGCAAGCTGCGCTGCTGCGGAGATGTCGCGCTGT 717
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Db 718 CTTTCCAGGAGAGCTGCTGTACTGGGGCATCGCGGAGGACCACTGGAGCGCTGCTGA 777
Qy 338 AGCGCGCGCTCGACGACCGCATCTCCGACACCTTACTCGGCGCGAGCGCGG 397
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Db 838 ACAGCGCGTGGACAGCGAGGCGCGCGACAGCGAGGCGCGCGCGCGCGCGCGCGCG 897
Qy 449 CAGGCGCTGGTGGAGCGCATCGCGCGGACCTTCGAGGAGCGCGCGCTGCTGGCGG 508
Db 898 TGGGCGCTGCATCGCGGACCTCGCGGACATGGTGGAGGCGCGACCTCGGCGCTGCTG 957
Qy 509 CGAGATCTCGTGTAGCGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 568
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Qy 569 CGAGCGGTGCGCGGAGTGGCGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 622
Db 1018 TCAGCACCTTGGCCAGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1077
Qy 623 ACCGAGCGAGGATAATTGAGCTATCTGATAGTTGTTGTTGTTGTTGTTGTTGTTGTT 682
Db 1078 ACAACGTTTCATCGTGGAGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1137
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Db 1138 GGTTCATGAGGCGCGCGAGTTCGCTTCTGCGAGCGCGCGCTGAGCTGATCGACC 1197
Qy 743 TACTGCGAATCAAGCGGATTAATCTCTGTTGTTGATGACAGTGTTCAGGCGAG-- 798
Db 1198 TGGTGGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1257
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Db 1258 GCAAGCGCGCGCGGCAAGTACTGAGCAAGGTTGGGCTGTTGCTGCGCGCTGCTGC 1317
Qy 842 GAATGATGAGATTTTGGTGAATTAAGCTTCCCGTCACTTCAATGTTGTTTCAAGAC 901
Db 1318 GGGCGCTGCGCATCTGTAGTGTGCGGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCG 1377
Qy 902 TCGGTTTGAATCTCAACGTTGCTACCGAGAGATGTTATGTTACTTGTCTTCAATTTGT 961
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Qy 1142 TTTGTGTTGTCAGTGGAAATGTTCTATTGGCATTACTATCACTTTTATCTACCATAGCT 1201
Db 1609 GCAGCATCTCTGAGCGGATCTCTGCTCATGGCTTCCAGTCACTTCAATCTCCACACT 1668
Qy 1202 TTGTGCACTGTATCATGAGCTCAA 1226
Db 1669 TCTCCCTCTCTACCTGAGCTCAA 1693

RESULT 2

PCT-US94-08449A-1
; Sequence 1, Application PC/TUS9408449A
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Potassium Channel Protein 1 and 2
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESS: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/08449A
; FILING DATE: SUBMITTED HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2127 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
PCT-US94-08449A-1

Query Match 21.7%; Score 277.4; DB 5; Length 2127;
Best Local Similarity 55.2%; Pred. No. 1.6e-54;
Matches 676; Conservative 0; Mismatches 501; Indels 48; Gaps 5;

Qy 38 TGACGTGGGCGGCGCGGTTTCGCTGTCGCGGAGCTGCTGAAGGACTTCCCGCTGC 97
Db 481 TCAACGTAGGCGGATCAAGTACTGCTGCTGCGGAGCTGCGAGGTTCCCGCTGA 540
Qy 98 GCCCGTGGAGCGGCTGACGCTGCGCTCGAGGCGGAGCTGCTGAGGTTGCGAGC 157
Db 541 CGCGCTGGGCGAGCTCAAGGCGCTGACCAACTTCGACGACATCTCAACGTGCGGATG 600
Qy 158 ACTACGACCGGAGCGCAAGAGTACTTCTTCGACCGGAGCTCGAGGCTTCGCTTCA 217
Db 601 ACTACGACGTCACCTGCAACAGAGTCTTCTTCGACCGCAACCGGCGGCTTCGCGACTA 660
Qy 218 TCCTGTCTACGTGCGGCGCGGCAAGTGGGCTTCGCGCGCGGATGTTGCGAGCTCT 277
Db 661 TCCTGACCTTCTGCGGCG---CGGCGAAGCTGCGGCTGCTGCGGAGATGTTGCGCTGT 717


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QY 278 CTTCTACAAACGAGATGATCTACTGGGCTCGAGGGCGCGCACTCGAGTACTCTCTCC 337
Db 718 CTTCTACGAGAGAGTGTGTACTGGGCTCGAGGGCGCGCACTCGAGTACTCTCTCA 777
QY 338 AGCGCGCTCGACGACCGCATGTCCGACACCTACACCTTCTACTCGCGCGAGAGCGG 397
Db 778 AGCGCGCTCTCTGACGAGATGAGAGTTCGCGAGATGTGAGCGGGAGAGAGG 837
QY 398 GCGTGTCTGGCGCGACGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 448
Db 838 AGCAGCGCTGACGACGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 897
QY 449 CCAGCGCTGCTGAGCGCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 508
Db 898 TGGGGCGCTGCAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 957
QY 509 CGCAGATCTGCTAGCGTGTGCGTGTGCTGATCGTGTCTTCTGATGTGTGTGTGCG 568
Db 958 GCAAGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1017
QY 569 CCAGCAGCTTCCCGACTGCGCGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 622
Db 1018 TCAGCAGCTTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1077
QY 623 ACCGAGCAGGATAATTGAAGCTATCTGCAATAGTGTGCTGCTGCTGCTGCTGCTG 682
Db 1078 ACAAGCTTCTATCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1137
QY 683 GGTTCATGCTTCCAAACAAAGTGTGAGTTTGTCAAGAGACCGCTGCAACATCATGAT 742
Db 1138 GGCTCATTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1197
QY 743 TACTGGCAATACGCGGTATTAATCTCTGCTGTGATGACAGTGTGTTACAGCGAG --- 798
Db 1198 TGGTGGCAATCTGCGCTTACTACATACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1257
QY 799 -----AATCTCAACTCCAGAGGCTGGAGTCACTTGAGGSPACTTA 841
Db 1258 GCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1317
QY 842 GAATGATGAGATTTTGGGTGATTAAGCTTGCCTGCTCACTTCACTTGTCTTCAACAC 901
Db 1318 GGGCGCTGCGCATCTGTACGATGATGCGCTTGGCGCGCGCGCGCGCGCGCGCGCG 1377
QY 902 TCGGTTGACTCTCAAACTGCTACCGAGAGATGTTATGTTACTTGTCTTCTTCTTGTG 961
Db 1378 TGGGCTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1437
QY 962 TTGCGCATGCAATCTTTAGTGACATTTCTAGCTTCTTGAACATGGCTGACCTGGAAA 1021
Db 1438 TGGCATCGCGCTCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1488
QY 1022 CATCAACAAAGACTTTACAGCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1081
Db 1489 CCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1548
QY 1082 CTACAGTTGGCTATGAGATATGTAATCTATACAGTGCCTGGAAAGATTTCTTGAGAG 1141
Db 1549 CGACGCTGAGCTATGCGACATGTTTCCCGAGGACACCGCGCGCGCGCGCGCGCG 1608
QY 1142 TTTGTGTTGCTGAGTGTGTTCTATGGGATTAACCTATCACTTTTATCTACCATAGCT 1201
Db 1609 GCAGCATCTGAGCGCATCTGCTCATGCGCTTCCAGTCACTCCATCTTCCACACT 1668
QY 1202 TTGTGAGTGTATCATGAGCTCAA 1226
Db 1669 TCTCCCGCTCTACCTGGAGCTCAA 1693
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RESULT 3

US-09-719-919A-18

; Sequence 18, Application US/09719919A

; Patent No. 6680180

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; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICAGEN Incorporated
; TITLE OF INVENTION: Kv6.2, a Voltage-Gated Potassium Channel Subunit
; FILE REFERENCE: 018512-001410US
; CURRENT APPLICATION NUMBER: US/09/719,919A
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/091,466
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: WO PCT/US99/14945
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 2022
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (149)..(1708)
; OTHER INFORMATION: human alpha subunit of heteromeric voltage-gated
; OTHER INFORMATION: potassium channel Kv6.2
; US-09-719-919A-18
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Query Match 20.3%; Score 258.8; DB 4; Length 2022;
Best Local Similarity 54.1%; Pred. No. 2.9e-50;
Matches 664; Conservative 0; Mismatches 522; Indels 42; Gaps 5;

QY 30 GGTGGTCTGAAGTGGCGCGCGCGGATTCGCTGTCCCGGAGCTGTGAAGACTT 89
Db 328 GATCCTGATCAACGTGGGGGCGAGAGGTATCTCTCCCTGGAGCACACTGACCGGTT 387
QY 90 CCGCTCGCGCGGTGAGCGGCTGCACGCTCGCGTCCGAGCGGACGCTGCTCGAGGT 149
Db 388 CCGCTGAGCGGCTGAGCAACTCAGGCTCTGTGGAGCTACAGAGATCTGTGAGCT 447
QY 150 GTGCGAGCTACGACCGCGAGCGCAACGAGTACTTTCGACCGGCACTTCGAGGCTT 209
Db 448 CTGCGATGATTACGACGAGGACAGCCAGGAGTCTTCTTCGACAGGAGCCAGCGCTT 507
QY 210 CGGCTTCATCTGCTTACGTGCGGCGCACGCGAGCTCGCTTCGCGCGCGGATGTG 269
Db 508 CGGGGTGATCGTGAAGTTCCTG---GCGCGCGGAAAGCTGGTCTTCTGAGGAGATGTG 564
QY 270 CGAGCTCTCTTTTACAAACGAGATGATCTACTGGGGCTGGAGGGCGCGCACCTCGAGTA 329
Db 565 CGCGCTCTCTTCCAGGAGGAGCTGGCTTACTGGGATCGAGGAGCCCACTTGGAGAG 624
QY 330 CTGTGCGCGCGCGCTCGACGACCGCATGTCCGACACCTACACCTTCTACTCGGCGGA 389
Db 625 GTGTGCTCGGAAAGTGTCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAG 684
QY 390 CGAGCGCGGCTGTGGCGCGCGA---CGAGGCGCGCGCGCGCGCGCGCGCGCGCGCTCC 446
Db 685 CAGGAGAGCTGACTGAGGCGAGCAGAGGAGAGCCCGCGCGCGCGCTGCGACTTCTCGCG 744
QY 447 CTCAGCGCTGTGCTGAGCGCATGCGGCGGACCTTCGAGAGCGCCACGCTGCTGCTGGC 506
Db 745 CTGGGCGCTGTGATGAACCGGCTGCGGAGATGTGTGAAACCCCGAGTCCGGGCTGCC 804
QY 507 CGGCGAGATCTCGCTAGCTGTGCTGGTGTGCTGATCGTGTCCATGCTGTGCTGTG 566
Db 805 CGGAAAGTCTTTCGCTTGGCTCTCCATCTCTTCTGCGGCGCCACAGCGCTCAGCCTGTG 864
QY 567 CGGCGAGCATTTGCCCGACTGGGCGC-----AAGCAGCGCGCGCGCACCAACCGAGCTTGA 620
Db 865 TGTCAGCACCATGCCCGACTCGGCGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 924
QY 621 TGACCGAGCAGGATTAATGAAGCTATCTGCTAGGTTGGTTTCACTGCGCGAGTGCATCGT 680
Db 925 CTACTATATTTTATCGTGGAGACCATCTGCGTGGGCTGGTTCTCTCCCTGGAGTTGCTG 984
QY 681 GAGGTTTCAATGTCTCCAAAAACAAGTGTGAGTTTGTCAAGAGAGCCCTGTAACATCATTTGA 740
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Db 985 GCGTTTGTCCAGGCCAAGACAGTGTGATCTTCCAGGGCCCTGGAACATCATCGA 1044
Qy 741 TTTTACTGGCAATCACGCCGATTTACATCTCTGTGTGATGACAGTGTTCAG----- 793
Db 1045 CATCTTGGCCATCTCCCATACTACGTGTGCTGGCGGTGTCTGAGGAGCCGCCGAGGA 1104
Qy 794 -----GGAGAACTCTCACTCCAGAGGGCTGAGTCACTCTTGAGGGTACT 839
Db 1105 CGCGAGAGCGCCAGCAGAGCTCTTACTTGAGAAAGTGGGGCTGGTCTCGTGTGCT 1164
Qy 840 TAGAATGATGAGGATTTTGGGTGATTAAAGTGTGCCCTGCTACTTCATTGCTTTCAGAC 899
Db 1165 GCGAGCGCTGGCATCTCTACGTGATGCGCTGGCTGCCACTGCTGGGGCTGCAGAC 1224
Qy 900 ACTCGGTTTGACTCTCAAGCTGTGCTACCGAGAGATGTTTGTACTGTCTTCTCATTTG 959
Db 1225 GCTGGGGCTCACCGTGGCGGCTTGCATGTGAGTTCGGGCTGCTCTCTCTCTGGC 1284
Qy 960 TGTGTGCATGGCAATCTTTAGTGCATTTCTCAGCTTCTTGAACATGGGCTGGACCTGGA 1019
Db 1285 CGTGGCCATCACCTCTCTCCCTTTGGTCTACGTGGCGGAGAGAGTCCGGCGGG- 1343
Qy 1020 AACATCCAAACAGGATTTACAGAGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTAT 1079
Db 1344 -----TGCTGGAGTTTACCAGCATCCCGCTCTTATTGGTGGGCCATCATCTCCAT 1395
Qy 1080 GACTACAGTGGCTATGAGAGATATGATCTATCAAGTGCCTGGAAGAAATCTTGGAGG 1139
Db 1396 GACAAAGTGGGCTACGGGAGCATGATGTCGCCGAGTGTCCAGCCAGATGGTGGCCCT 1455
Qy 1140 AGTTTGTGTGTCAGTGGAAATGTTCTATGTCGATTAACCTATCACTTTTATTCACATAG 1199
Db 1456 CAGCAGATCCTGAGCGGGATCTCATGATGGCTTCCGGGCAAGTCTATCTTCCACAC 1515
Qy 1200 CTTTGTGCACTGTATCATGAGCTCAAG 1227
Db 1516 CTTCTCCCACTCCTACCTGAGCTCAAG 1543

RESULT 4

US-09-719-919A-2
; Sequence 2, Application US/09719919A
; Patent No. 6680180
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICAGEN Incorporated
; TITLE OF INVENTION: Kv6.2, a Voltage-Gated Potassium Channel Subunit
; FILE REFERENCE: 018512-001410US
; CURRENT APPLICATION NUMBER: US/09/719,919A
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/091,466
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: WO PCT/US99/14945
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1518
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1518)
; OTHER INFORMATION: mouse alpha subunit of heteromeric voltage-gated
; OTHER INFORMATION: potassium channel Kv6.2
US-09-719-919A-2

Query Match 19.6%; Score 251; DB 4; Length 1518;
Best Local Similarity 53.2%; Pred. No. 1.6e-48;
Matches 648; Conservative 0; Mismatches 530; Indels 39; Gaps 4;
Qy 38 TGAACGTGGCGGGCGGCGGTATTCGCTGTCGGGAGCTGCTGAAGAGACTTCCCGCTGC 97

Db 185 TGAATGTGGTGGCCAGCGGTACTGCTGCTCGCTGGAGACCTTGGATGCTTCCCGCTGA 244
Qy 98 GCGCGTGAAGCCGCTGCACGGGTGCGCTCCAGCGCGAGCTGCTCGAGGTGTGCGAGC 157
Db 245 GCGCGCTGAGCAGGCTCCGCTGTGCGCGCAGCCATGAGGAGATCAAGAGCTCTCGGATG 304
Qy 158 ACTACGACCGCGAGCGCAACGAGTACTTCTTCGACCGGCACCTCGAGGGCTTCCGGTTCA 217
Db 305 ACTACGATGAGGACAGCCAGAGTCTTCTTCGACAGGAACCCAGCGCTTCCGGGTGA 364
Qy 218 TCCTGCTTACGTGCGCGGCCACGGAAGCTGCGCTTCGCGCCGCGGATGTGCGAGCTCT 277
Db 365 TCGTGAAGCTTCTG- - -GCCGCGGGAAGCTGTGTGCTTCTGCGAGAGATGTGCGCCCTGT 421
Qy 278 CTTTCTAACAGAGATGATCTACTTGGGGCTTGGAGGCGCGCACCTCGAGTACTTGTGCC 337
Db 422 CTTTCCGGAGGAGCTGAGCTACTTGGGCATCGAGGAACCACTTGGAGCGTGTCTGCC 481
Qy 338 AGCGCCGCTCGACGACCGCATGTCCGACACCTACCTTCTACTCGCGCGAGAGCCGG 397
Db 482 TGCAGAGCTGCTGAAGAGCTGAGAGCGCGCGAGCTGCGCCGGGAGAGGCTGCC 541
Qy 398 GCGTGTGGCGCGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCTCCCTCCAGCGCT 457
Db 542 AGCGCCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTCCAGTGGCGCGCA 601
Qy 458 GGTGAGCGCATCGCGCGACCTTCGAGGAGCGCGCGCTGCTGCGTGGCGCGCGCATCC 517
Db 602 GCATGAACAGCTGCGTGAATGTTGGAGGAGCCACAGTCGGGGCTTCCCGGGAAGTCT 661
Qy 518 TGGTACAGTGTGCGTGGTCTGCTGATCGTGTCCATGTTGGTGTGCTGTGCGCGCAGCAGT 577
Db 662 TCGCTCCCTCTCGTCTCTTCTGTCGCAACAGCGCTGTGACCTGTGTGTGAGCACCA 721
Qy 578 TGCCCGACTGGCGCAACGCGAGCGCGC-----GACAAACGCGACCTGGATGACCGAGCA 631
Db 722 TGCCCGACTTTCAGGGCTGAGGAGGCAAGGAGATGCACTAGAAAGTGTATTACATCT 781
Qy 632 GGATAATTGAAGCTATCTGCATAGTGTGTTTCACTCCGAGTGCATGCTGAGGTTTCTTG 691
Db 782 TCGTGGTGAATCCATCTGTGCGCTGCTGCTGCTGAGTGTTCCTGCTGAGTGTTCCTGCT 841
Qy 692 TCTCCAAAACAGTGTGAGTGTTCAGAGAGACCCCTGAAACATCATGATTACTGGCAA 751
Db 842 AGGCCCCGACAAATGTCACTTTCGCGCGCCCTGATGTATGATCATGACATTCAGCCA 901
Qy 752 TCAGCGCGTATTACATCTCTGTGTGTGATGACAGTGTTCAGCGGAG----- 798
Db 902 TCTCCCATATACTATGTCTGCTGCGAGTGTCTGACGAATCCCGGAGGCGAGGAGGC 961
Qy 799 -----AACTCTCAACTCCAGAGGCTGAGTCACTTTGAGGCTACTTAGAATGATGA 850
Db 962 CGAGCAGAGCTCTTACTCGAGAAAGTGGGTGTGCTGCTGCTGCTGCTGCGGCACTAC 1021
Qy 851 GGATTTTGGGTGATTAAGCTTGCCTGCACTTCATGCTGTCTTTCAGACACTCGTTTGA 910
Db 1022 GCATCTCTACGTAATGCGCTGCTGCTGCGCTGCTGCGGCTGCGAGCGCTGCGGCTCA 1081
Qy 911 CTCTCAACGTTGCTACGAGAGATGTTATGTTACTTGTCTTCACTTGTGTGCTGCTG 970
Db 1082 CTGTGCGCGCTGCGCGGAGAGTGTGCTCTCTGATGCTTCTTCTGCTGCTGCGGTTA 1141
Qy 971 CAATCTTTAGTGCATTTCTCAGCTTCTTGAACATGGGCTGGACCTTGAACATTCACAA 1030
Db 1142 CCCTCTTCTACCGTTCGTCTATGATCTGAGAAATGATCCGGAAGGG-----TCC 1192
Qy 1031 AGGACTTTACAGCATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1090
Db 1193 TGGAGTTTCACTAGCATCCCGCATCTTATTTGGTGGGCACTCATCTCCATCAGACCGTGG 1252
Qy 1091 GCTATGAGATATGATCTTATCTATCAGTGTGCTGGAAGAAATCTTGGAGGAGTGTGTTG 1150

Db 1253 GCTATGGGACATGTCCTCGCAGCGTCCGGGACAGATGGTGGCTCTGAGCAGCATCC 1312
Qy 1151 TCAGTGGAAATGTTCTATTGGCAATACCTATACATTTTATCTACATAGCTTTTGGAGT 1210
Db 1313 TTAGCGGATCCTTATCATGGCTTTCCAGCCACATCATCTTCCACAGCTTCTCTACT 1372
Qy 1211 GTTATCATGAGCTCAAG 1227
Db 1373 CCTACTGGAGCTGAAG 1389

RESULT 5

US-08-464-340A-3

; Sequence 3, Application US/08464340A

; Patent No. 5710019

; GENERAL INFORMATION:

; APPLICANT: LI, ET AL.

; TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; ADDRESS: CECCHI, STEWART & OLSTEIN

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WORD PERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/464,340A

; FILING DATE: June 5, 1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/08449

; FILING DATE: 28 JUL 1994

; ATTORNEY/AGENT INFORMATION:

; NAME: FERRARO, GREGORY D.

; REGISTRATION NUMBER: 36,134

; REFERENCE/DOCKET NUMBER: 325800-415

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2483 BASE PAIRS

; TYPE: NUCLEIC ACID

; STRANDEDNESS: SINGLE

; TOPOLOGY: LINEAR

; MOLECULE TYPE: CDNA

US-08-464-340A-3

Query Match 15.5%; Score 198.2; DB 1; Length 2483;
Best Local Similarity 50.9%; Pred. No. 2.5e-36;
Matches 625; Conservative 0; Mismatches 568; Indels 36; Gaps 5;

Qy 3 GACCTTCGGGCGAGCGGGCGGCTCGGTGTGTGAACGTGGCGGCGCGCGGTATTTC 62
Db 729 GAGCTCCGCTGCCAGCGACACATAGATAGTCTCAACGTGGGGGGCGTGGCGAGGT 788
Qy 63 GCTGTCCCGGAGCTGCTGAAGACTTCCCGCTGCGCGCGGAGCCGCGTGCACGGCTG 122
Db 789 GCTGTACGGGACCTCTCAGTCAGTACCCTGAGACCGCGCTGGCGAGCTCATCACTG 848
Qy 123 CGGCTCCGAGCGGAGCG-----TGCTCGAGGTGTGCGAGCACTACGACCGCGGCGCAA 176
Db 849 CTTGGCTGGGGGTACGACACCATCTTCTCCCTGTGTGCGACGACTACGACCGCGCAAGC 908
Qy 177 CGAGTACTTCTTCGACCGGCACTCGAGGCGCTTCGGCTTCATCTCGCTCTAGCTGGCGG 236

RESULT 6

PCT-US94-08449A-3

Db 909 CGAGTTCTACTTTTCAGAGGACCCCGACGCCCTTCAAGTGTGTC---ATCGAGGTGACTA 965
Qy 237 CACGGCAAGCTCGGCTTCGCGCGGAGTGTGCGAGCTCTCCTTCTACAAACAGATGAT 296
Db 966 TTTGGGGAGGTCCACATGAAGAGGCATCTCCCCCACTGCTTCAAGAACAGATGGA 1025
Qy 297 CTACTTGGGGCTGGAGGGCGGCACCTCGAGTACTGCTGCACGCGCGCTCGACGACCG 356
Db 1026 CTTCTGGAAGTGGACCTCAAGTTCCTGGACGACTGTTCGAAGAGCCACC----- 1075
Qy 357 CATGTCGACACCTACACCTTCTACTCGCCGACGAGCCGGGGTGTGCGGCGCGACGA 416
Db 1076 --TGAGCGAAGCGGAGGAGTGGAGGAGATCGCGCGCGCGTGCAGCTCATCTGGA 1133
Qy 417 GGGCGCGCCCGCGGGCGCGAGCGGCTCCCTCCAGCGCTGGCTGGAGCGCATGGCGCG 476
Db 1134 CGACCTGGGCGTGGACGCGCGCGGAGCGCTGGCGCGCTGCCAGAGTGGCTTGAA 1193
Qy 477 GACCTTCGAGGAGCCACGTCGTCGTCGGCGCGGAGATCCTGCTAGCGTGTGGTGGT 536
Db 1194 GTTCTCTGGAAGCGCGAGTCTGTCGTCGCGCGCGGGTGGTGGCGAGCTCTCTTCCT 1253
Qy 537 GTTCGTGATCGTGTCCATGTCGTGTGTCGCGCAGCAGCTTCCCGACTGGCGCAACGC 596
Db 1254 GCTCATCTCTGTCGTCGTCGTCGTCATGTGATGGACACCATCCCGAATCGAGGTCT 1313
Qy 597 AGCGCGCAACCGCAGCTGGATGACCGGA---GCAGGATATTGAAGCTATCTGCAT 653
Db 1314 GGACCGGAGGGCAACCGCGTGGAGCACCGCGCTGGAGACGCTGGAGACGGCGTGCAT 1373
Qy 654 AGTTGGTTCACTGCGAGTGCATCGTGAGGTTCATTGTCTCCAAAACAAAGTGTGAGT 713
Db 1374 TGGCTGTTTACCTTGGAGTACCTGTCGCGCTCTCTCGTCAACCAAGCTGCATTT 1433
Qy 714 TGTCAAGAGACCCCTGAACATCATTTGATTATCTGGCAATCACCGGTATTACATCTCT 773
Db 1434 CGGCTGCTCTTTCATGAACATTGTGGACGTGTGGCCATCTCCCTCTTACGTAGCCT 1493
Qy 774 GTTGATGACAGTGTTTACAGCGAGAACTCTCACTCCAGAGGCTGGAGTCACTTTGAG 833
Db 1494 CACGCTCACGCACCTGGGTCCCGCATGATGGAGCTGACCAACGTGCAGGCGCGTGA 1553
Qy 834 GGTACTTGAATGATGAGGATTTTGGGTGATTAAAGCTTGGCCGTCACATTCATTGGTCT 893
Db 1554 GCGCTCGGATCATGCGCATCGCGCATCTTCAAGCTGCGCGCCACCTCTCGGCGCT 1613
Qy 894 TCAGACACTCGTGTGACTCTCAAAAGTGTGCTACCGGAGATGGTTATGTTACTTGTCTT 953
Db 1614 CGAGACCTCACCTATGCTTCAAGCGCAGCTTCAAGGAACTGGGGCTGCTGCTCATGTA 1673
Qy 954 CATTGTGTTGCCATGGCAATCTTTAGTGACATTTCTCAGCTTCTTGAACATGGGCTGGA 1013
Db 1674 CTTGGCAGTGGTATCTTGTCTTCTGTC-----CCTGGGCTACACCATGGA 1721
Qy 1014 CTTGGAACATCCAAAGGACTTTACAGCATTTCTGCTGCTGCTGGTGGGTGATAT 1073
Db 1722 GCAGAGCATCCAGAGACCCCTGTTTAAAGAACATCCCCAGTCTTCTGTTGGGCGCATCAT 1781
Qy 1074 CTCTATGACTACAGTTCGCTATGAGATATGATCTCTATCACAGTGCCTGGAAGATTCT 1133
Db 1782 CACCATGACCAACCGTGGCTACGCGACATCTACCCCAAGACACGCTGAGCAAGCTCAA 1841
Qy 1134 TGAAGAGTGTGTGTTGTCAGTGGAAATTGTTTATTGGCATTACCTATCACTTTTATCTA 1193
Db 1842 CGCGGCATCAGCTTCTTGTGTGTGTCATTGCCATCGCCCTGCCCATCCACCCCATCAT 1901
Qy 1194 CCATAGCTTTGTGAGTGTATTATGAGC 1222
Db 1902 CAACAACCTTTGTCAGGTACTACAAAGC 1930

```

; Sequence 3, Application PC/TUS9408449A
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Potassium Channel Protein 1 and 2
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/08449A
; FILING DATE: SUBMITTED HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2483 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: cDNA
; PCT-US94-08449A-3

Query Match 15.5%; Score 198.2; DB 5; Length 2483;
Best Local Similarity 50.9%; Pred. No. 2.5e-36;
Matches 625; Conservative 0; Mismatches 568; Indels 36; Gaps 5;

QY 3 GACCTTCGGCGCAGCGCGCGCTCGGTGGTGTGAACGCTGGGCGGCGCCGGTATTC 62
DB 729 GAGCTCGGTGCCAGCGACGACATAGATAGTCTCAACGTGGGGGGCTCGGCGAGT 788
QY 63 GCTGTCGGGAGCTCTGAAGGACTTCCCGCTGGCGCGCGGTGAGCGCGCTCGACGGCTG 122
DB 789 GCTGTACGGGAGCTCTCAGTCAGTACACCTGAGACCGCGCTGGGAGCTCATCAACTG 848
QY 123 CCCTCCGAGCGGAGC-----TGCTCGAGGTGTCGACGACTAGACCGGAGCGCAA 176
DB 849 CTTGGCTGGGGGTACGACACCATCTTCCCTGTCGACGACTAGACCGCGGAGCG 908
QY 177 CGAGTACTTCTTCGACCGGACCTCGGAGCGCTTCGCGCTTCATCTGCTACGAGATGAT 236
DB 909 CGAGTCTACTTTGACAGGACCGCGGACGCTTCAAGTGTGTC---ATCGAGGTGACTA 965
QY 237 CCACGCGAGCTCGCTTCGCGCGGGATGTCGAGCTCTCTCTTACAGGATGAT 296
DB 966 TTTGGGGAGGTCCACATGAAGAGGGCATCTGCCCATCTGCTTCAAGAGAGATGA 1025
QY 297 CTACTGGGCGCTGGAGGGGCGCACCTCGAGTACTCTGCCAGCGCGCTCGACGCG 356
DB 1026 CTTCTGGAAGTGGACCTCAAGTTCTTGACGACGTGTTCCAGAGCCACC----- 1075
QY 357 CATGTCGACACCTACACCTTCTACTCGCGGACGAGCGCGGTGCTGGCGGCGAGA 416
DB 1076 --TGACGGAAGCGCGGAGGAGCTGGAGGAGATCGCGCGCGCTGCAGCTCATCTTGA 1133

; Sequence 3, Application PC/TUS9408449A
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Potassium Channel Protein 1 and 2
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/08449A
; FILING DATE: SUBMITTED HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2483 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: cDNA
; PCT-US94-08449A-3

RESULT 7
US-09-336-643A-17
; Sequence 17, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; FILING DATE: 1999-06-18
; PRIOR FILING DATE: 60/076,667
; PRIOR FILING DATE: 1998-08-07

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;; PRIOR APPLICATION NUMBER: 60/116,448
;; PRIOR FILING DATE: 1999-01-19
;; PRIOR APPLICATION NUMBER: PCT/US99/03826
;; PRIOR FILING DATE: 1999-02-22
;; NUMBER OF SEQ ID NOS: 87
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 17
;; LENGTH: 3102
;; TYPE: DNA
;; ORGANISM: H. sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (274)...(1705)
;; OTHER INFORMATION: K+Hnov11
US-09-336-643A-17

Query Match 15.5%; Score 197.8; DB 4; Length 3102;
Best Local Similarity 50.8%; Pred. No. 3.3e-36;
Matches 614; Conservative 0; Mismatches 547; Indels 48; Gaps 4;

QY 38 TGAACGTGGCGCGCGCGGTATTGCTGTCGCCGGAGTGTCTGAAGCACTTCCGGCTGC 97
DB 335 TCAATGTGGCGCGCTTCAAGAGAGCTGCGCTCCGACACGCTGCTGCGCTTCCCGGAGA 394
QY 98 GCCGCTGAGCGGCTGCACGCGCTCCGCTCCGAGCGCAGCTGCTCGAGGTGTGCGACG 157
DB 395 CGCGCTGGCGCGCTGCTGCTGCTGCCACTCGCGGAGGCCATTCTGAGGCTCTGCGATG 454
QY 158 ACTAGACCGGAGCGCAGCTACTTCTTCGACGGGCACTCGAGGCTTTCGCTTCA 217
DB 455 ACTAGACGACCTCAGCGGGAGTCTACTTCGACGGCAACCCCTGAGCTCTTCCCTACG 514
QY 218 TCTGCTCTACGTGGCGGCCACGCAAGCTCGCTTCCGCGCGGAGTGTGCGAGCTCT 277
DB 515 TGTGCTGATTTATC---ACACGGCAAGCTTCACTGCTGAGCTGATGTGCTTCT 571
QY 278 CTTTCTACACAGATGATCTACTGGGCTGGAGGGCGGCACTCGAGTACTGCTGCC 337
DB 572 CTTTCTAGCAGAGATCGAGTACTGGGCAATCAACGAGTCTTCTGACTCTCTGCTGCA 631
QY 338 AGCGCGCTCTGACGACCGCATGTCCGACACCTACACCTTCTACTCGCGCAGGAGCGG 397
DB 632 GTTACAGTACCATGGCGCAAGTAGCCCGAGCAGGAGAGTGGGACGAGCAGATG 691
QY 398 GGTGCTGGCGCGCG-----ACGAGCGCGCGCGCGCG 430
DB 692 ACCAGGAGACCAACGCTTCTTCTCGATGAGATCCTTGCCTTCTACACGACGCTCCA 751
QY 431 GGGCGGAGCGGCTCCCTCAGCGCTGCTCGGCGCATGGCGGACCTTCCGAGGAGC 490
DB 752 AGTTGATGGGAGCGCCCTCGGCAACTTCCGAGGAGCTGTGGCTGGCGCTGGCAACC 811
QY 491 CCACGTCTGCTGGCGCGCAGATCCTGCTAGCGTGTGCTGCTGCTGCTGCTGCTGCTG 550
DB 812 CCGGCTACTCAGTGTGAGCAGGGTCTTCAGCATCCTGTCCATCCTGCTGCTGCTGCTG 871
QY 551 CCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 607
DB 872 CCATCATCACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 931
QY 608 ACCGAGCCTGATGACCGGAGCAGGATAATTTGAAGCTATCTGATAGTGTGCTGCTG 667
DB 932 ACCCTGGCAGGACCTAGTTCGAAATCGTGGAGCATTTGGCATTCCTGCTGCTGCTG 991
QY 668 CCGAGTGCATCTGAGGTTTCATGCTCTCAAAAAAAGAGTGTGAGTGTGCTGAGGACCC 727
DB 992 TTGAGCTGGTGGCGAGGTTTGTGTGGCGCCCTGACTTCTCAAGTCTTCTCAAGATGCC 1051
QY 728 TGAACATCATTTACTTACGGCAATCACGCGCTATTACATCTGCTGCTGCTGCTGCTG 787
DB 1052 TAAACCTTATTGACCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1111
QY 788 TTACAGGCGAGAACTCTCAACTCCAGAGGGCTGGAGTCACTTGTAGGGTACTTAGATGA 847

DB 1112 TGGTGGAGACACACCTACTTTAGCCAACTTGGGAGGGTGGCCAGGTCTCTGAGGCTGA 1171
QY 848 TGAGGATTTTTGGGTGATTAAAGCTTCCCGTCACTTCATTTGTTTCAGACACTCGGTT 907
DB 1172 TGGGATCTTCCGCACTCTTAAAGCTGGCCAGGCACTCCACTGGCCTCCGCTCGGGGG 1231
QY 908 TGACTCTCAACGTTGCTTACCGAGAGATGTTATGTTACTTGTCTTCACTTGTGTTGCCA 967
DB 1232 CCACCTTTGAAATACAGCTACAAGAGTAGGGTGTCTTGTCTTACTCTCCGTGGGGA 1291
QY 968 TGGCAATCTTTAGTGCACTTTCTCAGCTTTTGAACATGGGCTGGACCTGGAAACATCCA 1027
DB 1292 TTTCCATCTTCTCGTGGTCCCTACACCATTTGAAAAGAGGAG-----A 1336
QY 1028 ACAAGGCTTTACAGCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1087
DB 1337 ACGAGGCTTGGCCACCATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1396
QY 1088 TTGCTATGAGATATATATCTATCAGCTGCTTGAAGAAATTTTGGAGGAGTTTGTG 1147
DB 1397 TGGGTACGGGATGTGTTCCAGGGACACGCGCAGGAAAGCTGACTGCTCTGCTGCA 1456
QY 1148 TTGTCAGTGAATGTTTCTATTTGTCATTACTATCTATCTATCTATCTATCTATCTAT 1207
DB 1457 TCTTGGCAGCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1516
QY 1208 AGTGTATC 1216
DB 1517 ACTTTTACC 1525

RESULT 8
US-09-181-339-6
; Sequence 6, Application US/09181339
; Patent No. 6610827
; GENERAL INFORMATION:
; APPLICANT: Forsayeth, John R.
; APPLICANT: Zhao, Byron
; APPLICANT: Chavez, Potassium C.
; TITLE OF INVENTION: POTASSIUM CHANNEL SUBUNIT POLYPEPTIDE
; TITLE OF INVENTION: AND POLYNUCLEOTIDE COMPOSITIONS AND USES THEREFOR
; FILE REFERENCE: 5865-0033.30
; CURRENT APPLICATION NUMBER: US/09/181,339
; CURRENT FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 60/063,450
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 2494
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (449)...(1924)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2494)
; OTHER INFORMATION: n = A,T,C or G
US-09-181-339-6

Query Match 14.3%; Score 182.4; DB 4; Length 2494;
Best Local Similarity 49.9%; Pred. No. 1e-32;
Matches 607; Conservative 0; Mismatches 561; Indels 48; Gaps 4;

QY 38 TGAACGTGGCGCGCGCGGTATTGCTGTCGCCGGAGTGTCTGAAGCACTTCCCGTGC 97
DB 504 TGAACGTGGCGCGCGGTATTGCTGTCGATCAAGTCAAGTCACTCTCGGCTTCCCTCACA 563
QY 98 GCCCGTGGCGGCTGCAAGGCTGCGCTCCGAGCGGAGCTGCTGAGGTGTGCGACG 157
DB 564 CACGACTGGGAAAGCTGCTTACCTGCCACTCTGAGGAGGCCCACTTCTGAGCTGTGTATG 623

QY 606 CAACCCAGCCTGGATGACCGGAGCAGGATAAATGAAGCTATCTGATAGGTGGTTTCAC 665
Db 1181 AAGCTGGCTGGACCTCAGCTGCTGGAATCTGGAGTATGTGTGCAITTAGCTGGTTTAC 1240
QY 666 TGCCGAGTGCATCGTCAAGTTCATTCTCCAAAACAAAGTGTAGTGTCTCAAGAGAC 725
Db 1241 CGGGAGTTTGTCTCGGTTCTGTGTGTGGGACAGGTGTGCTTCTTAAGAAAGT 1300
QY 726 CTGGAACATCATGATTTACTGCAATACCGCGTATTACATCTCTGTGTTGATACAGT 785
Db 1301 GCCAAACATATAGACCTCCTTGCCATCTTGCCCTTCTACATCACTCTCTGTTAGAG 1360
QY 786 GTTTCAGCGGAGAACCTC-----TCAACTCCAGAGGCTGGAGTCACTTGAGGGTACT 839
Db 1361 CCTAAGTGGAGCCAGACACGAGAGCTGGAGAACGTGGGGCGCATTTGCCAGTGT 1420
QY 840 TAGAATGATCAGGANTTTTGGGTGATTAAAGCTTGCCCGTCACTTCATTGGTCTTCAGAC 899
Db 1421 GAGGCTGCTCAGGGCTCTGGCATGCTAAAGCTGGGACACATTCACAGGATTACGCTC 1480
QY 900 ACTCGGTTTGACTCTAAAGTGTACCGAGAGATGTTATGTACTTGTCTTCAATTG 959
Db 1481 CTTGGGATGACAAATCACCAGTGTACGAAGATGCGGCTACTGCTCTATTCTATC 1540
QY 960 TGTGTCATGGCAATCTTTAGTGCACTTTCTCAGCTTCTTGAACTGGGCTGGACCTGGA 1019
Db 1541 CGTGGAACTCTATATTTCACTGTAGATATTTGCTGAGCAAGCAITTC----- 1593
QY 1020 AACATCCAAAGGATTTACAGCAATCTCTGCTGCTGCTGCTGGTGGTGAATTTCTCTAT 1079
Db 1594 -----CTGACACAACTTCACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1648
QY 1080 GACTACAGTTGGCTATGGAGATGATGATCTATCAGTGTCTGGAAGAAATCTTGGAGG 1139
Db 1649 GACTACTGAGGATATGGGACATATAGACACACACACACAGGAAATCTGCGCTT 1708
QY 1140 AGTTGTGTGTCAGTGAATTTCTTATTTGCAATTAATGCAATTAATTAATTAATTAAT 1199
Db 1709 CATGTATATATATCGGAAATCTTGTCTGCGCTTGGCTATGCTATTAATTAATTAAT 1768
QY 1200 CTT 1202
Db 1769 CTT 1771

RESULT 10
US-09-181-339-11
; Sequence 11, Application US/09181339
; Patent No. 6610827
; GENERAL INFORMATION:
; APPLICANT: Forsayeth, John R.
; APPLICANT: Zhao, Byron
; APPLICANT: Chavez, Raymond C.
; TITLE OF INVENTION: POTASSIUM CHANNEL SUBUNIT POLYPEPTIDE
; FILE REFERENCE: 5865-0033.30
; CURRENT APPLICATION NUMBER: US/09/181,339
; PRIOR FILING DATE: 1998-10-28
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 2266
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (308)...(1783)
US-09-181-339-11

Query Match 11.4%; Score 146; DB 4; Length 2266;
Best Local Similarity 48.0%; Pred. No. 2.3e-24;

Matches 585; Conservative 0; Mismatches 585; Indels 48; Gaps 4;
QY 37 CTGAACGTGGCGCGCGCGGTATTCGTGTCCCGGAGCTGCTGAAGGACTTCCCGCTG 96
Db 362 CTGAATGTGGGGGCTTTAGCAGTCTGTGACCAAGACCCCTCTCGCGTTTCTCAC 421
QY 97 CGCCGCTGAGCCCGCTGCACCGGTGCGCTCCGAGCGGACGCTGCTGAGGTGGAC 156
Db 422 ACCAGACTGGGGAAGCTGCTTACTTGGCATTTCTGAAGAGGCCATTCTGGAGCTGTGAT 481
QY 157 GACTACGACCGGAGCGCAACGAGTACTTCTTCACCGGCACTCGAGGCGCTTCGGCTTC 216
Db 482 GATTACAGTGGCGGATAGGATATCTACTTTGATCGAATCCCTCTCTTCAGATAT 541
QY 217 ATCTGTCTTACGTGGCGGCGCACGCAAGTGGCTTTCGCGCCGCGGATGTGAGGCTC 276
Db 542 GTTTTGAATT---TTTATTACACGGGGAAGTGTATGTCTATGGAGGAGCTGTGCGTATTC 598
QY 277 TCCCTTCTACACGAGATGATCTACTGGGCTGAGGCGCGGACCTTCGAGTACTGCTGC 336
Db 599 TCATTTGCGCAGGAGATCGAGTACTGGGCAATCAACGAGCTCTTCATGATTTCTTGTGC 658
QY 337 CAGCGCCGCTTCGACGACCGCATGTCCGACACCTTACCTTCTACTCGGCGGACGACCG 396
Db 659 AGCAATCGTACACAGGAACGCAAGGAGGAAAAACACGAGAAGGACTGGACCAAAAAAGC 718
QY 397 GCGGTGCTGGCGCGGAC-----GAGGCGCGCGCGGCG 429
Db 719 CATGATGTGAGTACCGACTCTCTGTTTGAAGAGTGTCTCTGTTTGAAGAAGAGCTGGAG 778
QY 430 GGGCGCAGGCGGCTCCCTCCAGGCGGTGTGAGGCGCATGCGGCGGACCTTCGAGGAG 489
Db 779 AAGTTTGACACACTCGCATTTGGTCACTCGGAAGAAATCTGGAATTAGATGAGAAAT 838
QY 490 CCAACGTGCTGCTGGCGCGGACAGATCTCGCTAGCGTGTGCGGTGTGCTGATCGTG 549
Db 839 CCAGCGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 898
QY 550 TCCATGTGTGTGTGCTGCGCAGCAGCTTGCAGGCTGGCGCAACGAGCGCGGACGACAA 609
Db 899 TCCATGTGTGTGTGCTGCGCAGCAGCTTGCAGGATGTCAGATGTCAGATGAGGATGGAAGTG 958
QY 610 CGCAGCTGATGACCGGAGCAGGATAATTGAAGCTATCTGCAATGCTGATGCTGCTGCTG 669
Db 959 GATGATCCGCTGCTGGAAGGAGTGGAGATCG-----CGTGCTGCTGCTGCTGCTGCTGCTG 1012
QY 670 GAGTGCATGCTGAGTTCATTGTCTCCAAAAACAAGTGTGAGTGTGTCAGAGACCGCTG 729
Db 1013 GAGCTGCGGCTGCGGCTGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1072
QY 730 AACATCATTTACTTGTGCAATCACGCGCTATTATCATCTCTGTGTTGATGACAGTGT 789
Db 1073 AACATCATTTGCTGCTCTATTTATTTCTTCTATGCGACGTTGGCTGTAGACACCAAG 1132
QY 790 ACAGCGAGAACTCTCAACTCCAGAGGCTGGAGTCACTTGGAGGTACTTAGAATGATG 849
Db 1133 GAGGAAGAGAGTGAAGATATTGAAACATGCGCAAGGTGCTCCAGATCTTACGCTTATG 1192
QY 850 AGGATTTTGGGTGATTAAGCTTGGCGCTCACTTCTTCTGCTTTCAGACACTCGGTTTG 909
Db 1193 AGGATTTTGGGTGATTAAGCTTGGCGCTCACTTCTTCTGCTTTCAGACACTCGGTTTG 1252
QY 910 ACTCTAAAGCTGCTACCGAGAGATGGTTATGTTACTTGTCTTCTTCTTCTTCTTCTTCT 969
Db 1253 ACCTGAGACACAGCTACCACTGAAGTTGGGCTTCTGCTTCTTCTTCTTCTTCTTCTTCT 1312
QY 970 GCATCTTTAGTGCACCTTCTCAGCTTCTTGAACATGGGCTGGACCTGGGAAACATCAAC 1029
Db 1313 TCCATTTTCTG-----TGCTTATCTCTCGGTGAGAAAGATGACCACACA 1360
QY 1030 AAGGACTTTTACAGCAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1089
Db 1361 TCCAGCCTCACCAGCAATCCCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1420

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QY 1090 GGCTATGGAGATGATGATCTCTATCAGATGCTCGGAGAAATCTTTGAGGAGTTTGTGTT 1149
Db 1421 GGGTATGGAGACACCCACCGGTCTCTTTGGCGGAAAGCTCTATCGCCAGCATGTCATC 1480
QY 1150 GTCAGTGAATTTGTTTATTTGCAATTAACCTATACATTTTATTTATCTACATAGCTTTGTCAG 1209
Db 1481 ATCTGTGGCATCTTGTGGTGGCCCTTCCATCACCATCATCTTCAACAAGTTTCCAAAG 1540
QY 1210 TGTATCATGAGCTCAAG 1227
Db 1541 TACTACAGAAGCAAAAG 1558

RESULT 11
US-09-336-643A-5
; Sequence 5, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2293
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (330)...(1800)
; OTHER INFORMATION: K-Hnov6
US-09-336-643A-5

Query Match 11.4%; Score 146; DB 4; Length 2293;
Best Local Similarity 48.0%; Pred. No. 2.3e-24;
Matches 585; Conservative 0; Mismatches 585; Indels 48; Gaps 4;

QY 37 CTGACCTGGCGCGCGCGGTTTCTGCTGCTCCGGGAGCTGCTGAAGACTTCCCGCTG 96
Db 384 CTGAATGTGGGGCTTTTAAGCACTGTGTTGACAAAGACCCCTCTCGGGTTTCTCTAC 443
QY 97 CGCGCGCTGACCGGCTGCACGCGCTGCGCTCCGAGCGGACGTCGTGCGAGGTGTCGAC 156
Db 444 ACCAGACTGGGAAGCTGCTTACTTGCCATTTGAAAGAGGCCATCTCGGAGCTGTGTAT 503
QY 157 GACTACACCGGAGCGCACGAGTACTTCTTCGACCGGCACTCGGAGGCTTCGCGTTC 216
Db 504 GATTACAGTGTGGCCGATAAGGAATACTACTTGTATCGGAATCCCTCTTTGTTTCAATAT 563
QY 217 ATCTGCTCTACTGCTCGCGGCCACCGCAAGCTGCGTTCTCGCGCGCGGAGTGTGCGAGCTC 276
Db 564 GTTTTGAAT--TTTATTACCGGGGAAGCTCATGTCTATGAGGAGCTGTGCGTATTC 620
QY 277 TCCTTTACACAGATGATCTACTTGGGCGCTGGAGGCGCGCACCTCGAGTACTCTGTC 336
Db 621 TCATTCTGCCAGGAGATCGAGTACTGGGGCATCAACGAGCTCTTCATTGATTTCTGCTGC 680
QY 337 CAGCGCGCTCGACGACCGCATGTCCGACACCTACACCTTCTACTCGGCGGACGAGCGG 396
Db 681 AGCAATCGCTACAGGACCGCAAGAGGAAAAACACGAGAGGACTGGGACCAAGAAAGC 740
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QY 397 GGCTGCTGGCGCCCGGAC-----GAGGCGCCGCCCGGC 429
Db 741 CATGATGTGATCCGACTCCTCGTTTGAAGAGTCGTCCTCTGTTTGAAGAAAGAGCTGGAG 800
QY 430 GGGCCGAGGGGCTCCTCCAGGCGCTGGCTGGAGCGCATGGCGGACCTTCGAGGAG 489
Db 801 AAGTTTGACACACTGCGAATTTGGTCAGCTCCGGAAGAAAATCTGGATTGAATGGAGAAT 860
QY 490 CCCACGCTGCTGCTGGCGCGCGCAGATCCTGGCTAGCGTGCCTGGTGGTGTTCGTGATCGTG 549
Db 861 CCAGGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 920
QY 550 TCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 609
Db 921 TCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 980
QY 610 CGCAGCCTGGATGACCGGAGCAGGATAATGAAGCTATCTGCATAGTTGTTTCACTGCC 669
Db 981 GATGATCCGGTGTGGAAGAGTGGAGTCG-----CGTGCATTGCTGCTGCTGCTGCTGCTG 1034
QY 670 GAGTGCATCTGAGGTTTCTTCTTCCAAAACAAGTGTGAGTTTGTCAAGAGACCCCTG 729
Db 1035 GAGCTTGGCGTCCGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1094
QY 730 AACATCATGTTTACTTGGCAATCACCGCTATACATCTCTGTTGATGACAGTGTGTT 789
Db 1095 AACATCATGTTGACTTTGCTCTTATTATTCCTTCTATGCCACGTTGGCTGTAGACACCAAG 1154
QY 790 ACAGCGAGAACTCTCAACTCCAGAGGCTGGAGTCACTTGAAGGTPACTTAGAATGATG 849
Db 1155 GAGGAAGAGAGTGAAGTATTTGAGAACATGGGCAAGTGTCCAGATCCTACGGCTTATG 1214
QY 850 AGGATTTTGGGTGATTAAGCTTCCCGCTCACTTCACTTGGTCTTCAAGACTCGGTTG 909
Db 1215 AGGATTTTCCGAATTTAAAGCTTCCCGCTCACTCGGTAGGACTTCGGTCTCTAGGTGCC 1274
QY 910 ACTCTCAAAAGCTTCTACCGAGAGATGTTATGTTTACTTGTCTTCTTCTTCTTCTTCTG 969
Db 1275 AACTGAGACACACTACCATGAATTTGGCTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCT 1334
QY 970 GCAATCTTTAGTGACATTTCTCAGCTTCTTCAACATGGGCTGGACCTGGAAACATCCAAC 1029
Db 1335 TCCATTTTCTCTG-----TGCCTTATCTACTCCGTTGGAGAAAGATGACCAACA 1382
QY 1030 AAGGACTTTACAGCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1089
Db 1383 TCCAGCTTACAGCATCTCCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1442
QY 1090 GGCTATGGAGATGATGATCTATCAGAGTGCCTGGAAAGAAATCTTTGAGGAGTTTGTGTT 1149
Db 1443 GGCTATGGAGACACCCACCGGTCACCTTGGCGGAAAGCTCATCGCCAGCACATGCATC 1502
QY 1150 GTCAGTGAATTTGTTTATTTGGCAATTAACCTATCACTTTTATCTACCATAGCTTTGTCCAG 1209
Db 1503 ATCTGTGCACTTTGGTGGTGGCCCTTCCCATCACCATCATCTTCAACAAGTTTCCAAG 1562
QY 1210 TGTATCATGAGCTCAAG 1227
Db 1563 TACTACAGAAGCAAAAG 1580
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RESULT 12
US-09-016-434-169
; Sequence 169, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
```


ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016.434
FILING DATE: HERWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAINOT12
CLONE: 1413667
US-09-016-434-169

Query Match	9.5%;	Score 122;	DB 4;	Length 267;
Best Local Similarity	68.8%;	Pred. No. 3.9e-19;		
Matches 183;	Conservative 0;	Mismatches 80;	Indels 3;	Gaps 17;
QY	48	CGCGCCCGGATTGCTGTGTCGCGGAGCTGCTGAAGACTTCCCGCTGCGCGCGTGAG	107	
Db	1	CGGCATCAAGTACTGCTGCTGCCCTGGACAACGCTGGACGAGTTCGCGCTGACGCGCTGGG	60	
QY	108	CGCGGTGCACGGCTGCCGCTCCGAGCGCGACGCTCTCGAGGTGTGGAGCATACGACGG	167	
Db	61	CGAGCTCAAGGCTGCACCAACTTCGACGACATCTCTCAAGTGTGGATGATACGAGCT	120	
QY	168	CGAGCGCAACGAGTACTTCTTCGACCGGCACCTCGAGGCCTTCGGCTTCATCTCTCTA	227	
Db	121	CACCTGCAACGAGTTCCTTCGACCGCAACCCGGGGGCGCTTCGGCACTATCTGACCTT	180	
QY	228	CGTGGCGGCGCACGCGAGCTGCCTTCGGCGCGCGGAGTGGCGAGCTCTCTCTCAAA	287	
Db	181	CTTGGCGG---CGGGCAAGCTTCGGGCTGTGCGGAGATGTGGCGCGCTCTCTTCAGGA	237	
QY	288	CGAGATGATCTACTGGGCGCTGGAGG	313	
Db	238	GGAGCTGTGTACTGGGCGATCGGG	263	

RESULT 13
US-09-181-339-8
; Sequence 8, Application US/09181339
; Patent No. 6610827
; GENERAL INFORMATION:
; APPLICANT: Forsayeth, John R.
; APPLICANT: Zhao, Byron
; APPLICANT: Chavez, Raymond C.
; TITLE OF INVENTION: POTASSIUM CHANNEL SUBUNIT POLYPEPTIDE
; TITLE OF INVENTION: AND POLYNUCLEOTIDE COMPOSITIONS AND USES THEREFOR
; FILE REFERENCE: 5865-0033.30

```

; CURRENT APPLICATION NUMBER: US/09/181.339
; CURRENT FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 60/063,450
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 1273
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(1273)
US-09-181-339-8

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	Query Match	9.0%;	Score 115.4;	DB 4;	Length 1273;
	Best Local Similarity	50.3%;	Pred. No. 2e-17;		
	Matches 377;	Conservative 0;	Mismatches 351;	Indels 21;	Gaps 3;
QY	482	TGAGGAGCCACGTCGTGCGCTGGCGCGCAGATCCTGGCTAGCGTGC	CGGTGGTGTTCG	541	
Db	318	TGGAGAAATCCAGGTA	CTGCTTGGCTTAAAGCTTATCGCTATCTCCTCTTGGAGCGTG	377	
QY	542	TGATCGTGTCCATGTTGGTGTGTCGTGGGCCAGCAGTTCGCCGAC	TGGCGCAGCGACCGCG	601	
Db	378	TGCTGGCCCTCCATCGTGGCCATGTGGTTCACAGCATGTTCGAGTTC	CCAGATGAGGATC	437	
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Db	792	CTGTGGGCATTTCCATTTTCTCTG-----TGCTTATCTACT	CCGTGGAGAAAG	839	
QY	1019	AAACATCCAAACAGGACTTTACAGCATTTCTGTCCTCTGCTGGT	GGGTGATATTCTCTA	1078	
Db	840	ATGACCACACATCCAGCCTCACGAGCATCCCATCTGCTGGTGG	GGCCACCATCAGCA	899	
QY	1079	TGACTACAGTTGGCTATGAGATATGATTCCTATCACAGTGCCT	GGAAGATTTCTTGGAG	1138	
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QY	1139	GAGTTTGTCTGTGTCAGTGGAAATGTTTCTATTGGCATTACCT	ATCATCTTTTATCTACATA	1198	
Db	960	GCACATGCATCATCTGTGGCATCTTGGTGGTGGCCCTTCCCAT	CACCATCTTCAACA	1019	
QY	1199	GCTTTGTGCAGTGTATTATCATGAGCTCAAG	1227		
Db	1020	AGTTTTCCAAAGTACTACCAGAGCAAAAG	1048		

RESULT 14

US-10-162-012-7
 ; Sequence 7, Application US/10162012
 ; Patent No. 6682597
 ; GENERAL INFORMATION:
 ; APPLICANT: Curtis, Rory A.J.
 ; APPLICANT: Silos-Santiago, Inmaculada
 ; APPLICANT: Gu, Wei
 ; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
 ; FILE REFERENCE: 10448-190001
 ; CURRENT APPLICATION NUMBER: US/10/162,012
 ; CURRENT FILING DATE: 2002-06-04
 ; PRIOR APPLICATION NUMBER: US 60/209,845
 ; PRIOR FILING DATE: 2000-06-06
 ; PRIOR APPLICATION NUMBER: US 09/875,321
 ; PRIOR FILING DATE: 2001-06-06
 ; PRIOR APPLICATION NUMBER: PCT/US01/18340
 ; PRIOR FILING DATE: 2001-06-06
 ; PRIOR APPLICATION NUMBER: US 60/209,257
 ; PRIOR FILING DATE: 2000-06-05
 ; PRIOR APPLICATION NUMBER: US 09/875,423
 ; PRIOR FILING DATE: 2001-06-05
 ; PRIOR APPLICATION NUMBER: PCT/US01/18398
 ; PRIOR FILING DATE: 2001-06-05
 ; PRIOR APPLICATION NUMBER: US 60/209,238
 ; PRIOR FILING DATE: 2000-06-05
 ; PRIOR APPLICATION NUMBER: US 09/875,363
 ; PRIOR FILING DATE: 2001-06-05
 ; PRIOR APPLICATION NUMBER: PCT/US01/18247
 ; PRIOR FILING DATE: 2001-06-05
 ; PRIOR APPLICATION NUMBER: US 60/227,068
 ; PRIOR FILING DATE: 2000-08-22
 ; PRIOR APPLICATION NUMBER: US 09/928,530
 ; PRIOR FILING DATE: 2001-08-13
 ; PRIOR APPLICATION NUMBER: PCT/US01/25475
 ; PRIOR FILING DATE: 2001-08-15
 ; PRIOR APPLICATION NUMBER: US 60/226,770
 ; PRIOR FILING DATE: 2000-08-21
 ; PRIOR APPLICATION NUMBER: US 09/934,421
 ; PRIOR FILING DATE: 2001-08-21
 ; PRIOR APPLICATION NUMBER: PCT/US01/26096
 ; PRIOR FILING DATE: 2001-08-21
 ; PRIOR APPLICATION NUMBER: US 60/279,281
 ; PRIOR FILING DATE: 2001-03-28
 ; PRIOR APPLICATION NUMBER: US 10/109,029
 ; PRIOR FILING DATE: 2002-03-28
 ; PRIOR APPLICATION NUMBER: PCT/US02/09728
 ; PRIOR FILING DATE: 2002-03-28
 ; PRIOR APPLICATION NUMBER: US 60/290,288
 ; PRIOR FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: US (not assigned)
 ; PRIOR FILING DATE: 2002-05-13
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 7
 ; LENGTH: 1341
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(1338)
 ; US-10-162-012-7

Query Match 8.9%; Score 113.4; DB 4; Length 1341;
 Best Local Similarity 47.0%; Freq. No. 5.9e-17;
 Matches 508; Conservative 0; Mismatches 546; Indels 27; Gaps 4;

Qy 152 GCGACGACTACGACCGGAGCGGAGTACTTCTTCGACCGGCACTCGAGGCTTCG 211
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Qy 212 GCTTCATCTGCTCTACGTCGCGGCGGACGCGGAGTCTTCGCGCGGAGTTCG 271
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Qy 272 AGCTCTCTCTTCAACAGAGATGATCTACTGGGCTTGGAGGGCGGCGCACCT-----CG 325
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 Qy 326 AGTACTGCTGCCAGCGCGCTCGACGACGCGATGTCGACACCTACACCTTCTACTCGG 385
 Db 287 TCGCGAGGAGGAGGCTGCCGCTGCGGCGCGGAGCGCCCTGCGCGCGGCGCTTCG 346
 Qy 386 CCGACGAGCGGCGGCTGCTGGGCGCGGAGGCGCGCGCGGCGGCGGCGGCGGCGCTC 445
 Db 347 CCGCGCAGCTGTGCTGCTTTTCGAGTTTCCGAGAGCTCTCAGGCGCGGCGGCTGCTG 406
 Qy 446 CCTCAGGCGCTGCTGAGGCGATGCGGCGGCTTCGAGGAGCGGCGGCGGCGGCTG 505
 Db 407 CCGTAGTCTCGTGTGCTCATCTCTGCTCTCCATCTGCTGCTTCTGCTCGAGCGCTGC 466
 Qy 506 CCGCGCAGATCTGGCTAGGCTGCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 565
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 Db 527 TCCCCGCTCGCTGAAATGGGCTTCAGCCAAATGCTGGAATTCACCCCGCTCGCTTCA 586
 Qy 620 ATGACCGGAGCAGGATTAATGAAGCTATCTGCATAGGTTGGTTCACTGCGGAGTGCATG 679
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 Qy 740 ATTTACTGGCAATCAAGCGCTTATTACATCTCTGTGTGA--TGACAGTGTTTACAGCG 796
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 Qy 1037 TTACGACATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1096
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 Qy 1097 GAGATATGATCTTATCAGAGTGGCTGGAAGATTTCTGAGAGGTTGTTGTTGCTGCTG 1156
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 Qy 1217 A 1217
 Db 1175 A 1175

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; Patent No. 5610827
; GENERAL INFORMATION:
; APPLICANT: Forsayeth, John R.
; APPLICANT: Zhao, Byron
; APPLICANT: Chavez, Raymond C.
; TITLE OF INVENTION: POTASSIUM CHANNEL SUBUNIT POLYPEPTIDE
; TITLE OF INVENTION: AND POLYNUCLEOTIDE COMPOSITIONS AND USES THEREFOR
; FILE REFERENCE: 585-0033.30
; CURRENT APPLICATION NUMBER: US/09/181.339
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 60/063,450
; FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 2799
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)...(1647)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2799)
; OTHER INFORMATION: n = A,T,C or G
US-09-181-339-2

Query Match      8.4%; Score 107.8; DB 4; Length 2799;
Best Local Similarity 48.1%; Pred. No. 1.4e-15;
Matches 620; Conservative 0; Mismatches 567; Indels 102; Gaps 7;

QY 9 CGGGCGACGCGGGCGGCTCGTGGTGTGTAACCTGGCGCGCGCGCGGTATTCGTGTC 68
DB 192 CTGGCGGCTAGAGACGARGCGCTCGGCGTGAACCTGGCGGAGTGGCGGCGTCTGAG 251
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QY 522 TAGCGGTGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 581
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QY 582 CGACT-----GGCGCAACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 617
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DB 1089 AGTGAAGTGTTCGCGCTCATGCGCATCTTCGCGTGTCTCAGCTGGCGGCGCATCCAC 1148
QY 888 TGGTCTTCAGACACTCGGTTTGAATCTCAAACTTGTCTACCGAGAGATGTTATGTTACT 947
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DB 1371 GCTGGCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1430
QY 1188 TATCTACCATAGCTTTTGTGCGAGTGTATC 1216
DB 1431 CATCTTCAACAGTTTTTCCACATCTTACC 1459
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Search completed: October 6, 2004, 20:35:57
Job time : 127 secs

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LOCUS	UI-R-CO-jl-g-04-0-UI-s1	UI-R-CO-jl-g-04-0-UI-3'	UI-R-CO	Rattus norvegicus	cdna	clone
DEFINITION	UI-R-CO-jl-g-04-0-UI-s1	UI-R-CO-jl-g-04-0-UI-3'	UI-R-CO	Rattus norvegicus	cdna	clone
ACCESSION	AI043703	AI043703.1	GI:3290438			
VERSION	AI043703	EST.				
KEYWORDS	Rattus norvegicus					
SOURCE	Rattus norvegicus					
ORGANISM	Rattus norvegicus					
REFERENCE	1 (bases 1 to 523)					
AUTHORS	Bonaldo,M.F., Lennon,G. and Soares,M.B.					
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery					
JOURNAL	Genome Res. 6 (9), 791-806 (1996).					
PUBMED	97044477					
COMMENT	8889548					
	Contact: Soares, MB					
	Coordinated Laboratory for Computational Genomics					
	University of Iowa					
	375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA					
	Tel: 319 335 8250					
	Fax: 319 335 9565					
	Email: bento-soares@uiowa.edu					

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	437.4	34.2	500	28	AQ402619	AQ402619 HS_5086A
3	433.6	33.9	509	29	CG639652	CG639652 OST371309
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RESULT 3
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DEFINITION OST371309, genomic survey sequence.
ACCESSION CG639652
VERSION CG639652.1 GI:37463501
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 509)
Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.

TITLE Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT Contact: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.

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ORIGIN
Query Match 33.9%; Score 433.6; DB 29; Length 509;

Best Local Similarity 93.0%; Pred.No. 3e-62;
Matches 465; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

QY 631 AGGATAAATTAAGAGCTATCTGCATAGGTTGGTTCACTGCCAGTGCATCTGAGGTTCAAT 690
Db 5 AGGATAAATTAAGAGCTATCTGCATAGGTTGGTTCACTGCCAGTGCATCTGAGGTTCAAT 64
QY 691 GCTCTCCAAAACAAGAGTGTGAGTTGTCAGAGACCCCTGAAACATCATTTACTTACTGGCA 750
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QY 751 ATCAC-GCGGTATTACATCTCTGTGTGTGATGACAGTGTGTTACAGGAGAACTCTCAACT 809
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QY 810 CCAGAGGGGTGGAGTCACTTGGGTGCTTGAAGATGAGGAGTATTTTGGGTGATTA 869
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QY 870 GCTTGGCCCGCTCACTTCATTTGGTCTTCAGACACTCGGTTTGTGACTCTCAACAGTTGTACCG 929
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Db 305 AGAGATGGTTATGTTACTTGTCTTCAATTTGTGTCATGGCAATCTTTAGTGCATTTTC 364
QY 990 TCAGCTTCTTGAACATGGGCTGGACCTGCAACATCCAAACAGGACTTTACCAGCATTC 1049
Db 365 TCAGCTTCTTGAACATGGGCTGGACCTGCAACATCCAAACAGGACTTTACCAGCATTC 424
QY 1050 TGTGCTGCTGCTGGTGGTGAATATCTCTATGACTACAGTTGGCTATGGAGATGATATCC 1109
Db 425 CGCTGCTGCTGGTGGTGAATATCTCTATGACTACAGTTGGCTATGGAGATGATATCC 484
QY 1110 TATCACAGTGCCTGGAGAA 1129
Db 485 TATCACAGTGCCTGGAGAA 504

RESULT 4
CG662016 484 bp DNA linear GSS 02-OCT-2003
LOCUS OST444129 Mus musculus 129SV/Ev Mus musculus genomic clone
DEFINITION OST444129, genomic survey sequence.
ACCESSION CG662016
VERSION CG662016.1 GI:37485865
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 484)
Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.

TITLE Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT Contact: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.

FEATURES
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 Db TGAGCTTCGAGCGTGTCTACCGGAAATGATGCTCTCTGCTCTTCATCTGCGTTGCCA 757
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 Db TGGCGATCTTCAAGTGCATCGACAGCTGCTGGAGCAGCGGCTCGACTTGAAGCGGAA 817
 QY ACAAGGACTTTACACAGCATCTCTGCTGCTGCTGCTGGGTGATTTATCTCTATGACTACAG 1087
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 QY TTGGCTATGGAGATATGATCTATACAGTGCCTCGGAGAAATCTTGGAGGAGTTTGTG 1147
 Db TGGGTACGGGACATGTACCGGCTGACGGTGGCAGCGCGGCTGCTGGGCGGGCTGTGCG 937
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RESULT 6
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 DEFINITION sequence.
 ACCESSION BU274588
 VERSION BU274588.1 GI:25545538
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
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 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 REFERENCE 1 (bases 1 to 772)
 Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 A Comprehensive Collection of Chicken cDNAs
 Curr. Biol. 12 (22), 1965-1969 (2002)
 22335534
 12445392
 Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.
 Location/Qualifiers
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 /mol_type="mRNA"
 /strain="Compton line 151"
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 ECoRI; Site_2: NotI; This normalized library was
 constructed from 1 million independent clones. cDNA
 synthesis was initiated using an oligo(dT) primer, using
 methylated C in the first strand synthesis reaction.
 Following this first strand reaction, double-stranded cDNA
 was blunted, ligated to NotI adapters, digested with

FEATURES

source
 CG582101 487 bp DNA linear GSS 02-OCT-2003
 LOCUS CG582101
 DEFINITION OST222985 Mus musculus 129Sv/Ev Mus musculus genomic clone
 OST222985, genomic survey sequence.
 ACCSSION CG582101
 VERSION CG582101.1 GI:37379484
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 487)
 Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
 Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
 Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
 Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
 Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
 Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,

ECoRI, size-selected, and cloned into the NotI and EcoRI
 compatible sites of a custom modified MCS of the
 pBluescript (KS+) vector. The library was normalized in 2
 rounds using conditions adapted from Soares et al., PNAS
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
 (1996): 791, except that a significantly longer
 reannealing hybridization was used."

ORIGIN

Query Match 28.3%; Score 361.4; DB 13; Length 772;
 Best Local Similarity 81.3%; Pred. No. 3.5e-50;
 Matches 482; Conservative 0; Mismatches 101; Indels 10; Gaps 5;
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 QY 692 TCTCCAAAACACAGTGTGATTTGTCAAGAGACCCCTGAACATCATTTGATTTACTGGCAA 751
 Db 190 TTTCAAAGAACAAAGTGTGATTTGTGAGAGACCTCTCAACATTTATTTACTGGCAA 249
 QY 752 TCACGCCGTATTACATCTCTGTGTTGATGACAGTGTTTACAGCGGAGAACTCTCAACTCC 811
 Db 250 TTACTCTTACTACATCTCTGTTCTAATGACAGTTTTTACAGGGGAAATTCGCAACTCC 309
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 Db 368 TGCTCTGTCATTTTCATTGTCCTTCAACACATTTGTTGCTGACTCTGAAGCGTTGTCAGAG 427
 QY 932 AGATGGTTATGTTACTTGTCTTCATTTGTTGTTGCCATGGCAATCTTTAGTGCACTTCTC 991
 Db 428 AGATGGTGTATGTCCTTGTCTTTATCTGTTGTTGCTATGCGCAATTTTCAGTGCATTTCCC 487
 QY 992 AGCTTCTTGAACATGGCTGGACCTGGAACATCCCAAGAGACTTTACCAGCATTCCTG 1051
 Db 488 AGCTGTTGAAATGGCTGGACTTTGGGACAAAGAAATAGGATTAAGCAGATCCCTG 547
 QY 1052 CTCGCTGCTGGTGGGTGATTAATCTCT-ATGACTACAGTTGGGTATGGAGATATGATTCCT 1110
 Db 548 CTCGCTGGTGGTGGGTGATCATCTCTCATGACCACAGTTGGTTACGCTGCATGTTGTCCTCC 607
 QY 1111 ATCACAGTGCCTGGA--GAATTCCTGGAG--AGTTGTTGTTGTCAGTGAATTTCT 1166
 Db 608 ATCACAGTACCGGAAAGGATTTCTTGGAGGAATCTGCGTGGTGTAGTGGCATCGTTTT 667
 QY 1167 ATTGGCATTAACCTA--TCACCTTTTATCTACCATAGCTTTGTGCACTGTTTATC 1216
 Db 668 ACTAGCCCTTGCCAAATCACCTTTTCATTATCATAGCTTTGTGCACTGTTTACC 720

TITLE Zhu, Q., Person, C. and Sands, A.T.
JOURNAL Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
COMMENT Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
 Contact: Zambrowicz BP
 OmniBank

LEADER Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
EMAIL Email: materials@lexgen.com
GENE Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
CLASS Class: Gene Trap. Location/Qualifiers

FEATURES source
 1. .487
 /organism="Mus musculus"
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 Best Local Similarity 88.9%; Pred. No. 7.7e-49;
 Matches 433; Conservative 0; Mismatches 48; Indels 5; Gaps 5;

637 ATTGAAGCTATCTGCATAGTGGTTGTTCACTGCG-AGTGCATCGTGAGTTCAATTGCTC 695
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 696 CAAACACAGTGTGAGTTGTTCAAGAGCCCTGACATCATTTACTTGGCAATCAC 755
 Db 61 CAAACACAGTGTGAGTTGTTCAAGAGCCCTGACATCATTTACTTGGCAATCAC 120
 756 GCGTATTACATCTCTGTGTTGATGACAGTGTGTTACAGCGGA-GAATCTCAACTCCAGA 814
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 1111 ATCACAG 1117
 Db 481 ATCACGG 487

RESULT 8
LOCUS AY417320
DEFINITION Mus musculus KCNbl gene, partial sequence, GSS 17-DEC-2003
ACCESSION AY417320
VERSION AY417320.1 GI:39773280
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2562)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
 Adams, M.D. and Cargill, M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
 Science 302 (5552), 1960-1963 (2003)

JOURNAL 14671302
PUBMED 14671302
REFERENCE 2 (bases 1 to 2562)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
 Adams, M.D. and Cargill, M.

TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment.

FEATURES source
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 /locus_tag="HCM6184"

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 Best Local Similarity 53.8%; Pred. No. 6.9e-34;
 Matches 650; Conservative 0; Mismatches 531; Indels 27; Gaps 4;

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 83 AGGACTTCGCGTGGCGGGTGGCGGGTGGCGGGTGGCGGGTGGCGGGTGGCGGGTGGCG 142
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 Db 494 CTGAGAGAGGAGAAACCTTGGGACCTTCG-----TGGAGAGGCGCAACTCATCGG 544
 503 TGGCGCGGAGATCTCGGTAGGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 562
 Db 545 TGGCGCGGAGATCTCGGTAGGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 604
 563 TGTGCGCGACGAGCTTGGCGGAGCTGGCGCAACGCGAGCGGCGGCGGCGGCGGCGGCGG 622

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725 TGAGGTTCTGCTCCCTGCGCCCAAGAAATGGAAGTCTTTTAAGGCGCCCTCCACGCCAT 784
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1025 CGAGCTGTGCTTCTTGGCGAGAGGATGAGGA-----TGACCAAGTTCA 1072
1040 CCAGCATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1099
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1253 AGCAGAAG 1260

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RESULT 9

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DEFINITION
Homo sapiens KCNB1 gene, DNA linear GSS 17-DEC-2003
genomic survey sequence.
ACCESSION
AY417318
VERSION
AY417318.1 GI:39773278
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2565)
Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 2565)
Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,

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TITLE
JOURNAL
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
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Best Local Similarity 53.7%; Pred. No. 3e-33;
Matches 645; Conservative 0; Mismatches 529; Indels 27; Gaps 4;
QY 30 GGTGGTCTGACAGTGGCGCGCGCCCGTATTGCTGTCGCGGAGCTGCTGAGGACTT 89
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QY 747 GGCATCACGCGCTATATCATCTCTGTTGTGATGACAGTGTTTACAGCGGAGACTCTCA 806
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QY 807 ACTCCAGAGGGCTGAGTCACTTGGGGTACTTAGAATGATGAGGATTTTGGGTGAT 866

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Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.

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TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 PUBMED 8889548
 COMMENT Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: benton-soares@uiowa.edu
 Oligo-dT track not found, Not I site shown in beginning of sequence
 is likely internal to the message. cDNA Library Preparation: M.
 Fatima Bonaldo, Ph.D. Clone distribution: clones will be available
 through Research Genetics This clone is also available through the
 I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE
 ID=1787504
 Seq primer: M13 Forward
 POLYA=No.

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 /mol_type="mRNA"
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 /db_xref="taxon:10116"
 /clone="UI-R-C2p-oh-e-08-0-UI"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="UI-R-C2p"
 /note="Vector: pT73D-pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-C2p
 library is a subtracted library derived from the UI-R-C1
 library, which is a subtracted library derived from the
 UI-R-C0 library. The UI-R-C0 library consisted of a
 mixture of individually tagged normalized libraries
 constructed from rat placenta, adult lung, brain, liver,
 kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day
 embryo. The tag is a string of 3-5 nucleotides present
 between the Not I site and the oligo-dT track which allows
 identification of the library of origin of a clone within
 the mixture. The subtracted library (UI-R-C2p) was
 constructed as follows: PCR amplified cDNA inserts from
 UI-R-C1 clones from which 3' ESTs had been derived was
 used as a driver in a hybridization with the UI-R-C1
 library in the form of single-stranded circles. The
 remaining single-stranded circles (subtracted library) was
 purified by hydroxyapatite column chromatography,
 converted to double-stranded circles and electroporated
 into DH10B bacteria (Life Technologies) to generate the
 UI-R-C2p library. This procedure has been previously
 described (Bonaldo, Lennon and Soares, Genome Research 6:
 791-806, 1996)"

ORIGIN
 Query Match 18.7%; Score 239; DB 9; Length 298;
 Best Local Similarity 88.9%; Pred. No. 6.4e-30;
 Matches 273; Conservative 0; Mismatches 25; Indels 9; Gaps 1;
 295 ATCTACTGGGCTGGAGGGCGGACCTCGAGTACTGCTCCAGCGCGCTCGACGAC 354
 298 ATCTACTGGGCTGGAGGGCGGACCTCGAGTACTGCTCCAGCGCGCTCGACGAC 239
 355 CGCATGTCCGACACCTTCTACTCGGCCGACGAGCGGGCGTGTGGCGCGCGAC 414
 238 CGCATGTCCGACACCTTCTACTCGGCCGACGAGCGGGCGTGTGGCGCGCGAG 188
 415 GAGGGCGCGCGGCGGCGGCGGCTCCCTCCAGCGCTGCTGAGCGCATGCGG 474
 187 CAGCCTCGTCCACCCGCGGCGGCGGCTCCCTCCGCGCGCTGCTGAGCGCATGCGG 128
 475 CGGACCTTCGAGGAGCCACGTCGCTCGCTGGCGGCGGACAGATCCTGGCTAGCGTGTGCGGTG 534

Db 127 CGGACCTTCGAGGAGCCACGTCGTCGTCGCGCGAGATCCTGGCCAGCGTGTCCGTG 68
 QY 535 GTGTTCTGTGATCGTGTCCATGGTGTCTGTGCGCCAGCAGCTTGCCTGCGCAAC 594
 Db 67 GTGTTCTGTGATCGTGTCTATGTTGTGCTGTGCGCCAGCAGCTTGCCTGCGGAGCTGCGGCGG 8
 QY 595 GCAGCGG 601
 Db 7 GCGGCGG 1
 RESULT 12
 LOCUS CE495701 301 bp DNA linear GSS 28-SEP-2003
 DEFINITION tigr-gss-dog-17000327301868 Dog Library Canis familiaris genomic,
 genomic survey sequence.
 ACCESSION CE495701
 VERSION CE495701.1 GI:36812482
 KEYWORDS GSS
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 REFERENCE 1 (bases 1 to 301)
 AUTHORS Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
 Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
 Venter, J.C.
 TITLE The dog genome: survey sequencing and comparative analysis
 JOURNAL Science 301 (5641), 1898-1903 (2003)
 MEDLINE 22875432
 PUBMED 14512627
 COMMENT Contact: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirknes@tigr.org
 Class: shotgun
 Location/Qualifiers
 1. 301
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /note="Site 1: BstXI; Libraries were prepared from
 peripheral blood"

ORIGIN
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 Best Local Similarity 98.6%; Pred. No. 1.3e-25;
 Matches 215; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 ATGACCTTCGCGCGCAGCGGGCGGCTCGTGGTGTGTAACGTGGCGCGCGCGGTAT 60
 Db 218 ATGACCTTCGCGCGCAGCGGGCGGCTCGTGGTGTGTAACGTGGCGCGCGGTAT 159
 QY 61 TCGCTGTCCGCGAGCTGCTGAAGGACTTCCCGCTGCGCGCGTGAAGCGCGCTGACGGC 120
 Db 158 TCGCTGTCCGCGAGCTGCTGAAGGACTTCCCGCTGCGCGCGTGAAGCGCGCTGACGGC 99
 QY 121 TGGCGCTCCAGCGCGAGCTGCTCGAGGTTGTCGACGACTACGACCGGAGCGCAACGAG 180
 Db 98 TGGCGCTCCAGCGCGAGCTGCTCGAGGTTGTCGACGACTACGACCGGAGCGCAACGAG 39
 QY 181 TACTTCTTCACCGGCACTCGGAGGCTTCGGCTTCAT 218
 Db 38 TACTTCTTCACCGGCACTCGGAGGCTTCGGCTTCAT 1
 RESULT 13
 BJ495239

LOCUS BJ495239 652 bp mRNA linear EST 08-AUG-2002
 DEFINITION BJ495239 MF01FSA cDNA Oryzias latipes cDNA clone MF01FSA038D18 5', mRNA sequence.
 ACCESSION BJ495239
 VERSION BJ495239.1 GI:22147165
 KEYWORDS EST.
 SOURCE Oryzias latipes (Japanese medaka)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
 REFERENCE 1 (bases 1 to 652)
 AUTHORS Kohara, Y., Shin-i, T., Kimura, T., Narita, T., Jindo, T. and Takeda, H.
 TITLE Medaka EST Project in Takeda's lab
 JOURNAL Unpublished (2001)
 COMMENT Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.
 FEATURES
 source
 1..652
 /organism="Oryzias latipes"
 /mol_type="mRNA"
 /strain="d-PR"
 /db_xref="taxon:8090"
 /clone="MF01FSA038D18"
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 /clone_lib="MF01FSA cDNA"
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 Best Local Similarity 62.5%; Pred. No. 2.1e-23;
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 34 GTCTGAACGTGGCGGCGCGCGGATTCGCTGTCCTGGGAGCTGCTGAAGACTTCGG 93
 78 GTACTCAATGTTGGGGGAACCGGTACGCTTCACTCGTGAGTGATCAAGGATTCCT 137
 94 CTCGCGCGGTGAGCGGCTGACGCTGCGCTCGGAGCGGAGCTGCTCGAGGTGTC 153
 138 CTCGCGCGGTGAGCGGCTGATGATGCGGACCGGAGGAGGCTTTAGACTGTGT 197
 154 GACGACTACGACCGGAGCGGACGAGTACTTTTCGACCGGACCTCGGAGGCTTCGGC 213
 198 GATGACTATGACGAGACCGGATGAGTTTCTTCGACCGGACCGACGAGGCTTTGTC 257
 214 TTCACTCTGCTTACGTCGCGGCGGACGAGCTGCGCTTCGCGCGGAGTGTGCGAG 273
 258 TTCACTGATGTGACGTTTC---GTCGCGCAACTCCGATTTGTTCTCGAGTGTGAG 314
 274 CTCCTCTTCTACACGAGATGATCTACTGGGCTCGAGGGCGGCGACCTCGAGTACTGC 333
 315 CTGCTCTTCTACTCAGAAATGCTTTACTGGGGTTGGAGAGCGTGACCTGGACTCTGC 374
 334 TGCAGCGCGGCTCGACGACCGGCTGCGACACCTACCTTCTACTCGGCGGAGGAG 393
 375 TGTGAGAAACGCTGATGACAGGATGTCTGATAGGACTGTGACACTCTTTTCGAGGG 434
 394 CCGGGCGTGTGGCGCGGACGAGGGCGGCGCGGCGGCGGAGCGGCTCCCTCCAGG 453
 435 GACATAGTGTGTGACGGGAGGAGCGCTGAGACCCGAGAGCTGCGTACACGATTCGG 494
 454 CGC-----TGGCTGGAGCGGATCGCGGAGCTTCGAGAGCGGAGCTCG 498
 495 CTCACCGGACGCGCAAGTGGCTCGAGAGATCGCAAAACAGTTGAGGAGCGCAACTCC 554
 499 TCGCTGCGCGCGGACGATCTCTGGCTAGCGTGTGCTGGTGTGTTCTGTATCGTGTCCATGGTG 558

Db 555 TCTATTCCAGCGAGCTTTTAGCTTCAGTTCTGTGATTTCTGTGATTCATTCATGATA 614
 Qy 559 GTGCTGTGCGCCAGCAGCTTGCCTGCGGACTGG 588
 Db 615 ATGCTGTGTCGACGAGCTACCGGATTGG 644
 RESULT 14
 FR0020615/c
 LOCUS FR0020615
 DEFINITION F. rubripes GSS sequence, clone 042H13bF8, genomic survey sequence.
 ACCESSION AL013498
 VERSION AL013498.1 GI:2679866
 KEYWORDS GSS; genome survey sequence.
 SOURCE Takifugu rubripes (Fugu rubripes)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Takifugu.
 REFERENCE 1 (bases 1 to 505)
 AUTHORS Elgar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umrana, Y., Williams, G. and Brenner, S.
 TITLE Direct Submission
 JOURNAL Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hmp.mrc.ac.uk
 COMMENT Vector: pBluescript II KS
 V type: phagemid
 PRIMER: KS
 DSCR:
 One pass dye-terminator sequencing of cosmid cloned genomic sequence.
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 Location/Qualifiers
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 /mol_type="genomic DNA"
 /db_xref="taxon:31033"
 /clone="042H13bF8"
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 Best Local Similarity 64.0%; Pred. No. 1.8e-22;
 Matches 318; Conservative 0; Mismatches 177; Indels 2; Gaps 2;
 675 CATCGTCAGGTTTCTCTCCAAAACAAGTGTGAGTTGTCAAGAGACCCCTGAACAT 734
 505 CATCGTCGTTTCTGTTGTGTCAGAAACAAGTG-GACTTCTCGGAGGCCCTGAACAT 447
 735 CATGATTTACTGGCAATACGCGGTATTACATCTCTGTGTTGATGACAGTGTACAGG 794
 446 AATCGAGCTGATGCCATCAGCCGCTANTACGTACCATGNGCTGCGCGGCGCGGAT 387
 795 CGAGAACTCTCACTCCAGAGGCTGAGTCACTTTCAGGCTACTTAGAATGATGAGAT 854
 386 GCGCGGCTGGGCTGGGTGTGTCGCGGGTGTGCTCGGGTGTGCGGATGATGCGGCT 327
 855 TTTTGGGTGATTAAAGCTTCCCGTCACTTCATTGTCCTTTCAGACACTCGGTTTACTCT 914
 326 GTTCTGGCTGATGAAGCTGCGCAGACACTTCTGGGCTGCGAGAGCTGGGANTGAGCT 267
 915 CAACGTTGCTACCGAGAGTGTATTGTTACTTGTCTTCTTGTCTCCATGGCAAT 974
 266 CACGCGTGTCTACAGGAGATGTTGATGCTGCTGTTGTTGCTGCTGCTGCTGCTGCT 207
 975 CTTTAGTGCACTTTCTCAGCTTCTTGAACATGGGCTGAGCTTGAACATGCAACAGGA 1034
 206 ATACAGCGCCCTGGCCAACTGTTGGAGCAGCGGCTGAGCTTGGGACGAGAAATCCGA 147
 1035 CTTTACAGCATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 1094
 146 GTAGCCAGCATCCCTCCCGCCCTGGTGGGTGATCATCTCCATGACGAGGTTGGNTA 87

QY 1095 TGGAGATATGATCTATACAGAGTCCCTGGAGAAATCTT-CGAGAGCTTTGTGTCTCA 1153
Db 86 CGGGGACGTTTACCCATACCATAGAGGGGGGGTGTCTCGGGGGGGTGTGCGGTGA 27
QY 1154 GTGGAATTTCTATTG 1170
Db 26 GCGGCATTGTTCTTG 10

RESULT 15
BF966122

LOCUS 602286371F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4375480 5',
DEFINITION mRNA sequence.

ACCESSION BF966122

VERSION BF966122.1 GI:12333337

KEYWORDS EST.

SOURCE

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 887)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10040 row: m column: 17

High quality sequence stop: 628.

Location/Qualifiers

1..887

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4375480"

/tissue_type="hippocampus"

/lab_host="DH10B"

/clone_lib="NIH_MGC_95"

/note="Organ: brain; Vector: pBluescriptR (modified

pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI

(gtcgag); Oligo-dT primed using primer

5'-TTTTTTTTTTTNN-3', size-selected for average

insert size 2.5 kb and normalized to 10^5. This is a

primary library enriched for full-length clones and

constructed using the Cap-trapper method (Carninci, in

preparation). Library constructed by M. Brownstein

(NIH/NHGRI, National Institutes of Health). Note: this

is a NIH_MGC Library."

FEATURES

source

ORIGIN

Query Match 15.2%; Score 193.8; DB 10; Length 887;
Best Local Similarity 81.5%; Pred. No. 2.9e-22;
Matches 286; Conservative 0; Mismatches 57; Indels 8; Gaps 5;

QY 1 ATGACCTTCGGGGCAGCGGGCGCCCTGGTGGTGTGACGTCGGGGCGGGCGCGCGGTAT 60
Db 480 ATGACCTTCGGGGCAGCGGGCGCG-CTCGTGGTGTGACGTCGGGGCGGGCGCGGTAT 538
QY 61 TCGCTGTCCCGGAGCTGTGAAGACTTCCCGCTCGCGCGGTGAGCGGGCTGCACCGGC 120
Db 539 TCGCTGTCCCGGAGCTGTGAAGACTTCCCGCTCGCGCGGTGAGCGGGCTGCACCGGT 598
QY 121 TCGCGCTCCGACCGGAGCTGTCTGAGGTGTGCGAGCTAGCACCGCGGAGCGCAACGAG 180

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 19, 2004, 11:54:10 ; Search time 5373 Seconds
(without alignments)
3428.399 Million cell updates/sec

Title: US-10-016-647-2

Perfect score: 2215
Sequence: 1 MFRSGAASVVLNVGGARY.....HELFKRSARYSRSLSTEFLN 425

Scoring table:
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-O=/cgn2_1/USPTO_spool/US10016647/runat_19042004_104945_10053/app_query.fasta_1.583
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosom62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10016647@cgn2_1_1_3731@runat_19042004_104945_10053 -NCPU=6 -ICPU=3
-NO_WMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pri.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
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27: em_sts.*
28: em_un.*

29: em_vi.*
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35: em_htg_rod.*
36: em_htg_mam.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2215	100.0	1278	6 AX511260	AX511260 Sequence
2	2215	100.0	1844	6 AX511262	AX511262 Sequence
3	2215	100.0	3670	9 AF454547	AF454547 Homo sapi
4	2199.5	99.3	1311	9 AB070604	AB070604 Homo sapi
5	2199.5	99.3	1947	6 AX641934	AX641934 Sequence
6	2199.5	99.3	1947	9 AF348982	AF348982 Homo sapi
7	2199.5	99.3	3703	9 AF454548	AF454548 Homo sapi
8	2122.5	95.8	1744	10 AF454549	AF454549 Rattus no
9	2120.5	95.7	3323	10 AF454551	AF454551 Mus muscu
10	2107	95.1	1302	9 AF450110	AF450110 Homo sapi
11	2107	95.1	1777	10 AF454550	AF454550 Rattus no
12	2105	95.0	3356	10 AF454552	AF454552 Mus muscu
13	2105	95.0	5775	6 AX641960	AX641960 Sequence
14	2076.5	93.7	2235	6 AX478109	AX478109 Sequence
15	1758	79.4	2312	6 AX392945	AX392945 Sequence
16	1649	74.4	1038	10 AB070605	AB070605 Rattus no
17	1113.5	50.3	151367	9 AC025750	AC025750 Homo sapi
18	1108	50.0	219807	2 AC098784	AC098784 Rattus no
19	1108	50.0	259704	2 AC112092	AC112092 Rattus no
20	1108	50.0	268099	2 AC133407	AC133407 Rattus no
21	1099.5	49.6	209523	10 AC084386	AC084386 Mus muscu
22	880.5	39.8	1401	9 HSA011021	HSA011021 Homo sapi
23	879.5	39.7	1702	5 GGU52139	GGU52139 Gallus gall
24	876	39.5	1580	6 AX641932	AX641932 Sequence
25	876	39.5	1560	9 AF348984	AF348984 Homo sapi
26	876	39.5	1560	9 AF450108	AF450108 Homo sapi
27	871.5	39.3	2775	10 RATKCB	RATKCB Rattus norv
28	868	39.2	2022	6 BD235203	BD235203 Voltage g
29	866	39.1	2523	10 RRA011020	RRA011020 Rattus ra
30	865.5	39.1	1518	6 BD235188	BD235188 Voltage g
31	865.5	39.1	1899	10 AF450109	AF450109 Mus muscu
32	865.5	39.1	3822	10 BC043936	BC043936 Mus muscu
33	857.5	38.7	2203	9 BC046629	BC046629 Homo sapi
34	855.5	38.6	1542	9 AF033383	AF033383 Homo sapi
35	855.5	38.6	2137	6 I81198	I81198 Sequence 1
36	855.5	38.6	2127	6 BD144650	BD144650 Potassium
37	801.5	36.2	3232	10 RATCDKX	RATCDKX Rat potassi
38	799.5	36.1	2455	9 HSU69962	HSU69962 Human delay
39	799.5	36.1	2736	9 AF450111	AF450111 Homo sapi
40	796.5	36.0	3599	9 AF338730	AF338730 Homo sapi
41	793.5	35.8	2727	3 LPKV2VGPC	LPKV2VGPC Loligo peal
42	793	35.8	2816	5 AF319664	AF319664 Ictalurur
43	789.5	35.6	3060	3 S68356	S68356 Aplysia sp.
44	788.5	35.6	3158	4 AY037947	AY037947 Oryctolag
45	787.5	35.6	2697	5 XLU20342	XLU20342 Xenopus lae

ALIGNMENTS

RESULT 1

AX511260 AX511260 1278 bp DNA linear PAT 27-SEP-2002
 LOCUS Sequence 1 from Patent WO0250271.
 DEFINITION AX511260
 ACCESSION AX511260
 VERSION AX511260.1 GI:23392138
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Fridde, C.J., Hilbun, E. and Turner, C.A.
 TITLE Novel human ion channel protein and polynucleotides encoding the same
 JOURNAL Patent: WO 0250271-A 1 27-JUN-2002;
 Lexicon Genetics Incorporated (US)
 FEATURES
 source Location/Qualifiers
 1.1278
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
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 Pred. No.: 6,29e-210 Length: 1278
 Score: 2215.00 Matches: 425
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0
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 QY 1 MetThrPheGlyArgSerGlyAlaAlaSerValValLeuAsnValGlyValAlaArgTyr 20
 Db 1 ATGACCTTCGGCGCGAGCGCGCGCTCGGTGCTGAACGTGGCGCGCGCGAT 60
 QY 21 SerLeuSerArgGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
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 QY 41 CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgS 60
 Db 121 TGGCGCTCCGAGCGCGACGTCTCGAGGTGTCGACGACTACGACCGCGCGCG 180
 QY 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheLeuLeuTyrValArgGlyHis 80
 Db 181 TACTTCTTCGACCGGCACCTCGAGGCTTCGCGCTTCATCTCTAGCTGCGCGCC 240
 QY 81 GlyLeuLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetileTyr 100
 Db 241 GGCAGCTCGCTTCGCGCGCGAGGTGCGAGCTCTCTCTCAACAGAGATGATCAT 300
 QY 101 TrpGlyLeuGluGlyAlaHisLeuGluTyrCysCysGlnArgArgLeuAspArgMet 120
 Db 301 TGGGCGCTGGAGCGCGCGACCTCGAGTACTCTGCGAGCGCGCTCGACCGCGCAT 360
 QY 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140
 Db 361 TCCGACACCTACACCTTCTACTCGCGCGAGCGCGCGCTGCTGGCGCGCGAGCGG 420
 QY 141 ArgProGlyGlyValAlaGluAlaProSerArgArgTyrLeuGluArgMetArgGthr 160
 Db 421 CGCGCGCGCGCGCGCGCGCGCTCTCGAGCGCTGCTGAGCGCATGCGCGCGAC 480
 QY 161 PheGluGluProThrSerSerLeuAlaAlaGlnLeuAlaSerValSerValPhe 180
 Db 481 TTCAGGAGCGCGCGCGCTGCTGCGCGCGCGAGATCTCTGCTGAGCGTGTGCTG 540
 QY 181 ValIleValSerMetValValLeuCysAlaSerThrLeuProAspTyrArgAsnAlaAla 200
 Db 541 GTGATCTGTCCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600

QY 201 AlaAspAsnArgSerLeuAspAspArgSerArgIleileGluAlaIleCysileGlyTyr 220
 Db 601 GCGGACACCGCGAGCTGGATGACCGGAGCAGATATTGAAGCTATCTGCATAGTTGG 560
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 LOCUS AX511262 1844 bp DNA linear PAT 27-SEP-2002
 DEFINITION Sequence 3 from Patent WO0250271.
 ACCESSION AX511262
 VERSION AX511262.1 GI:23392139
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Fridde, C.J., Hilbun, E. and Turner, C.A.
 TITLE Novel human ion channel protein and polynucleotides encoding the same
 JOURNAL Patent: WO 0250271-A 3 27-JUN-2002;
 Lexicon Genetics Incorporated (US)
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US-10-016-647-2 (1-425) x AB070604 (1-1311)

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QY	41	CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu	60
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AX641934

LOCUS

DEFINITION Sequence 3 from Patent WO02096944.

ACCESSION AX641934

VERSION AX641934.1 GI:28474564

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

1

Snyders,D.J., Ottschytch,N., Raes,A. and van Hoorick,D.

New heterotetrameric potassium channels and uses thereof

Patent: WO 02096944-A 3 05-DEC-2002;

Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)

FEATURES

source

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Percent Similarity:	97.48%	Conservative:	0
Best Local Similarity:	97.48%	Mismatches:	0
Query Match:	99.30%	Indels:	11
DB:	6	Gaps:	1

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LOCUS
DEFINITION
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complete cds, alternatively spliced.
ACCESSION
AF454551
VERSION
AF454551.1 GI:22164089
KEYWORDS
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
1 (bases 1 to 3323)
Vega-Saenz de Miera, E.C. and Rudy, B.
Kv10.1a and Kv10.1b: Two novel alternatively spliced potassium
channel subunits
Unpublished
JOURNAL
2 (bases 1 to 3323)
Vega-Saenz de Miera, E.C. and Rudy, B.
Direct Submission
Submitted (04-DEC-2001) Physiology and Neuroscience, New York
University School of Medicine, 550 First Avenue, New York, NY
10016, USA
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 VERSION AP450110.1 GI:31295623
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1302)
 AUTHORS Preisig-Muller R., Derst C., Mederos Y Schnitzler, M. and Daut, J.
 TITLE Cloning and characterization of two novel gamma Kv subunits
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1302)
 AUTHORS Preisig-Muller R., Derst C., Mederos Y Schnitzler, M. and Daut, J.
 TITLE Direct Submission
 JOURNAL Submitted (23-NOV-2001) University of Marburg, Institute of
 Physiology, Deutschhausstrasse 1-2, Marburg 35037, Germany
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301 TGGGCGCTGGAGGCGCGCACTGGAGTACTCTGCCAGCGCGCTAGACGACCGCATG 360
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Qy ArgProGlyGlyAlaGluAlaAlaProSerArgArgTrpLeuGluArgMetArgArgThr 160
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Qy PheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValValPhe 180
472 TTCGAGGAGCGCACCTGCTGGCTGGCGCGGAGATCTCTGGCAGCGTCTCGTGGTTC 531
Qy ValIleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArgAsnAlaAla 200
532 GTGATCGTGTCTATGTTGTTGCTGGCCAGCAGCTGCCGACTGCCGCGCGGCGCC 591
Qy AlaAspAsnArgSerLeuAspAspArgSerArg----- 211
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Qy -----IleIleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleValArgPhe 229
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712 ATCGTCTCAAAAACAAGTGTGAGTGTTCAGAGACCCCTGAAACATCATGACTTACTG 771
Qy AlaIleThrProTyrTyrIleSerValLeuMetThrValPheThrGlyGluAsnSerGln 269
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Qy LeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTrpValIle 289
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892 AAGCTTGGCCCGCACTTCATCGCGCTGCAGACCCCTGGGCTTGACTCTCAAGCATGCTAC 951
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1192 TTGGCATATACCTATCATCTTCATACCATAGCTTTGTGCACTGTATCCAGCTCAAG 1251
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1252 TTATGATCGCTCGATATAGTAGGACCTCTCCGCTGAGTTCCTGAAT 1299

RESULT 11
AF454550
LOCUS
DEFINITION
1777 bp mRNA linear ROD 09-AUG-2002
Rattus norvegicus voltage-gated potassium channel subunit Kv10.1b
mRNA, complete cds, alternatively spliced.
ACCESSION
AF454550
VERSION
AF454550.1 GI:22164087
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 1777)
Vega-Saenz de Miera, E.C. and Rudy, B.
Kv10.1a and Kv10.1b: Two novel alternatively spliced potassium
channel subunits
Unpublished
2 (bases 1 to 1777)
Vega-Saenz de Miera, E.C. and Rudy, B.
Direct Submission
Submitted (04-DEC-2001) Physiology and Neuroscience, New York
University School of Medicine, 550 First Avenue, New York, NY
10016, USA
FEATURES
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227..1528
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Query Match: 95.12% Indels: 14
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Qy 41 CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu 60
Db 347 TCGCGCTCGGAGCGCGACGCTGCTCGAGGTGTGCGACGACTACGACCGGAGCGCAACGAG 406
Qy 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheIleLeuLeuTyrValArgGlyHis 80
Db 407 TACTTCTTCGACCGGCACTCGAGGCGCTTCATCTGCTGTACGTGCGCGGCCAC 466
Qy 81 GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100

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527	Db		TGGGGCTGGAGGGCGGCACCTGGAGTACTGCTGCCAGCGCCCTAGACACCGCATG	586
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587	Db		TCCGACACCCACACCTTCCACGGCGCAGAGGAG-----CTGGCGCGCAGACGCT	637
141	Qy		ArgProGlyGlyAlaGluAlaAlaProSerArgArgTrpLeuGluArgMetArgArgThr	160
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161	Qy		PheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValPhe	180
698	Db		TTCAGAGAGCCACGCTCGCTCGCGCGCAGATCCTGGCCAGCGTGTCCGTGGTTC	757
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201	Qy		AlaAspAsnArgSerLeuAspAspArgSerArg-----	211
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212	Qy		-----IleIleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleValArgPhe	229
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290	Qy		LysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyr	309
1118	Db		AAGCTTCCCGGCACATTCACTCGCGCTGCACACCTCGGGCTTGACTCTCAAGCATGCTAC	1177
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1178	Db		CGAGAGATGTTATGTGCTCGTCTTCATCTGTGTGCTATGGCGATCTTCAGTGCACTC	1237
330	Qy		SerGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIle	349
1238	Db		TCTCAGCTCCTTGAGCAGGGTGGACTTGAGACGCTCCAACAGGACATTTGGCAGCATC	1297
350	Qy		ProAlaAlaCysTrpTrpValIleIleSerMetThrThrValGlyTyrGlyAspMetTyr	369
1298	Db		CCCGCTGCCTGTGGTGGTGATTATCTCTATGACTACAGTGGGCTATGGAGACATGTAT	1357
370	Qy		ProIleThrValProGlyArgIleLeuGlyGlyValCysValValSerGlyIleValLeu	389
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1418	Db		TTGGCATTACCTATCACTTTCATCTACCATAGTGTGTGCGAGTGCTACACAGAGCTCAAG	1477
410	Qy		PheArgSerAlaArgTyrSerArgSerLeuSerThrGluPheLeuAsn	425
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RESULT 12
AF454552

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DEFINITION	Mus musculus voltage-gated potassium channel subunit Kv10.1b mRNA, complete cds, alternatively spliced.							
ACCESSION	AP454552							
VERSION	AP454552.1	GI:22164091						
KEYWORDS								
SOURCE	Mus musculus (house mouse)							
ORGANISM	Mus musculus							
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.							
REFERENCE	1 (bases 1 to 3356)							
AUTHORS	Vega-Saenz de Miera, E.C. and Rudy, B.							
TITLE	Kv10.1a and Kv10.1b: Two novel alternatively spliced potassium channel subunits							
JOURNAL	Unpublished							
REFERENCE	2 (bases 1 to 3356)							
AUTHORS	Vega-Saenz de Miera, E.C. and Rudy, B.							
TITLE	Direct Submission							
JOURNAL	Submitted (04-DEC-2001) Physiology and Neuroscience, New York University School of Medicine, 550 First Avenue, New York, NY 10016, USA							
FEATURES	Location/Qualifiers							
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CDS								
polyA_signal								
ORIGIN	3162..3167							
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Best Local Similarity:	93.58%	Mismatches:	9					
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Db 638 TCCGACACCCACACTTCACGGCGCAGACGAG-----CTGGCGCGGACGACCT 688
QY 141 ArgProGlyGlyAlaGluAlaAlaProSerArgArgTrpLeuGluArgMetArgArgThr 160
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AX641960 5775 bp DNA linear PAT 21-FEB-2003
LOCUS
DEFINITION
Sequence 29 from Patent WO02096944.
ACCESSION
AX641960
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VERSION AX641960.1 GI:28474590
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Snyder,D.J., Otteschtych,N., Raes,A. and van Hoorick,D.
TITLE New heterotetrameric potassium channels and uses thereof
JOURNAL Patent: WO 02096944-A 29 05-DEC-2002;
Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)
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Score: 2105.00 Matches: 408
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Best Local Similarity: 93.58% Mismatches: 9
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 DEFINITION Sequence 39 from Patent WO0240541.
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 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Tang, Y.T., Yue, H., Nguyen, D.B., Hafalia, A.J., Elliott, V.S., Lu, Y.,
 Walla, N.K., Yao, M.G., Baughn, M.R., Gandhi, A.R., Ding, L.,
 Sanjanwala, M., Rankumar, J., Arvizu, C., Gietzen, K.J., Lal, P.G.,
 Azimzai, J., Khan, F.A., Thangavelu, K., Thornton, M., Lu, D.A.,
 Tribouley, C.M., Warren, B.A., Ison, C.H., Das, D., Raumann, B.E.,
 Policky, J.L. and Kearney, L.
 TITLE Transporters and ion channels
 JOURNAL Patent: WO 0240541-A 39 23-MAY-2002;
 Incyte Genomics, Inc. (US)
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 Best Local Similarity: 93.75% Indels: 9
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 QY 21 SerLeuSerArgGluLeuLeuIlyAspPheProLeuArgArgValSerArgLeuHisGly 40
 Db 488 TCGTGTCCCGGAGCTGCTGAAGGACTTCCCGTGGCGCGCGGTGAGCGCGCTGCACGGC 547
 QY 41 CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu 60
 Db 548 TCGCGCTCCGAGCGCAGCTGCTCGAGGTGTCGAGACTTACGACCGCGAGCGCAACGAG 607
 QY 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheIleLeuLeuTyrValArgGlyHis 80
 Db 608 TACTTCTTCGACCGGCACTCGAGGGCTTCGGCTTCATCTCTCTACGTGCGCGCGCAC 667
 QY 81 GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100
 Db 668 GGCAAGCTGGCTTCGCGCGCGGATGTGCGAGCTCTCTTCTTACAACGAGATGATCTAC 727
 QY 101 TrpGlyLeuGluGlyAlaHisLeuGluTyrCysGlnArgArgLeuAspAspArgMet 120
 Db 728 TGGGGCTCGAGGGCGCGCACCTCGAGTACTGTGTCAGCGCGCGCTCGACGACCGCATG 787
 QY 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140
 Db 788 TCCGACACCTACACCTTCTACTCGGCGCGAGCGCGGGGTGTGCGCGCGCGAGGGCG 847
 QY 141 ArgProGlyGlyAla-GluAlaAlaProSerArgArgTyrTrpLeuGluArgMetArgArgTh 160
 Db 848 CGCCCC---GGCGCGCGAGCGCGCTCCCTCCAGCGCTGGCTGAGCGCATGCGCGCGAC 904
 QY 160 rPheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValValPh 180
 Db 905 CTTCGAGGAGCCACATC-----CTGGCTAGCGGTGTGGTGTGT 945
 QY 180 eValIleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArgAsnAlaAl 200
 Db 946 CGTGATCGTGTCCATGGTGGTGTGTGCGCGCAGCAGCTTGGCGCGCTGCGCGCAACGAGC 1005
 QY 200 aAlaAspAsnArgSerLeuAspAspArgSerArgIleIleGluAlaIleCysIleGlyTyr 220
 Db 1006 CGCGCGAACCGCAGCGCTGGATGACCGAGCAGGATAATTGAAGCTATCTGATAGTTG 1065
 QY 220 pPheThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGluPheValIly 240
 Db 1066 GTTCACTCGCGAGTGCATCGTGGAGTTTCATTGTCTCCAAAACAAGTGTGAGTTGTCAA 1125
 QY 240 sArgProLeuAsnIleIleAspLeuLeuAlaIleThrProTyrTyrIleSerValLeuMe 260
 Db 1126 GAGACCCCTGAACATCATTCATTACTTGGCAATCACCGCGTATTACATCTCTGTGTGTAT 1185
 QY 260 tThrValPheThrGlyGluAsnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLe 280
 Db 1186 GACAGTGTTCAGCGGAGAACTCTCACTCCAGAGGGCTGGAGTCACCTTCAGGGTACT 1245
 QY 280 uArgMetMetArgIlePheTrpValIleLysLeuAlaArgHisPheIleGlyLeuGlnTh 300
 Db 1246 TAGAATGATGAGGATTTTTTGGGTGATTAAAGCTTGCCTTCATCTTGGTCTTCAGAC 1305
 QY 300 rLeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuValPheIleCy 320
 Db 1306 ACTCGGTTTGACTCTCAACAGTTGTACCGAGAGATGGTTATGTTACTTGTCTTCAATTG 1365

Thu Oct 7 10:52:18 2004

us-10-016-647-2.rge

Page 16

Search completed: April 19, 2004, 15:30:03
Job time : 5433 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 19, 2004, 10:49:57 ; Search time 556 Seconds
(without alignments)
3247.274 Million cell updates/sec

Title: US-10-016-647-2

Perfect score: 2215
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Scoring table:

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Dgapop 6.0, Dgapext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
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9: geneseqn2003cs:*

10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2215	100.0	1278	6	ABN83930 Human vol
2	2215	100.0	1844	6	ABN83931 Human vol
3	2199.5	99.3	1308	9	ADD01427 Human TCH
4	2199.5	99.3	1347	7	AB224711 Human pot
5	2199.5	99.3	5174	9	ADD01447 Human TCH
6	2105	95.0	5775	9	AB224716 Murine po
7	2095.5	94.6	1651	7	ABX72192 Human NOV
8	2076.5	93.7	2235	6	ABK83228 Human tra

9	1758	79.4	2312	6	ADD33662 Human TRI
10	1410.5	63.7	950	9	ADD01489 Mouse TCH
11	880.5	39.8	1401	2	AAD23803 Human Kv6
12	880.5	39.8	1401	5	AAS75631 DNA encod
13	876	39.5	1560	7	AB224710 Human pot
14	868	39.2	2022	3	AA249455 Human Vol
15	865.5	39.1	1518	3	Aaz49454 Mouse Vol
16	864.5	39.0	2370	9	ADb47439 Human CDN
17	855.5	38.6	2127	2	AA112461 Human K+
18	855.5	38.6	2127	2	AAV04873 Human K+
19	855.5	38.6	2127	9	ADb49122 Oligonuc
20	833	37.6	1634	6	ABQ49122 Oligonuc
21	833	37.6	1634	6	ABQ49123 Oligonuc
22	823.5	37.2	2499	6	AB235517 Human gen
23	797.5	36.0	1446	3	Aaz23804 Murine Kv
24	780.5	35.2	2565	3	Aaz36415 cDNA enco
25	780.5	35.2	3777	7	AB224713 Human pot
26	779.5	35.2	2577	6	AAL45289 Human KGN
27	766	34.6	3339	4	ABL01915 Drosophil
28	758	34.2	3441	4	ABL20763 Drosophil
29	720.5	32.5	1634	6	ABQ49124 Oligonuc
30	720.5	32.5	1634	6	ABQ49125 Oligonuc
31	715.5	32.3	3080	2	Aaz11900 Human pot
32	696	31.4	2044	9	ADb53347 Primary r
33	687	31.0	2517	3	Aaz51620 Human mem
34	685.5	30.9	1476	3	Aaz36410 cDNA enco
35	685.5	30.9	2421	3	Aaz36409 cDNA enco
36	685	30.9	2293	2	AA211899 Human pot
37	683	30.8	3102	2	AA211905 Human pot
38	683	30.8	5027	6	AB235328 Human gen
39	675	30.5	2573	6	AB267808 Human rec
40	667	30.1	3032	4	ABA09051 Human K c
41	661	29.8	461	6	ABK27494 DNA encod
42	642	29.0	1488	2	Aaz06653 hkv5.1 hu
43	642	29.0	1880	2	Aaz06652 hkv5.1 hu
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ALIGNMENTS

RESULT 1

ABN83930

ID ABN83930 standard; cDNA; 1278 BP.

XX AC ABN83930;

DT 06-SEP-2002 (first entry)

XX DE Human voltage-gated potassium channel-like protein encoding cDNA.

XX KW Human; voltage-gated potassium channel; ion channel; neuroprotective; therapeutic; diagnostic; pharmacogenomic; gene therapy; SNP;
KW single nucleotide polymorphism; foetal brain; brain; cerebellum;
KW pituitary; prostate; thymus; lymph node; bone marrow; trachea;
KW foetal liver; liver; testis; thyroid; salivary gland; stomach;
KW skeletal muscle; heart; uterus; adipose; hypothalamus; ovary; aorta;
KW 12 week old embryo; adenocarcinoma; osteosarcoma; Gene; ss.

XX OS Homo sapiens.

PH Key Location/Qualifiers

FT CDS 1..1278

FT /*tag= a

FT /product= "voltage-gated potassium channel-like protein"

FT replace(432,C)

FT /*tag= b

FT /standard_name= "single nucleotide polymorphism"

XX WO200250271-A2.

XX 27-JUN-2002.

XX

PF 10-DEC-2001; 2001WO-US048050.
 XX
 PR 20-DEC-2000; 2000US-0257932P.
 XX
 PA (LEXI-) LEXICON GENETICS INC.
 XX
 PI Fiddle CJ, Hilbun E, Turner CA;
 XX
 XX WPI; 2002-508799/34.
 DR P-PSDB; AB883073.
 XX
 PT Human ion channel polynucleotide useful in therapeutic, diagnostic and
 XX pharmacogenomic applications.
 XX
 PS Claim 1; Page 34; 36pp; English.
 XX
 CC The invention relates to a novel human ion channel polynucleotide that
 CC shares structural similarity with voltage-gated potassium channel
 CC proteins. The activity of the protein of the invention may be described
 CC as neuroprotective. The protein of the invention is useful in
 CC therapeutic, diagnostic and pharmacogenomic applications, for example to
 CC identify mutations associated with a particular disease, as a diagnostic
 CC or prognostic assay, or in gene therapy. The protein of the invention has
 CC been found to be expressed in human foetal brain, brain, cerebellum,
 CC pituitary, prostate, thymus, lymph node, bone marrow, trachea, foetal
 CC liver, uterus, adipose, hypothalamus, ovary, aorta, 12 week old embryo,
 CC heart, liver, adipose, hypothalamus, ovary, aorta, 12 week old embryo,
 CC adenocarcinoma and osteosarcoma cells. The current sequence represents
 CC the human voltage-gated potassium channel-like protein encoding cDNA

XX SQ Sequence 1278 BP; 237 A; 349 C; 376 G; 316 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2,59e-231 Length: 1278
 Score: 2215.00 Matches: 425
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0

US-10-016-647-2 (1-425) x ABN83930 (1-1278)

QY 1 MetThrPheGlyArgSerGlyAlaAlaSerValValLeuAsnValGlyGlyAlaArgTyr 20
 DB 1 ATGACCTTCGGCGGCGAGCGCGCGCTCGGGTGGTGAACGTGGCGCGCGCGCGGTAT 60
 QY 21 SerLeuSerArgGluLeuLeuLeuLysAspPheProLeuArgArgValSerArgLeuHisGly 40
 DB 61 TCGCTGTCCCGGAGCTGCTGAGGACATCCCGCTGGCGCGCGCTGAGCGCGCTGACCGGC 120
 QY 41 CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu 60
 DB 121 TGCCTGCTCGAGCGGACGTGCTGAGGTGTGCGACACTACGACCGCGAGCGCAACGAG 180
 QY 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheLeuLeuLeuTyrValArgGlyHis 80
 DB 181 TACTTCTTCGACGGGACATCGGAGGCTTCGCTTCATCTGCTCTAGTGGCGGCGCAC 240
 QY 81 GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetileTyr 100
 DB 241 GGCAAGCTCGCTTCGCGCGCGGATGTGCGAGCTCTCTCTTCTCAACGAGATGATCTAC 300
 QY 101 TrpGlyLeuGluGlyAlaHisLeuGluTyrCysGlnArgArgGluLeuAspArgMet 120
 DB 301 TGGGCGCTGGAGGCGCGCACCTCGAGTACTCTGCGAGCGCGCTCGACGCGCGATG 360
 QY 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140
 DB 361 TCCGACACCTACACCTTCTACTCGGCGGACGAGCGCGGCGTGTGGCGCGGAGCGCG 420
 QY 141 ArgProGlyGlyAlaGluAlaProSerArgArgTyrLeuGluArgMetArgArgThr 160
 DB 421 CGCCCCCGCGCGCGCGCGCTCCCTCCAGCGCTGGTGGAGCGATCGCGCGGAC 480

QY 161 PheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValPhe 180
 DB 481 TTCAGGAGCCACGTCGTCGTCGGCGCGCAGATCTGCTAGCTGCGTGGTGGTTC 540
 QY 181 ValIleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArgAsnAlaAla 200
 DB 541 GTGATCGTGTCCATGGTGGTGTGTCGGCCAGCAGCTGCCCCGACGCGCAGCC 600
 QY 201 AlaAspAsnArgSerLeuAspArgSerArgIleIleGluAlaIleCysIleGlyTrp 220
 DB 601 GCCGACAAACCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATG 660
 QY 221 PheThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGluPheValLys 240
 DB 661 TTCTACGCCGAGTGCATCGTGGATGATGATGATGATGATGATGATGATGATG 720
 QY 241 ArgProLeuAsnIleIleAspLeuLeuAlaIleThrProTyrTyrIleSerValLeuMet 260
 DB 721 AGACCCCTGAACATCATGATGATGATGATGATGATGATGATGATGATGATGATG 780
 QY 261 ThrValPheThrGlyGluAsnSerGlnLeuArgAlaGlyValThrLeuArgValLeu 280
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 QY 281 ArgMetMetArgIlePheTrpValIleLysLeuAlaArgHisPheIleGlyLeuGlnThr 300
 DB 841 AGAATGATGAGGATTTTGGGTGATTAAGCTTGGCGCTCCTCATTCATGCTTCAGACA 900
 QY 301 LeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuValPheIleCys 320
 DB 901 CTCGGTGTGACTCTCAACGCTTCTACCGAGAGATGATGATGATGATGATGATGAT 960
 QY 321 ValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeuGlu 340
 DB 961 GTTGCATGCGCACTTTAGTGCACTTTCTCAGCTTCTTGAACATGGCGCTGGAGCTG 1020
 QY 341 ThrSerAsnLysAspPheThrSerIleProAlaAlaCysTrpTrpValIleIleSerMet 360
 DB 1021 ACATCCAACAAGGACTTTACGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
 QY 361 ThrThrValGlyTyrGlyAspMetTyrProIleThrValProGlyArgIleLeuGlyGly 380
 DB 1081 ACTACAGTGGCTATGAGATATGATATCTATCAGCTGCTGCGGAGAGATTTCTGGAGA 1140
 QY 381 ValCysValValSerGlyIleValLeuLeuAlaLeuProIleThrPheIleTyrHisSer 400
 DB 1141 GTTTGTGTCAGTGGAAATTTGTTTATTTGGCATTAACCTATCACTTTTATACCATAGC 1200
 QY 401 PheValGluCysTyrHisGluLeuLysPheArgSerAlaArgTyrSerArgSerLeuSer 420
 DB 1201 TTTGTGCGAGTGTATCATGAGCTCAAGTTAGATCTGTAGGTATAGTAGGAGCCTCTCC 1260
 QY 421 ThrGluPheLeuAsn 425
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RESULT 2

ABN83931

ID ABN83931 standard; DNA; 1844 BP.

XX AC ABN83931;

XX AC ABN83931;

XX DT 06-SEP-2002 (first entry)

XX DE Human voltage-gated potassium channel-like protein encoding sequence.

XX DE Human; voltage-gated potassium channel; ion channel; neuroprotective;
 KW therapeutic; diagnostic; pharmacogenomic; gene therapy; SNP;
 KW single nucleotide polymorphism; foetal brain; brain; cerebellum;
 KW pituitary; prostate; thymus; lymph node; bone marrow; trachea;
 KW foetal liver; liver; testis; thyroid; salivary gland; stomach;
 KW skeletal muscle; heart; uterus; adipose; hypothalamus; ovary; aorta;

KW 12 week old embryo; adenocarcinoma; osteosarcoma; gene; ds.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT 5'UTR 1..456
 FT CDS /*tag= a
 FT /*tag= b
 FT /product= "voltage-gated potassium channel-like protein"
 FT /replace(888,C)
 FT /*tag= c
 FT /standard name= "single nucleotide polymorphism"
 FT 3'UTR 1735..1844
 FT /*tag= d
 PN WO200250271-A2.
 XX
 PD 27-JUN-2002.
 XX
 XX 10-DEC-2001; 2001WO-US048050.
 PF
 XX 20-DEC-2000; 2000US-0257932P.
 PR
 XX (LEXI-) LEXICON GENETICS INC.
 PA
 PI Friddle CJ, Hilbun E, Turner CA;
 XX
 DR WPI; 2002-508799/54.
 DR P-PSDB; ABB83073.
 XX
 DR Human ion channel polynucleotide useful in therapeutic, diagnostic and
 PT pharmacogenomic applications.
 PT
 XX
 PS Disclosure; Page 36; 36pp; English.
 CC The invention relates to a novel human ion channel polynucleotide that
 CC shares structural similarity with voltage-gated potassium channel
 CC proteins. The activity of the protein of the invention may be described
 CC as neuroprotective. The protein of the invention is useful in
 CC therapeutic, diagnostic and pharmacogenomic applications, for example to
 CC identify mutations associated with a particular disease, as a diagnostic
 CC or prognostic assay, or in gene therapy. The protein of the invention has
 CC been found to be expressed in human foetal brain, brain, cerebellum,
 CC pituitary, prostate, thymus, lymph node, bone marrow, trachea, foetal
 CC liver, liver, testis, thyroid, salivary gland, stomach, skeletal muscle,
 CC heart, uterus, adipose, hypothalamus, ovary, aorta, 12 week old embryo,
 CC adenocarcinoma and osteosarcoma cells. The current sequence represents
 CC the human voltage-gated potassium channel-like protein encoding DNA
 CC sequence
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 SQ Sequence 1844 BP; 314 A; 540 C; 596 G; 394 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 4,468-231 Length: 1844
 Score: 2215.00 Matches: 425
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-10-016-647-2 (1-425) X ABB83931 (1-1844)
 QY 1 MetThrPheGlyArgSerGlyValAlaSerValValLeuAsnValGlyGlyValArgTyr 20
 DB 457 ATGACCTTCGGCGCGAGCGGGCGGCTTCGGTGGTGTGACGTGGCGGGCGCGCGGTAT 516
 QY 21 SerLeuSerArgGluLeuLeuLysPheProLeuArgArgValSerArgLeuHisGly 40
 DB 517 TCGCTGTCCGGGAGCTGCTGAAGACTTCGCGTGGCGCGGTGAGCGCGGTGACGGC 576
 QY 41 CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu 60

577 TGCCGCTCCGAGCGCGACGCTGCTCGAGGTGTGCGAGCACTACGACCGCGAGCGCAACGAG 636
 QY 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheLeuLeuTyrValArgGlyHis 80
 DB 637 TACTTCTTGACCGGCACTCGGAGGCTTCGGGCTTCATCTGCTCTACGTCGCGGCCAC 696
 QY 81 GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetLleTyr 100
 DB 697 GGCAGAGCTGGCTTCGGCGCGGATGTGCGAGCTCTCTTCTACCAAGAGATGATCTAC 756
 QY 101 TrpGlyLeuGluGlyAlaHisLeuGluTyrCysGlnArgArgGluAspAspArgMet 120
 DB 757 TGGGGCTCGAGGCGCGCACCTCGAGTACTGTCTCCAGCGCGGCTCGACGCCCATG 816
 QY 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140
 DB 817 TCCGACACCTACACCTTCTACTCGCGCGAGCGGCGTGTGCGCGCGAGCGGCG 876
 QY 141 ArgProGlyGlyAlaGluAlaProSerArgArgTyrTrpLeuGluArgMetArgArgThr 160
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 DB 937 TTCAGAGAGCCACGCTCGCTGCGCGCGAGATCTCTGGTAGCGTGTCTGGTGTTC 996
 QY 181 ValIleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArgAsnAlaAla 200
 DB 997 GTGATCGTGTCCATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1056
 QY 201 AlaAspAspArgSerLeuAspAspArgSerArgGlyIleGluAlaIleCysIleGlyTyr 220
 DB 1057 GCCGCAACCGCGAGCTGGATGACCGAGGAGATTAATGAGCTATCTGCTAGGTGG 1116
 QY 221 PheThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGluPheValLys 240
 DB 1117 TTCACGCGAGTGCATCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1176
 QY 241 ArgProLeuAsnIleLeuAspLeuAlaIleThrProTyrTyrIleSerValLeuMet 260
 DB 1177 AGACCCCTGAACATCATGATTTACTTACGCAATCACGCGGTAATACATCTCTGTGTGATG 1236
 QY 261 ThrValPheThrGlyGluAsnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLeu 280
 DB 1237 ACAGTGTTCACGCGGAGAACTCTCAACTCCAGAGGCTGGAGTCACTTGAAGGTAATT 1296
 QY 281 ArgMetMetArgIlePheTrpValIleLysLeuAlaArgHisPheIleGlyLeuGlnThr 300
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 QY 301 LeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuValPheIleCys 320
 DB 1357 CTCGTTTGACTCTCAACGTTGCTACCGAGAGATGTTATGTTACTTCTTCATTGT 1416
 QY 321 ValAlaMetAlaIlePheSerAlaLeuSerGlnLeuGluHisGlyLeuAspLeuGlu 340
 DB 1417 GTTGCCATGGCAATCTTTAGTGCACTTCTCAGCTCTTGAACATGGGCTGGACCTGGAA 1476
 QY 341 ThrSerAsnLysAspPheThrSerIleProAlaAlaCysTrpTrpValIleIleSerMet 360
 DB 1477 ACATCCCAACAGGACTTTACCGACATTCCTGCTGCTGCTGGGGTGATTATCTCTATG 1536
 QY 361 ThrThrValGlyTyrGlyAspMetTyrProIleThrValProGlyArgIleLeuGlyGly 380
 DB 1537 ACTACAGTTGGCTATGGAGATATGATCTATCACAGTGCCTCGAAGAATTCITGGAGGA 1596
 QY 381 ValCysValValSerGlyIleValLeuLeuAlaLeuProIleThrPheIleTyrHisSer 400
 DB 1597 GTTGTGTGTGCTAGTGGAAATGTTCTATTGGCAATACCTATCATCTTTATCTACCATAGC 1656
 QY 401 PheValGlnCysTyrHisGluLeuLysPheArgSerAlaArgTyrSerArgSerLeuSer 420
 DB 1657 TTTGTGCGAGTGTATCATGAGCTCAAGTTTAGATCTGCTAGGTATAGTAGGAGCCTCTCC 1716

QY 421 ThrGluPheLeuAsn 425
 DB 1717 ACTGAATTCCTGNAT 1731

RESULT 3
 ADD01427
 ID ADD01427 standard; DNA; 1308 BP.
 XX AC
 XX ADD01427;
 XX DT
 XX 01-JAN-2004 (first entry)
 XX Human TCH136 coding sequence.

ds; gene; antidiabetic; antilipemic; antiarteriosclerotic; nootropic;
 KW neuroprotective; anabolic; antiinflammatory; immunosuppressive;
 KW cytostatic; antiasthmatic; antiarthritic; cerebroprotective;
 KW anti allergic; dermatological; cardiant; antiparkinsonian; neuroleptic;
 KW glucose transporter; potassium ion channel protein; diabetes;
 KW hyperlipemia; arteriosclerosis; digestive disorder; Crohn's disease;
 KW colitis; gastritis; ileitis; rectal inflammation; inflammatory disease;
 KW sepsis; prostatic hypertrophy; reproductive disorder; pneumonia;
 KW meningitis; hepatitis; myocarditis; asthma; immune disorder;
 KW multiple sclerosis; rheumatoid arthritis; Sjogren's disease; lupus;
 KW allergy; hay fever; allergic rhinitis; anaphylactic shock;
 KW atopic dermatitis; circulatory disorder; heart failure; cancer;
 KW Alzheimer's disease; Parkinson's disease; schizophrenia;
 KW hyperprolactinemia; Cushing's disease; vesicular glutamate transporter.
 XX Homo sapiens.

XX Key Location/Qualifiers
 FH 1..1308
 FT CDS

FT /*tag= a
 FT /product= "human TCH136 protein"
 FT /function= "voltage-dependent potassium ion channel"
 XX

PN WO2003054190-A1.
 XX
 XX 03-JUL-2003.
 XX
 XX 19-DEC-2002; 2002WO-JP013290.
 XX
 XX 21-DEC-2001; 2001JP-00389361.
 XX 25-DEC-2001; 2001JP-0032577.
 XX 26-DEC-2001; 2001JP-00394947.
 XX 26-DEC-2001; 2001JP-00395467.
 XX 06-FEB-2002; 2002JP-00030010.
 XX 08-FEB-2002; 2002JP-00033095.
 XX 06-JUN-2002; 2002JP-00165336.
 XX (TAKE) TAKEDA CHEM IND LTD.
 XX
 XX Nakanishi A, Sagiya Y, Uno Y;
 XX WPI; 2003-541817/51.
 XX P-PSDB; ADD01426.
 XX
 XX Glucose transporter TCH099, vesicular glutamate transporter TCH177 and
 PT potassium channel protein TCH136 and DNA encoding them for diagnosis,
 PT treatment and prevention of diabetes, hyperlipemia, arteriosclerosis and
 PT digestive disorders.
 XX
 XX Claim 62; SEQ ID NO 63; 221pp; Japanese.
 XX
 XX The invention relates to a novel glucose transporter TCH099, vesicular
 CC glutamate transporter TCH177 and voltage-dependent potassium ion channel
 CC protein TCH136. The sequences are useful in the treatment, prevention and
 CC diagnosis of a broad range of diseases including diabetes, hyperlipemia,
 CC arteriosclerosis, digestive disorders (such as Crohn's disease, colitis,
 CC gastritis, ileitis and rectal inflammation), inflammatory diseases,
 CC sepsis, prostatic hypertrophy, reproductive disorders, pneumonia,

CC meningitis, hepatitis, myocarditis, asthma, immune disorders (such as
 CC multiple sclerosis, rheumatoid arthritis, Sjogren's disease and lupus),
 CC allergies (such as hay fever, allergic rhinitis, anaphylactic shock and
 CC atopic dermatitis), circulatory disorders (such as heart failure), cancer
 CC (such as cancer of the lung, kidney, liver, ovary, prostate, stomach,
 CC pancreas, bladder, breast, fallopian tubes, or colon), central nervous
 CC system diseases (such as Alzheimer's, Parkinson's and schizophrenia) and
 CC secretory disorders (such as hyperprolactinemia and Cushing's disease). This
 CC sequence represents the coding sequence for the novel human voltage-gated
 CC potassium ion channel protein TCH136.

XX Sequence 1308 BP; 238 A; 362 C; 389 G; 319 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1,32e-229 Length: 1308
 Score: 2199.50 Matches: 425
 Percent Similarity: 97.48% Conservative: 0
 Best Local Similarity: 97.48% Mismatches: 0
 Query Match: 99.30% Indels: 11
 DB: 9 Gaps: 1

US-10-016-647-2 (1-425) x ADD01427 (1-1308)

QY 1 MetThrPheGlyArgSerGlyAlaAlaSerValValLeuAsnValGlyGlyAlaArgTyr 20
 DB 1 ATGACCTTCGGGCGCAGCGGGCGGCTCGGTGCTGTAACGTGGCGGCGCGGTAT 60
 QY 21 SerLeuSerArgGluLeuLeuLysAspPheProLeuArgArgValSerArgLeuHisGly 40
 DB 61 TCGGTGTCCCGGAGGTGCTGAAGGACTTCCCGCTCGCGCGGTGACCGGCG 120
 QY 41 CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu 60
 DB 121 TCGCGCTCCGAGCGCGAGCTGCTCGAGGTGTGGCAGCATACGACCGCGGCGCACAG 180
 QY 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheLeuLeuTyrValArgGlyHis 80
 DB 181 TACTTCTTCACCGGCACCTCGGAGGCTTCGGGCTTCATCTGCTACGTGGCGGCCAC 240
 QY 81 GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100
 DB 241 GGCAAGCTGGCTTCGCGCGCGGATGTGGAGCTCTCTTCTACACGAGATGATCTAC 300
 QY 101 TrpGlyLeuGluGlyAlaHisLeuGluTyrCysCysGlnArgArgLeuAspArgMet 120
 DB 301 TGGGGCTCGAGGGCGCGCACCTCGAGTACTGTCTGCGCGCGCTCGACGACCGCATG 360
 QY 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140
 DB 361 TCCGACACCTTACACCTTCTACTCGGCGCAGAGCGGGCGGTGCTGGCGCGCGAGGGCG 420
 QY 141 ArgProGlyGlyAlaGluAlaAlaProSerArgArgTyrLeuGluArgMetArgArgThr 160
 DB 421 CGCCCCGGCGGCGCGAGGGCGGCTCCCTCCAGCGCTGGCTGGAGCGCATGCGCGGACC 480
 QY 161 PheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValPhe 180
 DB 481 TTCGAGGAGCCACGCTGCTGCTGGCGCGCGACATCTGGCTAGCGTGGTGGTGTTC 540
 QY 181 ValIleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArgAsnAlaAla 200
 DB 541 GTGATCTGTTCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
 QY 201 AlaAspAsnArgSerLeuAspAspArgSerArg----- 211
 DB 601 GCCGCAACCGCGAGCTGGATGACCGGAGCAGGTACTCCGCGCGCGCTCGGAGGGAGCCC 660
 QY 212 -----IleIleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleValArgPhe 229
 DB 661 TCGGGGATAATTGAAGCTATCTCCATAGGTGTGGTTCCTGCGGAGTGCATCTGTAGGTTTC 720
 QY 230 IleValSerLysAsnLysCysGluPheValLysArgProLeuAsnIleLeuAspLeu 249

Db 721 ATTGTCCTCAAAAACAAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTACTG 780
 Qy 250 AlalleThrProTyrTyrIleSerValLeuMetThrValPheThrGlyValAsnSerGln 269
 Db 781 GCAATCACCCGCTATTACATCTCTGTGTGTATGACAGTGTTTACAGGCGAGACTCTCAA 840
 Qy 270 LeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTrpValIle 289
 Db 841 CTCCAGAGGCTGGAGTCACTTACCTTGAGGTACTTGAATGATGAGGATTTTGGGTGATT 900
 Qy 290 LysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyr 309
 Db 901 AGCTTCCCGGCACCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCA 960
 Qy 310 ArgGluMetValMetLeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeu 329
 Db 961 CGAGAGATGGTTATGTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1020
 Qy 330 SerGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIle 349
 Db 1021 TCTCAGCTTCTTGAACATGGCTGGACCTGGAACATCCCAACAGGACTTTACCAAGCAT 1080
 Qy 350 ProAlaAlaCysTrpIleValIleLeuSerMetThrValGlyTyrGlyAspMetTyr 369
 Db 1081 CTTGCTGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1140
 Qy 370 ProIleThrValProGlyArgIleLeuGlyValCysValValSerGlyIleValLeu 389
 Db 1141 CCTATCACAGTCCCTGGAAGAAATCTTGGAGGAGTTTGTGTGTCAGTGGAAATTTCTTA 1200
 Qy 390 LeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCysTyrHisLeuLeuLys 409
 Db 1201 TTGGGATTAACCTATCACTTTATCTACCATAGCTTTGTGACGTGTATCATGAGCTCAAG 1260
 Qy 410 PheArgSerAlaArgTyrSerArgSerLeuSerThrGluPheLeuAsn 425
 Db 1261 TTTAGATCTGTAGGTATAGTAGGACCTCTCCACTGAATTCCTGAAT 1308
 RESULT 4
 ABZ24711
 ID ABZ24711 standard; cDNA; 1947 BP.
 AC ABZ24711;
 XX
 XX 07-APR-2003 (first entry)
 DE Human potassium channel subunit Kv10.1 cDNA.
 XX Potassium channel; Kv10.1; human; anticonvulsant; antiarrhythmic;
 KW tranquilizer; cytostatic; virucide; nootropic; neuroprotective;
 KW epilepsy; long QT syndrome; muscular ataxia; arrhythmia; gene therapy;
 KW chromosome 2p21; gene; ss.
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH 596..1906
 CDS /*tag= a
 FT /*note= "Human Kv10.1"
 FT
 XX
 XX WO200296944-A2.
 XX
 XX 05-DEC-2002.
 XX
 XX 31-MAY-2002; 2002WO-BP006082.
 XX
 XX 31-MAY-2001; 2001EP-00202060.
 XX (VLA--) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
 PA
 XX
 XX Snyders DJ, Ottschysch N, Raes A, Van Hoorick D;
 PI
 XX WPI; 2003-140443/13.

DR P-PSDB; ABP58352.
 XX Novel voltage-gated heterotetrameric potassium channel useful for
 PT diagnosing, preventing and/or treating excitability disorders, comprises
 PT Kv2.1, Kv3.1, Kv5.1, Kv6.3, Kv10.1 or Kv11.1 potassium channel subunits.
 XX
 XX Claim 3; Page 50-53; 93pp; English.
 XX
 CC The present sequence is that of cDNA encoding human potassium channel
 CC subunit Kv10.1. The cDNA was obtained by PCR from a brain library. The
 CC invention relates to the cloning and characterisation of 3 novel voltage-
 CC gated potassium channel subunits that were identified in the human
 CC genome: Kv6.3 (located at 16q24.1), Kv10.1 (2p21) and Kv11.1 (9p24.2).
 CC yeast two-hybrid and co-immunoprecipitation experiments showed that these
 CC subunits do not form homotetrameric channels, but do form
 CC heterotetrameric channels with Kv2.1, Kv3.1 and/or Kv5.1. Co-expression
 CC of each of the novel subunits with Kv2.1, Kv3.1 and/or Kv5.1 results in
 CC currents that differ from typical Kv2.1 currents. Kv6.3, Kv10.1 and
 CC Kv11.1 alone do not reach the plasma membrane but are retained in the
 CC endoplasmic reticulum. Co-expression with Kv2.1 results in transport to
 CC the plasma membrane. The invention provides novel, voltage-gated
 CC heterotetrameric potassium channels comprising Kv2.1, Kv3.1, Kv5.1,
 CC Kv6.3, Kv10.1 or Kv11.1. These are useful for identifying a molecule that
 CC increases or decreases ion flux through the potassium channel. Nucleic
 CC acids encoding the heterotetrameric potassium channels are used in gene
 CC therapy to prevent or treat congenital or acquired excitability disorders
 CC including epilepsy, long QT syndrome, muscular ataxia, arrhythmia (all
 CC claimed), as well as hyperactivity disorders, mental disorders, mood
 CC disorders, behavioural disorders, anxiety disorders, hypokalaemic,
 CC periodic paralysis, spasticity disorders, myotonia and paramyotonia. The
 CC nucleic acids can be used to transfect cells. For example, stem cells are
 CC used in ex vivo procedures for cell transfection and gene therapy. The
 CC nucleic acids are also useful in diagnosis, and in the creation of
 CC transgenic or knockout animals
 XX
 SQ Sequence 1947 BP; 324 A; 596 C; 644 G; 383 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 2,37e-229 Length: 1947
 Score: 2199.50 Matches: 425
 Percent Similarity: 97.48% Conservative: 0
 Best Local Similarity: 97.48% Mismatches: 0
 Query Match: 99.30% Indels: 11
 DB: Gaps: 1
 US-10-016-647-2 (1-425) x ABZ24711 (1-1947)
 Qy 1 MetThrPheGlyArgSerGlyAlaAlaSerValValLeuAsnValGlyAlaArgTyr 20
 Db 596 ATGACCTTCGGGGCGCAGCGGGCGGCTCGGTGCTGCTGAACGTGGCGCGCCCGGTAT 655
 Qy 21 SerLeuSerArgGluLeuLeuLysAspPheProLeuArgArgValSerArgLeuHisGly 40
 Db 656 TCGCTGTCCCGGAGCTGCTGAAGGACTTCCCGTGGCGCGCGGTGACCGCGTGCACGC 715
 Qy 41 CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu 60
 Db 716 TGGCGTCCCGGCGCGACGCTGCTCGAGTGTGCGACGACTACGACCGGCGGCGACGAG 775
 Qy 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheIleLeuLeuTyrValArgGlyHis 80
 Db 776 TACTTCTTCGACCGGCGACCTCGGAGGCTTCGGTTCATCTCTGCTCTACGTCGCGCGCAC 835
 Qy 81 GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100
 Db 836 GGCAGCTGCGCTTCGCGCGCGGATGTGCGAGCTCTCTTCTACACGAGATGATCTAC 895
 Qy 101 TrpGlyLeuGluGlyAlaHisLeuGluTyrCysCysGlnArgArgLeuAspArgMet 120
 Db 896 TGGGCGCTGGAGGCGCGCACCTCGAGTACTGTGTCGAGCGCGCGCTCGACGACCGCATG 955
 Qy 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140

Db 956 TCCGACACCTACCTCTTACTCGCGCGAGCGCGCGCTGCTGGCGCGCGACGAGCG 1015
 Qy 141 ArgProGlyValAlaGluAlaAlaProSerArgArgArgArgArgArgArgArgArg 160
 Db 1016 CGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1075
 Qy 161 PheGluGluProThrSerSerLeuAlaAlaGlnLeuAlaSerValSerValValPhe 180
 Db 1076 TTCGAGGAGCCACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1135
 Qy 181 ValLeuValSerMetValValLeuValValValValValValValValValValVal 200
 Db 1136 GTGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1195
 Qy 201 AlaAspAsnArgSerLeuAspArgSerArg----- 211
 Db 1196 GCCGACAAACCGAGCTGGATGACCGGAGCAGGTACTCCGCGCGCGCTGGGAGGAGGCC 1255
 Qy 212 -----IleIleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleValArgPhe 229
 Db 1256 TCCGGGATTAATGAAGCTATCTCATAGGTGTTGCTGCGAGTGCATCTGAGGTTC 1315
 Qy 230 IleValSerLysAsnLysCysGluPheValLysArgProLeuAsnIleIleAspLeuLeu 249
 Db 1316 ATTGTCTCCAAACAAAGTGTAGTTGTCAAGAGACCCCTGAACATCATCTATTACTG 1375
 Qy 250 AlaIleThrProTyrTyrIleSerValLeuMetThrValPheThrGlyLysSerGln 269
 Db 1376 GCAATCAGCGCGTATTACATCTCTGTGTGATGACAGTGTTTACAGCGGAGAACTCTCA 1435
 Qy 270 LeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTrpValIle 289
 Db 1436 CTCAGAGGCTGGAGTCACTTACGAGGTACTTAGAATGATGAGGATTTTGGGTGATT 1495
 Qy 290 LysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyr 309
 Db 1496 AAGCTTGCCTGCTCACTTCACTTGTCTTCAGACACTCGTTCCTCAACAGCTTGCTAC 1555
 Qy 310 ArgGluMetValMetLeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeu 329
 Db 1556 CGAGAGATGTTATGTTACTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1615
 Qy 330 SerGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIle 349
 Db 1616 TCTCAGCTTCTTGAACATGGCTGGAGCTGGAACATCAACAGGACTTTTACAGCAT 1675
 Qy 350 ProAlaAlaCysTrpTrpValIleIleSerMetThrThrValGlyTyrGlyAspMetTyr 369
 Db 1676 CCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1735
 Qy 370 ProIleThrValProGlyArgIleLeuGlyGlyValCysValValSerGlyIleValLeu 389
 Db 1736 CCTATCACAGTGCCTGGAAGATTTCTGGAGGAGTTTGTGTGTCAGTGAATTTGTTCTA 1795
 Qy 390 LeuAlaLeuProIleThrPheIleThrHisSerPheValGlnCysTyrHisGluLeuLys 409
 Db 1796 TTGGCATTAACCTATCACTTTTATCTACCATAGCTTTGTGCGAGTGTATCATGAGTCAAG 1855
 Qy 410 PheArgSerAlaArgTyrSerArgSerLeuSerThrGluPheLeuAsn 425
 Db 1856 TTTAGATCTGCTAGGTATAGTAGGAGCCCTCTCCACTGAATTTCTGAT 1903

RESULT 5
 ADD01447
 ID ADD01447 standard; cDNA; 5174 BP.
 AC ADD01447;
 DT 01-JAN-2004 (first entry)
 DE Human TCH136 cDNA sequence.
 KW ds; gene; antidiabetic; antilipemic; antiarteriosclerotic; nootropic;

KW neuroprotective; anabolic; antiinflammatory; immunosuppressive;
 KW cytosolic; antiaesthetic; antiarthritic; cerebroprotective;
 KW antiallergic; antidiabetic; cardiatic; antiparkinsonian; neuroleptic;
 KW glucose transporter; potassium ion channel protein; diabetes;
 KW hyperlipemia; arteriosclerosis; digestive disorder; Crohn's disease;
 KW colitis; gastritis; ileitis; rectal inflammation; inflammatory disease;
 KW sepsis; prostatic hypertrophy; reproductive disorder; pneumonia;
 KW meningitis; hepatitis; myocarditis; asthma; immune disorder;
 KW multiple sclerosis; rheumatoid arthritis; Sjogren's disease; lupus;
 KW allergy; hay fever; allergic rhinitis; anaphylactic shock;
 KW atopic dermatitis; circulatory disorder; heart failure; cancer;
 KW Alzheimer's disease; Parkinson's disease; schizophrenia;
 KW hyperprolactinemia; Cushing's disease; vesicular glutamate transporter.
 XX Homo sapiens.
 OS WO2003054190-A1.
 PN 03-JUL-2003.
 PD 19-DEC-2002; 2002WO-JP013290.
 PF 21-DEC-2001; 2001JP-00389361.
 PR 25-DEC-2001; 2001JP-00392577.
 PR 26-DEC-2001; 2001JP-00394947.
 PR 26-DEC-2001; 2001JP-00395467.
 PR 06-FEB-2002; 2002JP-00030010.
 PR 08-FEB-2002; 2002JP-00033095.
 PR 06-JUN-2002; 2002JP-00165336.
 XX (TAKE) TAKEDA CHEM IND LTD.
 FA Nakanishi A, Sagiya Y, Uno Y;
 PI WPI; 2003-541817/51.
 XX Glucose transporter TCH099, vesicular glutamate transporter TCH177 and
 PT potassium channel protein TCH136 and DNA encoding them for diagnosis,
 PT treatment and prevention of diabetes, hyperlipemia, arteriosclerosis and
 PT digestive disorders.
 XX Claim 62; SEQ ID NO 83; 221bp; Japanese.

The invention relates to a novel glucose transporter TCH099, vesicular
 glutamate transporter TCH177 and voltage-dependent potassium ion channel
 protein TCH136. The sequences are useful in the treatment, prevention and
 diagnosis of a broad range of diseases including diabetes, hyperlipemia,
 arteriosclerosis, digestive disorders (such as Crohn's disease, colitis,
 gastritis, ileitis and rectal inflammation), inflammatory diseases,
 sepsis, prostatic hypertrophy, reproductive disorders, pneumonia,
 meningitis, hepatitis, myocarditis, asthma, immune disorders (such as
 multiple sclerosis, rheumatoid arthritis, Sjogren's disease and lupus),
 allergies (such as hay fever, allergic rhinitis, anaphylactic shock and
 atopic dermatitis), circulatory disorders (such as heart failure), cancer
 (such as cancer of the lung, kidney, liver, ovary, prostate, stomach,
 pancreas, bladder, breast, fallopian tubes, or colon), central nervous
 system diseases (such as Alzheimer's, Parkinson's and schizophrenia) and
 secretory disorders (such as hyperprolactinemia and Cushing's disease). This
 sequence represents the cDNA sequence for the novel human voltage-gated
 potassium ion channel protein TCH136.
 SQ Sequence 5174 BP; 1335 A; 1139 C; 1257 G; 1443 T; 0 U; 0 Other;

Alignment Scores:
 Pred. NO.: 1.01e-228 Length: 5174
 Score: 2199.50 Matches: 425
 Percent Similarity: 97.48% Conservative: 0
 Best Local Similarity: 97.48% Mismatches: 0
 Query Match: 99.30% Indels: 11
 Ds: 9 Gaps: 1
 US-10-016-647-2 (1-425) x ADD01447 (1-5174)

QY 1 MetThrPheGlyArgSerGlyAlaAlaSerValValLeuAsnValGlyValAlaArgTyr 20
 DB 485 ATGACCTTCGGGCGCAGCGCGCGCTCGGTGGTGTGAACGTGGCGGCGCGGTAT 544
 QY 21 SerLeuSerArgGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
 DB 545 TCGCTGTCCCGGAGCTGCTGAAGACATTCCCGCTGCGCGCGGTGAGCGCGCTGCACGCG 604
 QY 41 CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu 60
 DB 605 TCGCGCTCGAGCGCGAGCGTGTCTGAGGTGTGCGAGCTACGACCGCGAGCGCAACGAG 664
 QY 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheLeuLeuLeuTyrValArgGlyHis 80
 DB 665 TACTTCTTCGACCGGCACCTCGGAGGCTTCGCGCTTCATCTGCTCTAGCTGCGCGCGCAC 724
 QY 81 GlyValLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100
 DB 725 GGCAGCTGCGTTCGGCGCGCGGATGTGCGAGCTCTCTTCTACACGAGTGTATCTAC 784
 QY 101 TrpGlyLeuGluGlyAlaHisLeuGluTyrCysGlnArgArgGluLeuAspArgMet 120
 DB 785 TGGGCGCTGGAGGCGCGCACCTCGAGTACTGCTCCAGCGCGGCTCGACCGCGCATG 844
 QY 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140
 DB 845 TCCGACACCTACACCTTCTACTCGCGCGAGCGCGGCTGCTGGCGCGCGAGCGCG 904
 QY 141 ArgProGlyGlyValAlaGluAlaAlaProSerArgArgTyrLeuGluArgMetArgArgThr 160
 DB 905 CGCCCGCGCGGCGCGAGCGGCTCCCTCCAGCGCGCTGCTGCGAGCGCATGCGGCGGACC 964
 QY 161 PheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValPhe 180
 DB 965 TTCGAGGAGCCACCTGCTGCTGCGCGCGAGATCCTGGCTAGCGGTGCGGTGTTC 1024
 QY 181 ValIleValSerMetValValLeuCysAlaSerThrLeuProAspTyrArgAsnAlaAla 200
 DB 1025 GTGATCGTGTCTCATGGTGTGTGTGCGCCAGCAGCTGCGCGAGTGGCGNACGCGACC 1084
 QY 201 AlaAspAsnArgSerLeuAspArgSerArg----- 211
 DB 1085 GCGCAACCGCGAGCTGATACCGGAGCAGGTACTCGCGCGCGCTCGGAGGAGGCC 1144
 QY 212 -----IleIleGluAlaIleCysIleGlyTyrPheThrAlaGluCysIleValArgPhe 229
 DB 1145 TCGGGATTAATGAAGCTATCTGCTAGTGTGTGTCTGCTGCGAGTGTGCTGAGGTTC 1204
 QY 230 IleValSerLysAsnLysCysGluPheValLysA:GProLeuAsnIleIleAspLeuLeu 249
 DB 1205 ATTGCTCCAAAACAAAGTGTGAGTTTGTCAAGAGACCCCTCAACATCATTTGATTTACTG 1264
 QY 250 AlaIleThrProTyrTyrIleSerValLeuMetThrValPheThrGlyGluAsnSerGln 269
 DB 1265 GCAATCACCGCGTATTACATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1324
 QY 270 LeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTyrValIle 289
 DB 1325 CTCGAGGCGCTGAGTCACTTACCTTGAGGTACTTGAATGATGAGGATTTTGGGTGATT 1384
 QY 290 LysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyr 309
 DB 1385 AAGCTTGGCCCGCTCACTTCACTTGGCTTCAGACACTCGGTTCGACTCAAAACGTTTGTCTAC 1444
 QY 310 ArgGluMetValMetLeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeu 329
 DB 1445 CGAGAGATGGTATGTTACTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1504
 QY 330 SerGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIle 349
 DB 1505 TCTCAGCTTCTTGAACATGGCTGGACCTGGAAACATCCAAACAGGACTTTACCGAGCATT 1564
 QY 350 ProAlaAlaCysTrpTrpValIleLeuSerMetThrThrValGlyTyrGlyAspMetTyr 369

DB 1565 CCTGCTCCCTGCTGGTGGGTGAATATCTCTATCATTACAGTACAGTATGAGATATGAT 1624
 QY 370 ProfileThrValProGlyArgGlyLeuGlyValCysValValSerGlyValLeuValLeu 389
 DB 1625 CCTATCACAGTGGCTGGAGAAATCTTTGGAGGAGTTTGTGTTCAGTGAATTTCTTA 1684
 QY 390 LeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCysTyrHisGluLeuLys 409
 DB 1685 TTGGCAATCTACTATCATTCTTTTATCTACATAGCTTTGTGAGTGTATCATGAGCTCAAG 1744
 QY 410 PheArgSerAlaArgTyrSerArgSerLeuSerThrGluPheLeuAsn 425
 DB 1745 TTTAGATCTGCTAGTATAGTAGAGCCTCTCCACATGAATTCCTGAAT 1792
 RESULT 6
 ABZ24716
 ID ABZ24716 standard; cDNA; 5775 BP.
 XX
 AC ABZ24716;
 XX
 DT 07-APR-2003 (first entry)
 XX
 DE Murine potassium channel subunit Kv10.1 - flag sequence.
 XX
 KW Potassium channel; Kv10.1; mouse; transgenic mouse; gene; ss.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 3424..4749
 FT /*tag= a
 FT /note= "flag"
 XX
 FN WO200296944-A2.
 XX
 PD 05-DEC-2002.
 XX
 PF 31-MAY-2002; 2002WO-EP006082.
 XX
 PR 31-MAY-2001; 2001EP-00202060.
 XX
 PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
 XX
 PI Snyders DJ, Otteschytch N, Raes A, Van Hoorick D;
 XX
 XX WPI; 2003-140443/13.
 XX
 PT Novel voltage-gated heterotetrameric potassium channel useful for
 PT diagnosing, preventing and/or treating excitability disorders, comprises
 PT Kv2.1, Kv3.1, Kv5.1, Kv6.3, Kv10.1 or Kv11.1 potassium channel subunits.
 XX
 PS Example; Page 80-82; 93pp; English.
 XX
 CC The present sequence is that of a construct used in the creation of a
 CC potassium channel subunit Kv10.1 transgenic mouse. In an example from the
 CC invention, the construct was microinjected into the pronucleus of a one-
 CC cell embryo, and then incubated in a foster mother of the FVB/Nlco mouse
 CC strain. The invention provides novel, voltage-gated heterotetrameric
 CC potassium channels comprising Kv2.1, Kv3.1, Kv5.1, Kv6.3, Kv10.1 or
 CC Kv11.1. These are useful for identifying a molecule that increases or
 CC decreases ion flux through the potassium channel (claimed). Nucleic acids
 CC encoding the heterotetrameric potassium channels are used in gene therapy
 CC to prevent or treat congenital or acquired excitability disorders
 CC including epilepsy, long QT syndrome, muscular ataxia, and arrhythmia
 CC (all claimed)
 XX
 SQ Sequence 5775 BP; 1327 A; 1530 C; 1532 G; 1386 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 2,42e-218 Length: 5775
 Score: 2105.00 Matches: 408
 Percent Similarity: 94.72% Conservative: 5

25-SEP-2001; 2001US-0324800P.
 25-SEP-2001; 2001US-0324802P.
 27-SEP-2001; 2001US-0325684P.
 17-OCT-2001; 2001US-0330143P.
 14-NOV-2001; 2001US-0332131P.
 14-NOV-2001; 2001US-0332240P.
 14-NOV-2001; 2001US-0332779P.
 21-NOV-2001; 2001US-0332115P.
 04-DEC-2001; 2001US-0337621P.
 03-JAN-2002; 2002US-0345783P.
 16-JAN-2002; 2002US-0350251P.
 02-APR-2002; 2002US-00114270.
 (CURA-) CURAGEN CORP.
 Guo X, Kekuda R, Miller CE, Malyankar UM, Spytek KA,
 Patturajan M, Liu X, Gusev VY, Li L, Vernet CM, Zerhusen BD,
 Gorman L, Shenoy SG, Pena CEA, Smithson G, Burgess CE, Gerlach V,
 Padigaru M, Shinkets RA, Gangoli EA, Taupier RJ, Casman SJ, Ji W,
 Anderson DW, Leite MW, Rastelli L, Edinger SR, Stone DJ,
 MacDougall JR, Rothenberg ME, Mazur A, Millet I, Peyman JA,
 Ellerman K;
 WPI; 2003-046858/04.
 P-PSDB; ABUS4564.
 New isolated NOVX polypeptide useful for treating atherosclerosis,
 metabolic disorders, diabetes, obesity, infectious disease, anorexia,
 neurodegenerative disorders, Alzheimer's disease and cancer.
 Claim 17; Page 136; 666pp; English.
 The invention relates to human polypeptides, termed NOVX, and the
 polynucleotides encoding them. The polypeptides and polynucleotides are
 useful for diagnosing disease, and screening for potential therapeutic
 agents. The sequences are useful for treating metabolic disorders,
 cardiomyopathy, diabetes, hypertension, congenital heart defects, aortic
 stenosis, atrial septal defect (ASD), atrioventricular canal defect,
 ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular
 septal defect (VSD), valve diseases, tuberculous sclerosis, scleroderma,
 atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative
 disorders, Alzheimer's disease, Parkinson's disease, immune disorders,
 haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease
 and cancer. Sequences ABX72170-ABX72275 represent human NOVX
 polynucleotides of the invention
 XX Sequence 1651 BP; 292 A; 476 C; 510 G; 373 T; 0 U; 0 Other;
 SQ

Alignment Scores:
 Pred. No.: 4,11e-218 Length: 1651
 Score: 2095.50 Matches: 411
 Percent Similarity: 91.54% Conservative: 0
 Best Local Similarity: 91.54% Mismatches: 3
 Query Match: 94.60% Indels: 35
 DB: 7 Gaps: 3

US-10-016-647-2 (1-425) x ABX72192 (1-1651)

QY 1 MetThrPheGlyArgSerGlyValAlaSerValValLeuAsnValGlyValAlaArgTyr 20
 Db 58 ATGACCTTCGGCGGAGCGGGCGGCGCTCGGTGGTCTGACGTGGCGGCGCGGTAT 117
 QY 21 SerLeuSerArgGluLeuLeuLysAspPheProLeuArgArgValSerArgLeuHisGly 40
 Db 118 TCGCTGTCCCGGAGCTGCTGAAGACCTCCCGCTGCCGCGGTGAGCGCGTGCACGCG 177
 QY 41 CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu 60
 Db 178 TCCCGCTCCGACGGAGCTGCTCGAGGTGTGCGACGACTACGACCGGAGCGCAACGAG 237
 QY 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheLeuLeuLeuTyrValArgGlyHis 80
 Db 238 TACTTCTTCGACCGGCACTTCGAGAGGCTTCGGCTTCACTCCTGCTCTAGTGGCGGCCAC 297

QY 81 GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetLeuTyr 100
 Db 298 GGCAGAGCTGGCTTCGGCGCGCGGATGTGCGAGCTCTCTTCTACCAACAGATGATCTAC 357
 QY 101 TrpGlyLeuGluGlyAlaHisLeuGluTyrCysCysGlnArgArgLeuAspAspArgMet 120
 Db 358 TGGGGCTCGAGGGCGCGCACCTCGAGTACTGCTGCGAGCGCGCTCGACACCGCATG 417
 QY 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140
 Db 418 TCCGACCACTACACCTTCTACTCGGCGGAGCGGGCGTGTCTGGCGCGCGACGAGGCG 477
 QY 141 ArgProGly-----GlyAlaGluAlaAlaPro--- 149
 Db 478 CGCCCCGGCGCGAGCGCGCTCCCTCCAGCGCGTGGCTGGAGCGCATCGCGCGGACCTT 537
 QY 150 -----SerArgArgTyrTrpLeuGluArgMetArgArgThrPhe 161
 Db 538 CGAGGAGCCACGCTGCTGCTGGCGCGAGCGCTGGCTGGAGCGCATCGCGCGGACCTTC 597
 QY 162 GluGluProThrSerSerLeuAlaAlaGlnLeuLeuAlaSerValSerValValPheVal 181
 Db 598 GAGGAGCCACGCTGCTGCTGGCGCGAGATCTCTGGCTAGCGTGTCTGGTGTGTCTG 657
 QY 182 IleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArgAsnAlaAla 201
 Db 658 ATCGTGTCCATGTGTGTGTGCGCGCAGCACGTTCCCGACCTGGCGCAACCGAGCGGCC 717
 QY 202 AspAsnArgSerLeuAspAspArgSer----- 210
 Db 718 GACCAACCGGAGCTGATGACCGAGCAGTACTCCGCGCGCGCTGGAGGAGCGGCTCTCC 777
 QY 211 -----ArgIleIleGluAlaIleCysIleGlyTrpPheThrAlaGluCys 225
 Db 778 GGTGTGTCTTTCGACAGGATAATGAAGCTATCTGCATAGTGTGTCTCTGCCGAGTGC 837
 QY 226 IleValArgPheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsnIle 245
 Db 838 ATCGTGGGTTCATTGTCTCCAAAACAAAGTGTGAGTGTTCGCAAGAGACCCCTGAACATC 897
 QY 246 IleAspLeuLeuAlaIleThrProTyrTyrIleSerValLeuMetThrValPheThrGly 265
 Db 898 ATTGATTATCTGCAATACGCGGTATTACATCTCTGTGTATGACAGTGTTCAGGC 957
 QY 266 GluAsnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIle 285
 Db 958 GAGAACTCTCACTCCAGAGGCTGGAGTCACTTGAGGGTACTTAGATGATGAGGATT 1017
 QY 286 PheTrpValIleLysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeu 305
 Db 1018 TTTTGGGTGATTAAAGCTTGGCGCTCACTTCATTGGTCTTCAGACACTCGGTTCAGTCTC 1077
 QY 306 LysArgCysTyrArgGluMetValMetLeuValPheIleCysValAlaMetAlaIle 325
 Db 1078 AAACGTGTCTACCGAGAGATGGTATGTACTTGTCTTANTTGTGTGCGATGCGCAATC 1137
 QY 326 PheSerAlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAsp 345
 Db 1138 TTTAGTGCACTTCTCAGCTTCTTGAACATGGCTGGACCTGGAAACATCCAAACAAGGAC 1197
 QY 346 PheThrSerIleProAlaAlaCysTrpTrpValIleIleSerMetThrThrValGlyTyr 365
 Db 1198 TTTACCAAGCATTCCTGCTGCTGCTGGGTGATTATCTCTATGACTACAGTGGGTAT 1257
 QY 366 GlyAspMetTyrProIleThrValProGlyValArgIleLeuGlyValCysValValSer 385
 Db 1258 GGAGATATGATCTCTATCAGTGCCTGGAGAAATCTTGGAGAGATTGTGTGTGTCAGT 1317
 QY 386 GlyIleValLeuLeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCysTyr 405
 Db 1318 GGAATTGTTCTATTGGCATTACCTATCATTCTTATCTACCATAGCTTTGTGTCAGTGTAT 1377

muscle, immunological disorders (e.g. scleroderma, erythematous, allergies), cell proliferation (e.g. leukaemia, cervical or breast cancer)

CC muscle, immunological disorders (e.g. scleroderma, systemic lupus erythematosus, allergies), cell proliferative disorders such as cancers (e.g. leukaemia, cervical or breast cancers), neurodegenerative disorders

QY 220 pPheThrAlaGluCysIleValAlaGpPheIleValSerLysAsnLysCysGluPheVally 240

Qy 220 pPheThrAlaGluCysIleValArgpPheIle

ValSerLysAsnLysCysGluPheVally 240

Db 1066 GTTCACTCCGAGTCATCGTCAGGTTTCATTGCTCTCCAAACACAGTGTGAGTTGTCAA 1125
 QY 240 sArgProLeuAenillelleAspLeuLeuAlaileThrProTyrrilleSerValLeuMe 260
 Db 1126 GAGACCCCTGACATCATTTACTGGCAATCAACGCCGCTATTACATCTCTGTGTTGAT 1185
 QY 260 tThrValPheThrGlyGluAenSerGlnLeuGlnArgAlaGlyValThrLeuArgValLe 280
 Db 1186 GACAGTGTTTACAGCGGAGACTCTCACTCCAGAGGGCTGAGTCACCTTGAGGGTACT 1245
 QY 280 uArgMetMetArgillePheThrValilleYsLeuAlaArgHisPheilleGlyLeuGlnTh 300
 Db 1246 TAGAATGATGAGCAATTTTGGGTGATTAAAGCTTCCCGCTCACTTCATTGGTCTTTCAGAC 1305
 QY 300 rIeuGlyLeuThrLeuYsArgCysTyrrArgGluMetValMetLeuLeuValPheilleCy 320
 Db 1306 ACTCGGTGTGACTCTCAACAGTTGTACCGAGAGATGTTATGTTACTTGTCTTCAATTG 1365
 QY 320 sValAlaMetAlailePheSerAlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeuGl 340
 Db 1366 TGTTCGCCATGGCAATCTTTAGTCACCTTCTCAGCTTCTTGAAACATGGCTGGACCTGGA 1425
 QY 340 uThrSerAsnIysAspPheThrSerIleProAlaAlaCysTrpThrValillelleSerMe 360
 Db 1426 AACATCCCAACAGGACTTTACAGCAATTCCTGCTGCTGCTGGTGGGTATATCTCAT 1485
 QY 360 tThrThrValGlyTyrrGlyAspMetTyrrProilleThrValProGlyArgilleLeuGlyGl 380
 Db 1486 GACTACAGTGGCTATGAGATATGATCTATCATGCTGCTGGAAGAATCTTGGAGG 1545
 QY 380 yValCysValValSerGlylleValLeuLeuAlaLeuProilleThrPheilleTyrrHis 400
 Db 1546 AGTTTGTGTGTGACAGTGAATTTGTTATTTGGCATTACCTATCATCTTTTATCTACCATAG 1605
 QY 400 rPheValGlnCysTyrrHisGluLeuYsPheArgSerAlaArg 414
 Db 1606 CTTTGTGACGTGTTATCATGAGCTCAAGTTAGATTCTGCTAGG 1648
 RESULT 9
 AAD33662
 ID AAD33662 standard; cdna; 2312 BP.
 XX
 AC AAD33662;
 XX
 DT 01-JUL-2002 (first entry)
 XX
 DE Human TRICH-17 cDNA.
 KW Human; transporter and ion channel; TRICH-17; transport disorder; angina;
 KW amyotrophic lateral sclerosis; cystic fibrosis; diabetes; neuromuscular disorder;
 KW cardiac disorder; polymyositis; diabetes; neurological disorder; cancer;
 KW depression; schizophrenia; anaemia; Wilson's disease; Cushing's disease;
 KW cell proliferated disorder; infertility; arteriosclerosis; gene therapy;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; allergy;
 KW myasthenia gravis; multiple sclerosis; metabolic disorder; hypertension;
 KW acquired immune deficiency syndrome; immunological disorder; scleroderma;
 KW endocrine disorder; autoimmune thyroiditis; rheumatoid arthritis; goitre;
 KW cardiac myopathy; amnesia; toxic myopathy; Addison's disease; infection;
 KW epilepsy; mental disorder; myocarditis; Crohn's disease; Grave's disease;
 KW muscle disorder; stroke; dementia; anxiety; AIDS; asthma; cirrhosis;
 KW gene; ss.
 XX
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 325..1845
 FT /*tag= a
 FT /product= "Human TRICH-17 protein"
 XX
 PN WC0200212340-A2.
 XX
 PD 14-FEB-2002.
 XX

PF 01-AUG-2001; 2001WO-US024217.
 XX 03-AUG-2000; 2000US-0223269P.
 PR 10-AUG-2000; 2000US-0224456P.
 PR 18-AUG-2000; 2000US-0226410P.
 PR 25-AUG-2000; 2000US-0228140P.
 PR 31-AUG-2000; 2000US-0230067P.
 PR 08-SEP-2000; 2000US-0231434P.
 XX (JNCY-) INCYTE GENOMICS INC.
 FA Yue H, Thornton M, Ramkumar J, Tang YT, Azimzai Y, Baughn MR;
 XX Yang J, Yao MG, Lal P, Wallia NK, Gandhi AR, Hafalia AYA, Nguyen DB;
 PI Patterson C, Elliott VS, Tribouley CM, Lu DAM, Xu Y, Reddy R;
 PI Hernandez R, Borowsky ML, Lo TP, Lu Y, Policky JL, Greene BD;
 PI Sanjanwala WS, Raumann BE, Burford N, Ison CH, Lee EA, Ding L;
 PI Das D, Kallisch RA, Khan FA, Seilhamer JJ;
 XX WFI; 2002-206330/26.
 DR P-PSDB; AAE211173.
 XX
 DR New human transporters and ion channels polypeptides and polynucleotides
 PT for diagnosing, preventing or treating transport, neurological, muscle,
 FT immunological and cell proliferative disorders.
 XX
 PS Claim 91; Page 217; 230pp; English.
 XX
 CC The invention relates to human transporter and ion channel polypeptides
 CC designated TRICH and nucleic acid molecules encoding such polypeptides.
 CC TRICH sequences are useful for diagnosis, treatment and prevention of
 CC transport, muscle, neurological, immunological and cell proliferative
 CC disorders. Transport disorders include akinesia, amyotrophic lateral
 CC sclerosis, ataxia telangiectasia, cystic fibrosis, Becker's muscular
 CC dystrophy, diabetes mellitus, diabetes insipidus, myasthenia gravis,
 CC myocarditis, prostate cancer, diabetic neuropathy associated with transport
 CC e.g. polymyositis, bradyarrhythmia, dermatomyositis, angina, neurological
 CC disorders associated with transport e.g. amnesia, bipolar disorder,
 CC depression, Tourette's disorder, schizophrenia, other disorders
 CC associated with transport e.g. neurofibromatosis, sickle cell anaemia,
 CC Wilson's disease, cataracts, infertility, hyperglycaemia, hypoglycaemia,
 CC goitre, Cushing's disease, hypercholesterolaemia and cystinuria. Cell
 CC proliferated disorders include cancer, actinic keratosis, cirrhosis,
 CC arteriosclerosis, atherosclerosis, bursitis, hepatitis and psoriasis.
 CC Neurological disorders include Alzheimer's, Pick's and Parkinson's
 CC disease, amyotrophic lateral sclerosis, epilepsy, stroke, Huntington's
 CC disease, multiple sclerosis, dementia and other extrapyramidal disorder,
 CC motor neuron disorder, prion disease, metabolic disease of the nervous
 CC system and other developmental disorders of the central nervous system,
 CC neuromuscular disorders, metabolic, endocrine and toxic myopathies,
 CC periodic paralysis, mental disorders including mood anxiety; and
 CC immunological disorders include acquired immune deficiency syndrome
 CC (AIDS), adult respiratory distress syndrome, Addison's disease,
 CC allergies, asthma, atherosclerosis, osteoporosis, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, Crohn's disease, atopic dermatitis,
 CC Grave's disease, glomerulonephritis, rheumatoid arthritis, scleroderma,
 CC systemic lupus erythematosus, systemic sclerosis, ulcerative colitis,
 CC haemodialysis uretisis, viral, bacterial, fungal, parasitic, protozoal,
 CC hematitic infections and trauma, and muscle disorders include cardiac
 CC myopathy, myocarditis, polymyositis, arrhythmias and hypertension. The
 CC TRICH polynucleotides are used in gene therapy. The present sequence is
 CC human TRICH-17 cDNA
 XX
 SQ Sequence 2312 BP; 475 A; 607 C; 674 G; 556 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 4,43e-181 Length: 2312
 Score: 1758.00 Matches: 351
 Percent Similarity: 83.37% Conservative: 0
 Best Local Similarity: 83.37% Mismatches: 0
 Query Match: 79.37% Indels: 70
 DB: 6 Gaps: 1

US-10-016-647-2 (1-425) x AAD33662 (1-2312)

Qy 5 ArgSerGlyAlaAlaSerValValLeuAsnValGlyGlyAlaArgTyrSerLeuSerArg 24
 Db 790 CGCAGCGGGCGCGCTCGGTGCTGCAACGTGGGGCGCGCGGTATTCGTGTCGCCG 849
 Qy 25 GluLeuLeuLysAspPheProLeuArgArgValSerArgLeuHisGlyCysArgSerGlu 44
 Db 850 GAGCTGCTGAGGACTTCGCGCTGCGCGCGCTGAGCGCGCTGCAAGCTGCGCTCCGAG 909
 Qy 45 ArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGluTyrPhePheAsp 64
 Db 910 CGCAGCTGCTCGAGGTGCGAGCGACTACGACCGCGAGCGCAACGAGTACTTCTTCGAC 969
 Qy 65 ArgHisSerClnAlaPheGlyPheLeuLeuTyrValArgGlyHisGlyLysLeuArg 84
 Db 970 CGGACTCGGAGCGCTTCGCGCTTCATCTGCTCTAC----- 1005
 Qy 85 PheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyrTrpGlyLeuGlu 104
 Db 1005 ----- 1005
 Qy 105 GlyAlaHisLeuGluTyrCysCysGlnArgArgLeuAspArgMetSerAspThrTyr 124
 Db 1005 ----- 1005
 Qy 125 ThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAlaArgProGlyGly 144
 Db 1005 ----- 1005
 Qy 145 AlaGluAlaAlaProSerArgArgTyrLeuGluArgMetArgThrPheGluGluPro 164
 Db 1006 -----CGCGCTCCCTCCAGCGCTGCGTGGAGCGCATCGCGGACCTTCGAGGAGCGCC 1059
 Qy 165 ThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValValPheValIleValSer 184
 Db 1060 ACCTGCTGCTGCGCGCGAGATCTCGCTAGCGTCTCGTGGTGTCTGTGATCTGTGTC 1119
 Qy 185 MetValValLeuCysAlaSerThrLeuProAspTyrArgAsnAlaAlaAlaAspAsnArg 204
 Db 1120 ATGGTGGTGTGCGCGAGCAGCTTGGCGGACGTGGCGCAACGCGCGCGCAACCGC 1179
 Qy 205 SerLeuAspArgSerArgIleIleGluAlaIleCysIleGlyTrpPheThrAlaGlu 224
 Db 1180 AGCTTGATGACCGGAGCAGGATTAATGAAGCTATCTGCATAGGTGGTTCATCGCCGAG 1239
 Qy 225 CysIleValArgPheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsn 244
 Db 1240 TGCACTGCTGAGGTTCATTGTCTCAAAACAAAGTGTGAGTGTCAAGAGACCCCTGAAC 1299
 Qy 245 IleIleAspLeuLeuAlaIleThrProTyrTyrIleSerValLeuMetThrValPheThr 264
 Db 1300 ATCATTGATTACTGGCAATCACCGCGTATTACATCTCTGTGTGATGACAGTGTTTACA 1359
 Qy 265 GlyGluAsnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArg 284
 Db 1360 GCGGAGAACTCTCACTCAGAGGGCTGGAGTCACCTTCAGGGTACTAGATGATGAGG 1419
 Qy 285 IlePheTrpValIleLysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThr 304
 Db 1420 ATTTTGGGTGATTAAAGCTTGCCCGCTCATCTTCATTGGTCTTCAGACACTCGGTTTGACT 1479
 Qy 305 LeuLysArgCysTyrArgGluMetValMetLeuLeuValPheIleCysValAlaAlaMetAla 324
 Db 1480 CTCRAACGTGTACCGAGAGATGGTATGTACTTCTTCTATTGTGTTCATGTCATGCA 1539
 Qy 325 IlePheSerAlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLys 344
 Db 1540 ATCTTTAGTGCATTTCTCAGCTTCTGAACATGGCTGGACCTGGAACATCCAAACAG 1599
 Qy 345 AspPheThrSerIleProAlaAlaCysTyrTrpValIleIleSerMetThrThrValGly 364
 Db 1600 GACTTTACAGCATTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1659

Qy 365 TyrGlyAspMetTyrProIleThrValProGlyArgIleLeuGlyGlyValCysValVal 384
 Db 1660 TATGGAGATATGATATCTATCAGATGCTCCGGAAGAAATTTTGAGGAGTTTGTGTGTC 1719
 Qy 385 SerGlyIleValLeuLeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCys 404
 Db 1720 AGTGAATTTGTTCTTATGGCATTACCTATCATTATTTATCATTACCATAGCTTTGTGCAGTGT 1779
 Qy 405 TyrHisGluLeuLysPheArgSerAlaArgTyrSerArgSerLeuSerThrGluPheLeu 424
 Db 1780 TATCATGAGCTCAAGTTTAGTCTGCTAGTATAGTAGGAGCCTCTCCACTGAATTCCTG 1839
 Qy 425 Asn 425
 Db 1840 AAT 1842
 RESULT 10
 ADD01469
 ID ADD01469 standard; cDNA; 950 BP.
 XX
 AC ADD01469;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Mouse TCH136 cDNA sequence fragment.
 KW ds; antidiabetic; antilipemic; antiarteriosclerotic; nootropic;
 KW neuroprotective; anabolic; antiinflammatory; immunosuppressive;
 KW cytoskeletal; antiasthmatic; antiarthritic; cerebroprotective;
 KW antiallergic; dermatological; cardiant; antiparkinsonian; neuroleptic;
 KW glucose transporter; potassium ion channel protein; diabetes;
 KW hyperlipemia; arteriosclerosis; digestive disorder; Crohn's disease;
 KW colitis; gastritis; ileitis; rectal inflammation; inflammatory disease;
 KW sepsis; gastric hypertrophy; reproductive disorder; pneumonia;
 KW meningitis; hepatitis; myocarditis; asthma; immune disorder;
 KW multiple sclerosis; rheumatoid arthritis; Sjogren's disease; lupus;
 KW allergy; hay fever; allergic rhinitis; anaphylactic shock;
 KW atopic dermatitis; circulatory disorder; heart failure; cancer;
 KW Alzheimer's disease; Parkinson's disease; schizophrenia;
 KW hyperprolactinemia; Cushing's disease; vesicular glutamate transporter.
 XX Mus sp.
 XX WO2003054190-A1.
 PN 03-JUL-2003.
 XX 19-DEC-2002; 2002WO-JP013290.
 XX 21-DEC-2001; 2001JP-00389361.
 PR 25-DEC-2001; 2001JP-00392577.
 PR 26-DEC-2001; 2001JP-00394947.
 PR 26-DEC-2001; 2001JP-00395467.
 PR 06-FEB-2002; 2002JP-00030010.
 PR 08-FEB-2002; 2002JP-0003095.
 PR 06-JUN-2002; 2002JP-00165336.
 XX (TAKA) TAKEDA CHEM IND LTD.
 PA Nakanishi A, Sagiya Y, Uno Y;
 FI WPI; 2003-541817/51.
 XX
 DR Glucose transporter TCH099, vesicular glutamate transporter TCH177 and
 PT potassium channel protein TCH136 and DNA encoding them for diagnosis,
 PT treatment and prevention of diabetes, hyperlipemia, arteriosclerosis and
 PT digestive disorders.
 XX
 PS Example 21; SEQ ID NO 105; 221pp; Japanese.
 XX
 CC The invention relates to a novel glucose transporter TCH099, vesicular
 CC glutamate transporter TCH177 and voltage-dependent potassium ion channel
 CC protein TCH136. The sequences are useful in the treatment, prevention and

Alignment Scores:
 Pred. No.: 1,1e-85 Length: 1401
 Score: 880.50 Matches: 182
 Percent Similarity: 62.24% Conservative: 85
 Best Local Similarity: 42.42% Mismatches: 125
 Query Match: 39.75% Indels: 37
 DB: 2 Gaps: 8

US-10-016-647-2 (1-425) x AAZ23803 (1-1401)

QY	4	GlyArgSerGlyAlaAlaSerValValLeuAsnValGlyGlyAlaArgTyrSerLeuSer	23
DB	34	GGGGGACCCCGCCCGCCAGCTCATCATCAAGTGGGGGCTGCGCGCTGGCA	93
QY	24	ArgGluLeuLeuLysAspPheProLeuArgArgValSerArgLeuHisGlyCysArgSer	43
DB	94	TGGCGCGCTGGCGGATCCCGCTGCGCGCTGGAGCGCTGCGCGCTGCGCGCGC	153
QY	44	GluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGluTyrPhePhe	63
DB	154	CACGACGACCTGCTGCGCGTGTGACGACTACGAGCTGAGCGCGCGAGGTTCCTTC	213
QY	64	AspArgHisserGluAlaPheGlyPheLeuLeuLeuTyrValArgGlyHisGlyLysLeu	83
DB	214	GACCGACGCGCTGCGCGCTTCCGCGCCATCGTGGCGCTTTTGGCGCA---GGGAGCTG	270
QY	84	ArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyrTrpGlyLeu	103
DB	271	CGACTGCTGGGGCGCGTGGCGCTGGCGCTTCCGCGAGAGCTGCGCTACCTGGGCGATC	330
QY	104	GluGlyAlaHisLeuGluTyrCysGlnArgArgLeuAspArgMetSerAspThr	123
DB	331	GACGAGCGCGCTGGAGCGCTGCTGCGCGCGCTGCGCGCGCGAGGAGGCGG	390
QY	124	TyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAlaArgProGly	143
DB	391	-----GCCGAGCGCGCGCGCGG	408
QY	144	-----GlyAlaGluAlaAlaProSerArg-----	151
DB	409	CCGACGAGCGCGCGCGAGCGAGCGCGCGCGCTGCGAGCTCGCGCGCGGCTG	468
QY	152	---ArgTrpLeuGluArgMetArgArgThrPheGluGluProThrSerSerLeuAlaAla	170
DB	469	CACGCGCGCGCGCGCGCTGCGCGAGCTGCTGCGCGCGCTGCGCGCGCTGCGCGCG	528
QY	171	GlnIleLeuAlaSerValSerValPheValIleValSerMetValValLeuCysAla	190
DB	529	AAGCTCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	588
QY	191	SerThrLeuProAspTrpArgAsnAlaAlaAlaAspAsnArgSerLeuAspArgSer	210
DB	589	AGCACCATGCGGACATCGC---GCCGAGGAGCGCGCGCGAGTGTCTCCCGCAAGTGC	645
QY	211	Arg-----IleIleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleVal	227
DB	646	CGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	705
QY	228	ArgPheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsnIleLeuAsp	247
DB	706	CGCTCCCTGCGAGCGCGAGAGTGGCTTCTGCGCGCGCGCTGCTGCGCGCGCTGAC	765
QY	248	LeuLeuAlaIleThrProTyrTrpIleSerValLeuMetThrValPheThrGlyGluAsn	267
DB	766	ATCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	825
QY	268	SerGln-----LeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIle	285
DB	826	GGGACCAAGCTCTGAGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	885
QY	286	PheTrpValIleLysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeu	305
DB		-----	
DB	856	CTCTACGTGATGCGCTGGCGCGCACTCGCTGGGGCTGGCTTGGCTGGCGCTGACCATG	945
QY	306	LysArgCysTyrArgGluMetValMetLeuLeuValPheIleCysValAlaMetAlaIle	325
DB	946	CGCGCTGCGCGCGCGAGTTCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1005
QY	326	PheSerAlaLeuSerGlnLeuLeuHisGlyLeuAspLeuGluThrSerAsnLysAsp	345
DB	1006	TTGCGGCACTGTGCGACCTGGCGGCGCGAGCTGGGC-----GGCGCGCGGAC	1056
QY	346	PheThrSerIleProAlaAlaCysTrpTrpValIleIleSerMetThrThrValGlyTyr	365
DB	1057	TTCTCCAGCGTGGCGCGCGAGCTATTGTGGCGCTCATCTCCATGACACCGTGGGTAC	1116
QY	366	GlyAspMetTyrProIleThrValProGlyArgIleLeuGlyValCysValValSer	385
DB	1117	GCGACATGTTCGCGCGCGAGCTGCGCGCGAGGTGGTGGCTCAGCAGCATCTCTCAGC	1176
QY	386	GlyIleValLeuLeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCysTyr	405
DB	1177	GCGATCTGCTCATGCGCTTCCCGGTCCATCTCCATCTTCCACACCTTTTGGCGCTCTAC	1236
QY	406	HisGluLeuLysPheArgSerAlaArg	414
DB	1237	TCCGAGCTCAAGGAGCAGCAGCAGCGC	1263
DE	RESULT 12		
AA	AS75631	standard; cDNA; 1401 BP.	
XX	AS75631		
DT	13-FEB-2002	(first entry)	
XX	DNA encoding novel human diagnostic protein #11435.		
XX	Human; chromosome mapping; gene mapping; gene therapy; forensic;		
XX	food supplement; medical imaging; diagnostic; genetic disorder; ss.		
OS	Homo sapiens.		
XX	WO200175067-A2.		
XX	11-OCT-2001.		
XX	30-MAR-2001; 2001WO-US008631.		
XX	31-MAR-2000; 2000US-00540217.		
XX	23-AUG-2000; 2000US-00649167.		
XX	(HYSE-) HYSEQ INC.		
XX	Drmanac RT, Liu C, Tang YT;		
XX	WPI; 2001-639362/73.		
XX	P-PSDB; ABG11444.		
XX	New isolated polynucleotide and encoded polypeptides, useful in		
XX	diagnostics, forensics, gene mapping, identification of mutations		
XX	responsible for genetic disorders or other traits and to assess		
XX	biodiversity.		
PS	Claim 1; SEQ ID NO 11435; 103pp; English.		
XX	The invention relates to isolated polynucleotide (I) and polypeptide (II)		
XX	sequences. (I) is useful as hybridisation probes, polymerase chain		
XX	reaction (PCR) primers, oligomers, and for chromosome and gene mapping,		
XX	and in recombinant production of (II). The polynucleotides are also used		
XX	in diagnostics as expressed sequence tags for identifying expressed		
XX	genes. (I) is useful in gene therapy techniques to restore normal		
XX	activity of (II) or to treat disease states involving (II). (II) is		
XX	useful for generating antibodies against it, detecting or quantitating a		
XX	polypeptide in tissue, as molecular weight markers and as a food		

XX WPI: 2003-140443/13.
 DR P-PSDB; ABP59351.
 XX Novel voltage-gated heterotetrameric potassium channel useful for
 PT diagnosing, preventing and/or treating excitability disorders, comprises
 PT Kv2.1, Kv3.1, Kv5.1, Kv6.3, Kv10.1 or Kv11.1 potassium channel subunits.
 XX
 XX Disclosure; Page 45-48; 93pp; English.

XX The present sequence is the coding sequence of the human potassium
 CC channel subunit Kv6.3 gene. The coding sequence was cloned from genomic
 CC DNA by PCR. The invention relates to the cloning and characterisation of
 CC 3 novel voltage-gated potassium channel subunits that were identified in
 CC the human genome: Kv6.3 (located at 16q24.1), Kv10.1 (2p21) and Kv11.1
 CC (9p24.2). Yeast two-hybrid and co-immunoprecipitation experiments showed
 CC that these subunits do not form homotetrameric channels, but do form
 CC heterotetrameric channels with Kv2.1, Kv3.1 and/or Kv5.1. Co-expression
 CC of each of the novel subunits with Kv2.1, Kv3.1 and/or Kv5.1 results in
 CC currents that differ from typical Kv2.1 currents. Kv6.3, Kv10.1 and
 CC Kv11.1 alone do not reach the plasma membrane but are retained in the
 CC endoplasmic reticulum. Co-expression with Kv2.1 results in transport to
 CC the plasma membrane. The invention provides novel voltage-gated
 CC heterotetrameric potassium channels comprising Kv2.1, Kv3.1, Kv5.1,
 CC Kv6.3, Kv10.1 or Kv11.1. These are useful for identifying a molecule that
 CC increases or decreases ion flux through the potassium channel. Nucleic
 CC acids encoding the heterotetrameric potassium channels are used in gene
 CC therapy to prevent or treat congenital or acquired excitability disorders
 CC including epilepsy, long QT syndrome, muscular ataxia, arrhythmia (all
 CC claimed), as well as hyperactivity disorders, mental disorders, mood
 CC disorders, behavioural disorders, anxiety disorders, hypokalaemic
 CC periodic paralysis, spasticity disorders, myotonia and paramyotonia. The
 CC nucleic acids can be used to transfect cells. For example, stem cells are
 CC used in ex vivo procedures for cell transfection and gene therapy. The
 CC nucleic acids are also useful in diagnosis, and in the creation of
 CC transgenic or knockout animals

XX Sequence 1560 BP; 276 A; 499 C; 485 G; 300 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.01e-85	Length:	1560
Score:	876.00	Matches:	183
Percent Similarity:	63.07%	Conservative:	80
Best Local Similarity:	43.88%	Mismatches:	124
Query Match:	39.55%	Indels:	30
DB:	7	Gaps:	9

US-10-016-647-2 (1-425) x AB224710 (1-1560)

Qy	11	ValValLeuValLeuValGlyGlyAlaArgTyrSerLeuSerArgGluLeuLeuLysAspPhe	30
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Qy	31	ProLeuArgValSerArgLeuHisGlyCysArgSerGluArgAspValLeuGluVal	50
Db	241	CCGCTGAGCGCGCTGAGCAACTCAGCTCTGTCGAGACTACGAGGAGATCGTCAGCTC	300
Qy	51	CysAspAspTyrAspArgGluArgAsnGluTyrPhePheAspArgHisSerGluAlaPhe	70
Db	301	TGGGATGATTACGACGAGGACGCCAGGAGTTCTTCTTCGACAGAGGCCCGCGCTTC	360
Qy	71	GlyPheLeuLeuValArgGlyHisGlyCysLeuArgPheAlaProArgMetCys	90
Db	361	GGGGTATCGTGCAGCTTCCTGGCGGCC--GGGAGCTGCTGCTTCGACGAGATGTGC	417
Qy	91	GluLeuSerPheTyrAsnGluMetIleTyrTgPlyLeuGluGlyAlaHisLeuGluTyr	110
Db	418	GCCTCTGCTTCAGAGGAGCTGGGCTACTGGGGCATCGAGGAGGCCACCTGGAGAGG	477
Qy	111	CysCysGlnArgLeuAspAspArgMetSerAspThrTyrThrPheTyrSerAlaAsp	130
Db	478	TGCTGCTGGGAGGCTGCTGAGGAAGCTGGAGGAGCTGGAGGAGCTGCCCAAGCTGCAC	537

Qy	131	GluProGlyValLeu-----GlyArgAspGluAlaArgProGlyGlyAlaGluAlaAla	148
Db	538	AGGAGGAGCTACTGAGGACGACGAGGAGACCGCGCGCC-----GCTCG	585
Qy	149	ProSerArgArgTyr-----LeuGluArgMetArgThrPheGluGluProThr	165
Db	586	CACCTCTCGCGCTGGGCTGTGATGAACCGGCTGGCGAGATGGTGAAGAACCCGAG	645
Qy	166	SerSerLeuAlaAlaGlnIleLeuAlaSerValSerValPheValIleValSerMet	185
Db	646	TCGGGCTGCGCGGAGAGTTCGCTTGCCTCTCCATCTCTTCGTCGTCACACGAC	705
Qy	186	ValValLeuCysAlaSerThrLeuProAspTrpArgAsnAlaAlaAlaAsnArgSer	205
Db	706	GTCAGCTGTGTGTGTCAGCACCATCCCGCTCAGG-----GCAGAGGAGGACCGGC	759
Qy	206	LeuAspAspArgSer-----ArgIleleGluAlaIleCysIleGlyTyrPhe	221
Db	760	GAATGCTCTCGAAGTGTCTATATTTTCATCTGTCGAGACCATCTCGTGGCTGTTTC	819
Qy	222	ThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGluPheValLysArg	241
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Qy	262	ValPheThrGlyGlu-----AsnSerGlnLeuGlnArgAlaGly	274
Db	940	GAGAGCGCGGAGGAGCGGAGCGGAGCGGAGCTCTACCTGGAGAGGTGGG	999
Qy	275	ValThrLeuArgValLeuArgMetMetArgIlePheTrpValleLysLeuAlaArgHis	294
Db	1000	CTGTGCTGCTGTCGTCGAGCGCTCGGCATCTCTACGTGATCGCTGGCTCGGCAC	1059
Qy	295	PheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMet	314
Db	1060	TCGCTGGGCTGACAGACGCTGGGCTCAGCTGGCGCGTTGCACACGTGATTCGGCTG	1119
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Db	1120	CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1179
Qy	334	---GluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIleProAlaAla	352
Db	1180	AAGGAGTCCGGCGGGTGTGGAG-----TTCACGACATCCCGCGCTCC	1224
Qy	353	CysTrpTrpValIleIleSerMetThrValGlyTyrGlyAspMetTyrProIleThr	372
Db	1225	TATTGGTGGGCTCATCTCCATGACACGCTGGCTGACGGGACATGGTGGCGGAGT	1284
Qy	373	ValProGlyArgIleLeuGlyGlyValCysValValSerGlyIleValLeuAlaLeu	392
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RESULT 14
 AA249455
 ID AA249455 standard; DNA; 2022 BP.
 XX
 AC AA249455;
 XX
 DT 04-APR-2000 (first entry)
 XX
 DE Human Voltage-gated Potassium channel monomer, Kv6.2 gene.
 XX
 KW Voltage gated potassium channel; Kv6.2; human; excitability; ion flux;
 KW resting potential; alpha subunit; modulator; hearing/vision problem;
 KW migraine; central nervous system; CNS; seizure; neuroprotective agent;

KW psychotic disorder; reporter; treatment; detection; antibody; probe;
 KW primer; ds.
 OS Homo sapiens.

XX Location/Qualifiers
 XX 149..1708
 CDS

FT /tag= a
 FT /products "Human Kv6.2 polypeptide"

FT /note= "Voltage gated potassium channel subunit"

FT 1535..1543
 FT misc_feature

FT /tag= b
 FT /note= "This region encodes the amino acid sequence ELK

FT which is represented in the specification as the
 FT topographical error Kv6.2 (an insertion of the protein
 FT name)"

XX WO200001811-A1.

XX 13-JAN-2000.

XX 30-JUN-1999; 99WO-US014945.

XX 01-JUL-1998; 98US-0091466P.

XX (ICAG-) ICAGEN INC.

XX Jegia TJ;

XX WPI; 2000-126937/11.

XX P-PSDB; AAY44565.

XX New voltage-gated potassium channel alpha subunit, useful for identifying
 PT modulators of voltage-gated channel activity useful for treating central
 PT nervous system disorders e.g. migraines and as neuroprotective agents.
 XX Claim 5; Page 66-67; 80pp; English.

XX The present sequence is the gene encoding the human Kv6.2 monomer, which
 CC is an alpha subunit of a heteromeric voltage-gated potassium channel. It
 CC is isolated from brain tissue and maintains the resting potential and
 CC controls the excitability of a cell. Kv6.2 polypeptide can be used to
 CC identify compounds, that modulate the ion flux through heteromeric
 CC voltage-gated potassium channels. Such modulators are used as
 CC neuroprotective agents and for treating CNS disorders, such as migraines,
 CC hearing and vision problems, psychotic disorders and seizures. It can
 CC also be used as reporter molecules in assays and to produce antibodies.
 CC Kv6.2 DNA sequence can be used to produce specific primers or probes for
 CC detection purposes

XX SQ Sequence 2022 BP; 372 A; 653 C; 585 G; 412 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4,39e-84 Length: 2022
 Score: 868.00 Matches: 182
 Percent Similarity: 62.83% Conservative: 80
 Best Local Similarity: 43.65% Mismatches: 125
 Query Match: 39.19% Indels: 30
 DB: 3 Gaps: 9

US-10-016-647-2 (1-425) x AA249455 (1-2022)

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 QY 31 ProLeuArgValSerArgLeuHisGlyCysArgSerGluArgAspValLeuGluVal 50
 Db 389 CCGCTGAGCGGCTGAGCAACTCAGGCTCTCTCGAGCTACGAGAGATCGTGAGCTC 448
 QY 51 CysAspAspTyrAspArgGluAsnGluTyrPhePheAspArgHisSerGluAlaPhe 70
 Db 449 TCGATGATATTACGACGAGGACCCAGGAGTTCCTTCCTCGACGAGGAGCCCGCCTTC 508

QY 71 GlyPheIleLeuLeuTyrValArgGlyHisGlyLysLeuArgPheAlaProArgMetCys 90
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 QY 91 GluLeuSerPheTyrAsnGluMetIleTyrTrpGlyLeuGluGlyAlaHisLeuGluTyr 110
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 QY 111 CysCysGlnArgArgLeuAspArgMetSerAspThrTyrThrPheTyrSerAlaAsp 130
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 QY 131 GluProGlyValLeu-----GlyAcqAspGluAlaArgProGlyGlyAlaGluAla 148
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 QY 149 ProSerArgArgTrp-----LeuGluArgMetArgArgThrPheGluGluProThr 165
 Db 734 CACTCTCGCGCTGGGGCCTGTGCATGAACCGGTCGCGAGATGGTGGAAAACCCGACG 793
 QY 166 SerSerLeuAlaAlaGlnIleLeuAlaSerValSerValValPheValIleValSerMet 185
 Db 794 TCCGGGCTGCCGGGAAGTCTTCGCTTGCCTCTCCATCTCTCTCTGCGCCACACACGCC 853
 QY 186 ValValLeuCysAlaSerThrLeuProAspTrpArgAsnAlaAlaAlaAspAsnArgSer 205
 Db 854 GTCAGCCTGTGTCTACGACCACTGCCCGACCTCAGG-----GCAGAGGAGGACCGAGG 907
 QY 206 LeuAspAspArgSer-----ArgIleIleGluAlaIleCysIleGlyTrpPhe 221
 Db 908 GAATGCTCTCGGAAGTCTACTATATTTTCATCGTGAGACCATCTCGTGGCTGTTC 967
 QY 222 ThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGluPheValLysArg 241
 Db 968 TCCCTGAGTCTGCTCGCTGGGTTTTCAGGCCCAAGCAAGTGTCACTTCTTCCAGGG 1027
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 QY 275 ValThrLeuArgValLeuArgMetMetArgIlePheTrpValIleLysLeuAlaArgHis 294
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 QY 295 PheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMet 314
 Db 1208 TCGTGGGGCTGCAGACGCTGGGGCTCACGCTGCGCGTTCACATGTGATGTGGCGCTG 1267
 QY 315 LeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeu--- 333
 Db 1268 CTCCTTCTCTTCGCGCGGCGGCATCACCTCTTCTCCCTTGTGTCTACGTGGCGGAG 1327
 QY 334 ---GluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIleProAlaAla 352
 Db 1328 AAGGAGTCCGGGCGGGTGTGGAG-----TTCACCAACATCCCGCGCTCC 1372
 QY 353 CysTrpTrpValIleIleSerMetThrValGlyTyrGlyAspMetTyrProIleThr 372
 Db 1373 TATTGGTGGGCGCATCATCTCATGAACGCTGGGCTACGGGACATGTGTCGCCCGCAGT 1432
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 Db 1433 GTGCCAGCGCAGATGGTGGCCCTCAGCAGCATCTCTGAGCGGATCTCTCATCATGCGCTTC 1492
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 Db 1493 CCGGCCACGCTATCTTCCACACCTTCTCCCACTCTCTACCTGAGGCTCAAG 1543

RESULT 15

AAZ49454
ID AAZ49454 standard; DNA; 1518 BP.

XX AC AAZ49454;

XX DT 04-APR-2000 (first entry)

XX DE Mouse voltage-gated Potassium channel monomer, Kv6.2 gene.

XX KW Voltage gated potassium channel; Kv6.2; mouse; excitability; ion flux;
KW resting potential; alpha subunit; modulator; hearing/vision problem;
KW migraine; central nervous system; CNS; seizure; neuroprotective agent;
KW psychotic disorder; reporter; treatment; detection; antibody; probe;
KW primer; ds.

XX OS Mus sp.

XX FH Location/Qualifiers

XX mat_peptide

XX 1. .1518

XX /*tag= a

XX /label= Mouse_Kv6.2_polypeptide

XX /note= "Voltage gated potassium channel subunit"

XX FT misc_feature

XX 1381. .1389

XX /*tag= b

XX /note= "This region encodes the amino acid sequence ELK,

XX which is represented in the specification as the

XX typographical error Kv6.2 (an insertion of the protein

XX name)"

XX PN WO200001811-A1.

XX PD 13-JAN-2000.

XX PF 30-JUN-1999; 99WO-US014945.

XX PR 01-JUL-1998; 98US-0091466P.

XX PA (ICAG-) ICAGEN INC.

XX PI Jegla TJ;

XX P2; 2000-126937/11.

XX P-PSDB; AAY44564.

XX New voltage-gated potassium channel alpha subunit, useful for identifying
PT modulators of voltage-gated channel activity useful for treating central
PT nervous system disorders e.g. migraines and as neuroprotective agents.

PS Claim 5; Page 65-66; 80pp; English.

CC The present sequence is the gene encoding the mouse Kv6.2 monomer, which
CC is an alpha subunit of heteromeric voltage-gated potassium channel. It is
CC isolated from brain tissue and maintains the resting potential and
CC controls the excitability of a cell. Kv6.2 polypeptide can be used to
CC identify compounds that modulate the ion flux through heteromeric
CC voltage-gated potassium channels. Such modulators are used as
CC neuroprotective agents and for treating CNS disorders, such as migraines,
CC hearing and vision problems, psychotic disorders and seizures. It can
CC also be used as reporter molecules in assays and to produce antibodies.
CC Kv6.2 DNA sequence can be used to produce specific primers or probes for
CC detection purposes

XX SQ Sequence 1518 BP; 271 A; 467 C; 470 G; 310 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 5.38e-84 Length: 1518
Score: 865.50 Matches: 179
Percent Similarity: 62.71% Conservative: 85
Best Local Similarity: 42.52% Mismatches: 118
Query Match: 39.07% Indels: 39
DB: 3 Gaps: 9

US-10-016-647-2 (1-425) x AAZ49454 (1-1518)

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QY 31 ProLeuArgValSerArgLeuHisGlyCysArgSerGluArgAspValLeuGluVal 50
DB 238 CCGCTGAGCGCGCTGAGCAGGCTCCGCTGTGGCGAGCATGAGGAGATCACCGAGCTC 297

QY 51 CysAspTyrAspArgGluArgAsnGluTyrPhePheAspArgHisSerGluAlaPhe 70
DB 298 TGCATGACTACGATGAGGAGCAGCAGGAGTCTCTTCGACAGGAAACCCCGAGCGCTTC 357

QY 71 GlyPheLeuLeuLeuTyrValArgGlyHisGlyLysLeuArgPheAlaProArgMetCys 90
DB 358 GGGGTGATCGAGCTTCCTGGCGCG--GGAAGCTGGTCTTCGCGAGAGATGTC 414

QY 91 GluLeuSerPheTyrAsnGluMetIleTyrTrpGlyLeuGluGlyAlaHisLeuGluTyr 110
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QY 111 CysCysGlnArgArgLeuAspAspArgMetSerAspThrTyrThrPheTyrSerAlaAsp 130
DB 475 TGCTGCTGCGCAAGCTGCTGAAGAAGCTG-----GAG 507

QY 131 GluProGlyValLeuGlyArgAspGluAla-----ArgProGlyGly 144
DB 508 GAGCGCGCGAGCTGCGCGGAGGAGCTGCCAGCGCGCAGCAGCAGCGCGAGCGCTGC 567

QY 145 AlaGluAlaProSerArgArgTrp-----LeuGluArgMetArgArgThrPhe 161
DB 568 CACTCCGAGGTGCGAGCTTCACGATGGCGCGCAGCATGAACGAGCTGCGTGAATCGTG 627

QY 162 GluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValAlaPheVal 181
DB 628 GAGGACACACAGTCGGGCTGCCCGGAGAGTCTTCGCTGCTCCTCGGTCTTCGTCG 687

QY 182 IleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArgAsnAlaAla 201
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QY 218 IleGlyTrpPheThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGlu 237
DB 802 GTGGCTGGTTCGCTGGAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 861

QY 238 PheValLysArgProLeuAsnIleLeuAspLeuAlaIleThrProTyrTyrIleSer 257
DB 862 TCTTTCGCGCGCGCGCTGAAATGATCATCGATTCAGCATTCCTCCCATCTACTATGTGTCG 921

QY 258 ValLeuMetThrValPheThrGlyGlu-----AsnSerGlnLeu 270
DB 922 CTCGAGTGTCTGACGAATCCCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 981

QY 271 GlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTrpValIleLys 290
DB 982 GAGAAAGTGGGTGTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1041

QY 291 LeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyrArg 310
DB 1042 CTGCTCGCCTCCCTGGGCTGCAGAGCTGGGCTCACTGTGCGCGCTGCGCGCGA 1101

QY 311 GluMetValMetLeuLeuValPheIleCysValAlaValAlaPheSerAlaLeuSer 330
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QY 349 IleProAlaAlaCysTyrTrpValIleIleSerMetThrThrValGlyTyrGlyAspMet 368
 Db 1207 ATCCCCGCATCCTATGTGGGCCATCTCCATGACGCCGTGGCTATGGGACATG 1266
 QY 369 TyrProIleThrValProGlyArgIleLeuGlyGlyValCysValValSerGlyIleVal 388
 Db 1267 GTCCCTCGCAGCGTCCCGGACAGATGGTGGCTCTGACGACATCCTTAGCGGATCCTT 1326
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 Db 1327 ATCATGGCTTTCCCGACCCATCCATCTTCCACAGGTTCTCTCACTCCTACCTGGAGCTG 1386
 QY 409 Lys 409
 Db 1387 AAG 1389

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

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2163.799 Million cell updates/sec

Title: US-10-016-647-2

Perfect score: 2215

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Fgapop 6.0 , Fgapext 7.0
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Searched: 682709 seqs, 277475446 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	855.5	38.6	2127	1	US-08-464-340A-1
4	855.5	38.6	2127	5	PCT-US94-08449A-1
5	715.5	32.3	3080	4	US-09-336-643A-7
6	697	31.5	2494	4	US-09-181-339-6
7	685.5	30.9	2266	4	US-09-181-339-11
8	685	30.9	2293	4	US-09-336-643A-5
9	683	30.8	3102	4	US-09-336-643A-17
10	659	29.8	2799	4	US-09-181-339-2
11	635	28.7	2483	1	US-08-464-340A-3
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14	593.5	26.8	1805	1	US-07-955-916-6	Sequence 6, Appli
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17	574	25.9	1599	1	US-08-288-405A-9	Sequence 9, Appli
18	564.5	25.5	3424	4	US-09-336-643A-9	Sequence 9, Appli
19	558.5	25.2	2118	4	US-09-016-434-1304	Sequence 1304, Ap
20	545	24.6	2064	4	US-09-178-109-3	Sequence 3, Appli
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23	545	24.6	2121	4	US-09-178-109-1	Sequence 1, Appli
24	538	24.3	2104	4	US-09-142-791A-5	Sequence 5, Appli
25	473.5	21.4	1273	4	US-09-181-339-8	Sequence 8, Appli
26	424.5	19.2	774	4	US-09-181-339-4	Sequence 4, Appli
27	411.5	18.6	625	4	US-09-181-339-1	Sequence 1, Appli
28	383.5	17.3	696	1	US-07-955-916-5	Sequence 5, Appli
29	254.5	11.5	1080	4	US-09-328-352-2971	Sequence 2971, Ap
30	227.5	10.3	267	4	US-09-016-434-169	Sequence 169, App
31	224	10.1	870	4	US-09-489-039A-3103	Sequence 3103, Ap
32	224	10.1	888	4	US-09-252-991A-11022	Sequence 11022, A
33	214.5	9.7	3232	4	US-09-177-650-1	Sequence 1, Appli
34	214.5	9.7	3232	4	US-09-177-650-1	Sequence 95, Appli
35	214.5	9.7	3287	4	US-09-105-058C-19	Sequence 19, Appli
36	214.5	9.5	2169	4	US-09-105-058C-22	Sequence 22, Appli
37	211.5	9.5	900	4	US-09-105-058C-3	Sequence 3, Appli
38	210.5	9.5	2273	4	US-09-177-650-88	Sequence 88, Appli
39	210.5	9.5	2273	4	US-09-177-650-88	Sequence 580, App
40	208	9.4	870	4	US-09-540-236-580	Sequence 34, Appli
41	208	9.4	89047	4	US-09-596-002-34	Sequence 5, Appli
42	206.5	9.3	900	4	US-09-105-058C-5	Sequence 7, Appli
43	196	8.8	735	4	US-09-105-058C-7	Sequence 1890, Ap
44	192.5	8.7	786	4	US-09-134-000C-1890	Sequence 1, Appli
45	187	8.4	3074	4	US-09-813-148-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-719-919A-18
; Sequence 18, Application US/09719919A
; Patent No. 6680180
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICAGEN Incorporated
; TITLE OF INVENTION: Kv6.2, a Voltage-Gated Potassium Channel Subunit
; FILE REFERENCE: 018512-001410US
; CURRENT APPLICATION NUMBER: US/09/719,919A
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/091,466
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: WO PCT/US99/14945
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 18
; LENGTH: 2022
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (149)..(1708)
; OTHER INFORMATION: human alpha subunit of heteromeric voltage-gated
; OTHER INFORMATION: potassium channel Kv6.2
US-09-719-919A-18

Alignment Scores: 2.77e-98 Length: 2022
Pred. No.: 865.00 Matches: 182
Score: 865.00 Conservative: 80
Percent Similarity: 62.83% Mismatches: 125
Best Local Similarity: 43.65% Indels: 30
Query Match: 39.19% Gaps: 9
DB: 4

US-10-016-647-2 (1-425) x US-09-719-919A-18 (1-2022)

QY 11 ValValLeuAsnValClyGlyAlaArgTyrSerLeuSerArgGluLeuLeuLysAspPhe 30
 Db 329 ATCTGATCAAGCTGGGGGAGGAGGATCTCCCTCCCTGGAGCAGACTGGACCGGTTTC 388
 QY 31 ProLeuArgValSerArgLeuHisGlyCysArgSerGluArgAspValLeuGluVal 50
 Db 389 CCGCTGAGCGCTGAGCAAACTCAGGCTCTGCGAGCTACGAGGAGATCTGCGAGCTC 448
 QY 51 CysAspAspTyrAspArgGluArgGlnTyrPhePheAspArgHisSerGluAlaPhe 70
 Db 449 TCGGATGATTACGACGAGCAGCAGGAGGAGTCTCTTCGACAGAGGCCCGCCCTTC 508
 QY 71 GlyPheLeuLeuTyrValArgGlyHisGlyLysLeuArgPheAlaProArgMetCys 90
 Db 509 GGGGTGATCTGAGCTTCTCGCGGCC---GGGAAGCTGGTCTTCGACGAGATGTC 565
 QY 91 GluLeuSerPheTyrAsnGluMetIleTyrTrpGlyLeuGluGlyAlaHisLeuGluTyr 110
 Db 566 GCGCTGTCTCTCAGGAGGAGCTGGCTACTTGGGCTATCGAGAGGCCACCTCGAGAGG 625
 QY 111 CysCysGlnArgArgLeuAspArgMetSerAspThrTyrPheTyrSerAlaAsp 130
 Db 626 TGTCTGCTGGGAGCTGTGAGGAGCTGGAGAGCTGGAGAGCTGGCCAGCTGCAC 685
 QY 131 GluProGlyValLeu-----GlyArgAspGluAlaArgProGlyGlyAlaGluAla 148
 Db 686 AGGAGGAGCTACTGAGGAGCAGAGGAGGAGCCCGCGGCC---GCCCTCG 733
 QY 149 ProSerArgArgTrp-----LeuGluArgMetArgArgThrPheGluGluProThr 165
 Db 734 CACTCTCGCGTGGGGCTGTGCTGAACCGGCTGGCGAGATGTTGGAAACCCGAG 793
 QY 166 SerSerLeuAlaAlaGlnIleLeuAlaSerValSerValPheValIleValSerMet 185
 Db 794 TCGGGCTCGCCGGGAGGTCTTCGCTTCCCTCTCCATCTCTCGTGGCCACACGCC 853
 QY 186 ValValLeuCysAlaSerThrLeuProAspTrpArgAsnAlaAlaAlaAspArgSer 205
 Db 854 GTCAGCTGTGTGTCAGCACCATCGCCGACCTCAGG-----GCAGAGGAGCAGGCG 907
 QY 206 LeuAspAspArgSer-----ArgIleIleGluAlaIleCysIleGlyTrpPhe 221
 Db 908 GAATGCTCTCGGAGTGTACTATATTTTCATCGTGGAGACCATCTGGTGGCTGGTTC 967
 QY 222 ThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGluPheValLysArg 241
 Db 968 TCCCTGGAGTCTCTGCTGGGTTTGTCCAGGGCCCAAGACAGTGTCTCTCCAGGGG 1027
 QY 242 ProLeuAsnIleIleAspLeuAlaIleThrProTyrTyrIleSerValLeuMetThr 261
 Db 1028 CCCTGAACATCATCATCTGGCCATCTCCCATCTCTCCATCTAGTGTGCTGGCGTGTCT 1087
 QY 262 ValPheThrGlyGlu-----AsnSerGlnLeuGlnArgAlaGly 274
 Db 1088 GAGGAGCCCGGAGCAGCGGAGGAGCGCCGAGGAGGAGCTCTTACGTGAGAGGTGGGG 1147
 QY 275 ValThrLeuArgValLeuArgMetMetArgIlePheTrpValIleLysLeuAlaArgHis 294
 Db 1148 CTGGTCTGCTGTGCTGGAGCTGGCGATCTCTCTGATGCTGGCTGGCTGGCTGGCCAC 1207
 QY 295 PheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMet 314
 Db 1208 TCGCTGGGCTGCAGACGCTGGGCTCACCGTGGCGCTTGACATGTGAGTTCGGCTG 1267
 QY 315 LeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeu--- 333
 Db 1268 CTCTCTCTCTCTGCGCGTGGCCATCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1327
 QY 334 ---GluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIleProAlaAla 352
 Db 1328 ARGAGTCCCGGGGCTGTGGAG-----TTCCAGGATCCCGCCCTCC 1372

QY 353 CysTrpTrpValIleIleSerMetThrThrValGlyTyrGlyAspMetTyrProIleThr 372
 Db 1373 TAITGTGGGCCATCATCTCCATGACACAGGTGGGTACGGGACATGGTGGCCCGCAGT 1432
 QY 373 ValProGlyArgIleLeuGlyGlyValCysValValSerGlyIleValLeuLeuAlaLeu 392
 Db 1433 GTCCAGGCGCAGATGGTGGCCCTCAGCAGCATCTCAGCGGGATCTCATCATGGCCTTC 1492
 QY 393 ProIleThrPheIleTyrHisSerPheValGlnCysTyrHisGluLeuLys 409
 Db 1493 CCGGCCACGCTATCTTCCACACCTTCTCCACTCTCTACTGGAGCTCAAG 1543

RESULT 2
 US-09-719-919A-2
 ; Sequence 2, Application US/09719919A
 ; Patent No. 6680180
 ; GENERAL INFORMATION:
 ; APPLICANT: Jegla, Timothy James
 ; APPLICANT: ICAGEN Incorporated
 ; TITLE OF INVENTION: Kv6.2, a Voltage-Gated Potassium Channel Subunit
 ; FILE REFERENCE: 018512-001410US
 ; CURRENT APPLICATION NUMBER: US/09/719,919A
 ; CURRENT FILING DATE: 2001-02-22
 ; PRIOR APPLICATION NUMBER: US 60/091,466
 ; PRIOR FILING DATE: 1998-07-01
 ; PRIOR APPLICATION NUMBER: WO PCT/US99/14945
 ; PRIOR FILING DATE: 1999-06-30
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 1518
 ; TYPE: DNA
 ; ORGANISM: Mus sp.
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1518)
 ; OTHER INFORMATION: mouse alpha subunit of heteromeric voltage-gated
 ; OTHER INFORMATION: potassium channel Kv6.2
 US-09-719-919A-2

Alignment Scores:
 Pred. No.: 3,51e-98 Length: 1518
 Score: 865.50 Matches: 179
 Percent Similarity: 62.71% Conservative: 85
 Best Local Similarity: 42.52% Mismatches: 118
 Query Match: 39.07% Indels: 39
 DB: 4 Gaps: 9

US-10-016-647-2 (1-425) x US-09-719-919A-2 (1-1518)

QY 11 ValValLeuAsnValGlyGlyAlaArgTyrSerLeuSerArgGluLeuLeuLysAspPhe 30
 Db 178 ATCTGATGATGTGGTGGCCAGCGGTACTCTGCTCCCTGGAGCACCCTGGATGCTTC 237
 QY 31 ProLeuArgValSerArgLeuHisGlyCysArgSerGluArgAspValLeuGluVal 50
 Db 238 CCGCTGAGCGCTGAGCAGGCTCCGCGCTGTGCGCAGCCATGAGGAGATCAGCGAGCTC 297
 QY 51 CysAspAspTyrAspArgGluArgAsnGluTyrPhePheAspArgHisSerGluAlaPhe 70
 Db 298 TCGGATGATGATGATGAGGAGCAGCGAGGAGTCTTCTTCGACAGGAGACCCAGCGCTTC 357
 QY 71 GlyPheIleLeuLeuTyrValArgGlyHisGlyLysLeuArgPheAlaProArgMetCys 90
 Db 358 GGGGTGATCTGAGCTCTCTGCGCGCGG---GGAAAGCTGGTGTCTTCGAGAGATGTGC 414
 QY 91 GluLeuSerPheTyrAsnGluMetIleTyrTrpGlyLeuGluGlyAlaHisLeuGluTyr 110
 Db 415 GCGCTGTCTCTCGGAGGAGCTGAGCTACTGCGGATCGAGGAAACCACTGGAGCGC 474
 QY 111 CysCysGlnArgArgLeuAspArgMetSerAspThrTyrPheTyrSerAlaAsp 130
 Db 1111 CysCysGlnArgArgLeuAspArgMetSerAspThrTyrPheTyrSerAlaAsp 130

475 TGCTGCTCGCAAGCTGCTGAAGAAGCTG-----GAG 507
QY 131 GluProGlyValLeuGlyArgAspGluAla-----ArgProGlyGly 144
DB 508 GAGGCGCGGAGCTGCGCGGAGAGAGCTGCCAGCGCAGCAGCGCGAGCTGC 567
QY 145 AlaGluAlaAlaProSerArgArgTrrp-----LeuGluArgMetArgArgThrPhe 161
DB 568 CACTCCGAGGTGCAGGCTTCAGATGGCGCGCGAGCATGAACACGAGCTGCGTGAATGGTG 627
QY 162 GluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValValPheVal 181
DB 628 GAGGACCCACAGTGGCGCTGCCGGGAGGCTTCGCTGCCCTCCCTCGCTCTTGTG 687
QY 182 IleValSerMetValValLeuCysAlaSerThrLeuProAspTrrpArgAsnAlaAla 201
DB 688 GCAACACGGCTGTGAGCTGTGTGTGAGCACCAGTCCGCGGACTTCAGG-----GCTGAG 741
QY 202 AspAsnArgSerLeuAspAspArgSer-----ArgIleIleGluAlaIleCys 217
DB 742 GAGGCAAGGAGAGATGACATAGAAAGTGCTATTATCTTCGTGGTGGAAATCCATCTGT 801
QY 218 IleGlyTrrpPheThrValSerIleValArgPheIleValSerLysAsnLysCysGlu 237
DB 802 GTGGCTGCTTCCTCGTGGAGTTTTCCTGCGCTTGTCCAGGCGCCGCAACAAATGTGAG 861
QY 238 PheValLysArgProLeuAsnIleIleAspLeuAlaIleThrProTrrpTrrpIleSer 257
DB 862 TTCCTCCGCGGCGCTCAATGTATCATGACATTCATAGCCATCTCCCATATCATGTGTG 921
QY 258 ValLeuMetThrValPheThrGlyGlu-----AsnSerGlnLeu 270
DB 922 CTCGAGTGTCTGACGATCCCGGAGCGAGCGAGCGGAGCGAGCGAGCTCTACTGTG 981
QY 271 GlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTrrpValLys 290
DB 982 GAGAAAGTGGGTTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1041
QY 291 LeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTrrpArg 310
DB 1042 CTGGCTCCGCACTCCCTGGGCTGAGAGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1101
QY 311 GluMetValMetLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeuSer 330
DB 1102 GAGTTTGTCTCTGATGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1161
QY 331 GlnLeuLeuGluHis-----GlyLeuAspLeuGluThrSerAsnLysAspPheThrSer 348
DB 1162 TATGTAGCTGAGATGAGTCCGGAAGGCTCTCTGAG-----TTCACTAGC 1206
QY 349 IleProAlaAlaCysTrrpTrrpValIleIleSerMetThrThrValGlyTrrpGlyAspMet 368
DB 1207 ATCCCGCATCTCTATGTTGGCCATCATCTCCATGACGACGCTGGGCTATGGGAGCATG 1266
QY 369 TyrProIleThrValProGlyArgIleLeuGlyValCysValValSerGlyIleVal 388
DB 1267 GTCCCTCGCAGGCTCCCGGAGCATGTTGCTGCTGAGCATCTCTTAGCGGATCCTT 1326
QY 389 LeuLeuAlaLeuProIleThrPheIleTrrpHisSerPheValGlnCysTrrpHisGluLeu 408
DB 1327 ATCATGGCTTCCGAGCAGCATCTCATCTTCCACAGTCTCTCTACTCTCTACTGAGCTG 1386
QY 409 Lys 409
DB 1387 AAG 1389

RESULT 3

US-08-464-340A-1

; Sequence 1, Application US/08464340A

; Patent No. 5710019

; GENERAL INFORMATION:

; APPLICANT: Li, ET AL.

; TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins

NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,340A
FILING DATE: June 5, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/08449
FILING DATE: 28 JUL 1994
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-415
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2127 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: cDNA
US-08-464-340A-1
Alignment Scores:
Pred. No.: 1-12e-96 Length: 2127
Score: 855.50 Matches: 178
Percent Similarity: 60.94% Conservative: 81
Best Local Similarity: 41.88% Mismatches: 141
Query Match: 38.62% Indels: 25
DB: 1 Gaps: 8
US-10-016-647-2 (1-425) x US-08-464-340A-1 (1-2127)
QY 11 ValValLeuAsnValGlyGlyAlaArgTrrpSerLeuSerArgGluLeuLeuLysAspPhe 30
DB 474 ATCATCATCAACGTAGCGCGCATCAAGTACTCGCTCGCTGGACCGCTGCGAGGTTTC 533
QY 31 ProLeuArgArgValSerArgLeuHisGlyCysArgSerGluArgAspValLeuGluVal 50
DB 534 CCCTGACGCGCTGGCGCGAGCTCAAGGCTGACCACTTCGACGACATCTCTCAAGTG 593
QY 51 CysAspAspTrrpAspArgGluArgAsnGluTrrpPhePheAspArgHisSerGluAlaPhe 70
DB 594 TGGCATGACTATACGACGTACCTGCAACAGAGTTCTTCTCGACCGCAACCGCGGGGCTTC 653
QY 71 GlyPheIleLeuLeuTrrpValArgGlyHisGlyLysLeuArgPheAlaProArgMetCys 90
DB 654 GGCACTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 710
QY 91 GluLeuSerPheTrrpAsnGluMetIleTrrpGlyLeuGluGlyAlaHisLeuGluTrrp 110
DB 711 GCGCTGTCTCTCCAGGAGGAGTGTGTACTGTTGGGATCGCGGAGGAGCACCTGGAGCGG 770
QY 111 CysCysGlnArgArgLeuAspAspArgMetSerAspThrTrrpThrPheTrrpSerAlaAsp 130
DB 771 TGTTCGACGCGCGCTTACCTGCAAGAGTTCGAGAGTTCGCGAGATGTTGGAGCGGAG 830
QY 131 GluProGlyValLeu-----GlyArgAspGluAlaArgProGlyGlyAlaGlu 146

Db	831	GAAGAGACGACGCGCTGGACAGCAGAGGGCGCGACAGCAGGAGGCCCGCGGAGGCGGAG	890
Qy	147	AlaAlaProSerArgArgTgTtLeuGluArgMetArgThrPheGluGluProThrSer	166
Db	891	GGCGCGCTGGGG--CGCTGATCGCGCGACTGCGGACATGTTGGAGAGCGCGCACTCG	947
Qy	167	SerLeuAlaAlaGlnIleLeuAlaSerValSerValPheValIleValSerMetVal	186
Db	948	GGGCTGCTGCGCAAGAGTTCGCGCTGCTCGGTGGTCTCTTCGTGACCGTCACCGCGCTC	1007
Qy	187	ValLeuCysAlaSerThrLeuProAspTrpArgAsnAlaAlaAlaAspAsnArg----	204
Db	1008	AACCTCTCCGTGACACCTTGCCAGCGCTGAGGAGGAGGAGGAGGAGGCCACTGTTC	1067
Qy	205	SerLeuAspAspArgSerArgIleIleGluAlaIleCysIleGlyTrpPheThrAlaGlu	224
Db	1068	CAGATGTGCCACAAACGCTTCATCGTGGAGTCGGTGTGCGTGGCGTGGTTCCTCCCTGGAG	1127
Qy	225	CysIleValArgPheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsn	244
Db	1128	TTCTCTCTGGGCTCATTCAGGCGCCACAGAGTTGCGCTTCTCGCGAGCCCGCTGACG	1187
Qy	245	IleIleAspLeuLeuAlaIleThrProTyrTyrIleSerValLeuMetThr---ValPhe	263
Db	1188	CTGATCGACCTGGTGGCACTCTGCCCTACTACATCAGCGTGTGTTGGAGCGGCGGCC	1247
Qy	264	ThrClyGlu-----AsnSerClnLeuGlnArgAlaGlyValThrLeu	277
Db	1248	GCAGGCGCTGCGAAGCCGGCGGGCAACAGCTACCTGACAGAGTGGGGCTGTGTGCTG	1307
Qy	278	ArgValLeuArgMetMetArgIlePheTrpValIleLysLeuAlaArgHisPheIleGly	297
Db	1308	CGCGTCTCGGGCGCTGCGCATCTGTACGTGATGCGCCTGCGCGGCCACTCCCTGGGG	1367
Qy	298	LeuGlnThrLeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuVal	317
Db	1368	CTGCAGACGTGGGGCTACGGCGCGCGTGTGACCCGCGAGTTCGGGCTCTCTGCTGCTC	1427
Qy	318	PheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeuGluHisGlyLeu	337
Db	1428	TTCTCTGCGTGGCCATCGCCCTCTTCGCGCCCTGCTCTACGTCTCAGCAGAACGAGATG	1487
Qy	338	AspLeuGluThrSerAsnLysAspPheThrSerIleProAlaIaCysTrpTrpValIle	357
Db	1488	-----GCCGACACCCCGAGTTCACAGCATCCCTCCCTGCTACTCGTGGGCTGTC	1538
Qy	358	IleSerMetThrThrValGlyTyrGlyAspMetTyrProIleThrValProGlyArgIle	377
Db	1539	ATCACCATGACAGCGTGGACTATGGCGACATGGTCCCCAGGAGCACCCCGGCGCAGGTA	1598
Qy	378	LeuGlyGlyValCysValValSerGlyIleValLeuLeuAlaLeuProIleThrPheIle	397
Db	1599	GTGCGCCCTGACGACATCTCGAGCGGATCTGCTCATGGCCTTCCACGTCACCTCCATC	1658
Qy	398	TyrHisSerPheValGlnCysTyrHisGluLeuLys-----Phe	410
Db	1659	TTCCACACCTTCTCCCCCTCTACCTGGAGCTAAACAGGACGACAGAGGGGTGATGTTTC	1718
Qy	411	ArgSerAlaArgTyr	415
Db	1719	CGGAGGGCGCAGTTC	1733

RESULT 4

RESULT 4
PCT-US94-08449A-1

PCI-US94-08449A-1
: Sequence 1, Application PC/TUS9408449A

; SEQUENCE I, APPLICATION:
; GENERAL INFORMATION:

GENERAL INFORMATION:
APPLICANT: LI, ET AL.

TITLE OF INVENTION: Potassium Channel Protein 1 and 2

NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

ADDRESSEE: CECCHI, STEWART & OLSTEIN

STREET: 6 BECKER FARM ROAD

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CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/08449A
FILING DATE: SUBMITTED HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-105
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2127 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
PCT-US94-08449A-1

Alignment Scores:
Pred. No.: 1.12e-96
Score: 855.50
Percent Similarity: 60.94%
Best Local Similarity: 41.88%
Query Match: 38.62%
DB: 5
Length: 2127
Matches: 178
Conservative: 81
Mismatch: 141
Indels: 25
Gaps: 8

US-10-016-647-2 (1-425) x PCT-US94-08449A-1 (1-2127)

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[illegible]

RESULT 7

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RESOLUT
US-09-181-339-11
; Sequence 11, Application US/09181339
; Patent No. 6610827
; GENERAL INFORMATION:
; APPLICANT: Forsaveth, John R.
; APPLICANT: Zhao, Byron
; APPLICANT: Chavez, Raymond C.
; TITLE OF INVENTION: POTASSIUM CHANNEL SUBUNIT POLYPEPTIDE
; TITLE OF INVENTION: AND POLYNUCLEOTIDE COMPOSITIONS AND USES THEREFOR
; FILE REFERENCE: 5865-0033.30
; CURRENT APPLICATION NUMBER: US/09/181,339
; CURRENT FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 60/063,450
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 2266
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (308) ... (1783)
US-09-181-339-11

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Alignment Scores:		
Pred. No.:	2.65e-75	Length:
Score:	685.50	Matches:
Percent Similarity:	52.9%	Conservative:
Best Local Similarity:	33.5%	Mismatches:
Query Match:	30.9%	Indels:
DB:	4	Gaps:
		286

US-10-016-647-2 (1-425) x US-09-181-339-11 (1-2266)

QY 1 MetThrPheGly-----ArgSerGlyAlaAlaSer-----ValValLeuAen 14
Db 308 ATGGTCTTTGGTGAGTTTTCATCGCCTCGACAGCAGGAAACTGTGCAACCTGAAT 367
QY 15 ValGlyGlyAlaArgTyrSerLeuSerArgGluLeuLeuLysAspPheProLeuAenArg 34
Db 368 GTGGGGGGCTTTAAGCAGTCTGTGACCAAGACCCCTCTCGGGTTCCTCACCACGA 427
QY 35 ValSerArgLeuHisGlyCysArgSerGluArgAspValLeuGluValCysAspAspTyr 54
Db 428 GTGGGGGGCTTTAAGCAGTCTGTGACCAAGACCCCTCTCGGGTTCCTCACCACGA 487

428	Db	CTGGGGAAGCTGCTTACTTGCCTCCATTCTGAAAGAGCCCATCTCTGGAGCTGTGTGATGATTAC	487
55	QY	AspArgGluArgAsnGluTyrPhePheAspArgHisSerGluAlaPheGlyPheIleLeu	74
488	Db	AGTGTGCCGATAAGGAATACTACTTTGATCGGAATCCCTCTCTGTTTCAGATATGTTT	547
75	QY	LeuTyrValArgGlyHisGlyLysLeuArgPheAlaProArgMetCysGluLeuSerPhe	94
548	Db	AATTTTATTATC---ACGGGGAAGCTGCATGTCTATGAGAGAGCTGTGCGTATTCTTCATTC	604
95	QY	TyrAsnGluMetIleTyrTrpGlyLeuGluGlyAlaHisLeuGluTyrCysCysGlnArg	114
605	Db	TGCCAGGATGAGTACGACTGGGGCATCAACAGAGCTCTTTCATTGATCTTCTGTCGAGCAAT	664
115	QY	ArgLeu-----	122
665	Db	CGGTACCCAGAAACGCAAGGAGGAAAAACCGAGAGAGGACTGGGACCCAGAAAAGCCATGAT	724
123	QY	ThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArg-----	133
725	Db	GTGAGTACCGACTCCTCGTTTGAAGAGTCGTCTCTGTTTGAGAAGAGCTGGAGAGTTT	784
138	QY	AspGluAlaArgProGlyGlyAlaGluAlaAlaProSerSerArgTrpLeuGluArgMet	157
785	Db	GACACACTCGGATTTGGTCTCAGCTCCGG-----AAGAAAAATCTGGATTAG-----	829
158	QY	ArgArgThrPheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSer	177
830	Db	-----ATGGAGATCCAGCGTACTGCTGTCCGCTAAGCTTATCGCTATCTCTCTCC	880
178	QY	ValValPheValIleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArg	197
881	Db	TTGAGCGTGTGTGGCTCCATCGTGGCCATGTGCGTTCACAGCATGTCGGAGTTCGAG	940
198	QY	AsnAlaAlaAlaAspAsnArgSerLeuAspAspArgSerArgIleIleGluAlaIle---	216
941	Db	AAT-----GAGGATGAGAGTGGATGAT-----CCGGTGCTGGAGAGTGGAG	985
217	QY	-----CysIleGlyTrpPheThrAlaGluCysIleValArgPheIleValSerLysAsn	234
986	Db	ATCGCGTGCATTGCTTGTTACCGGGAGCTTGGCGTCCGCTGGCTGGCTGCTCTGT	1045
235	QY	LysCysGluPheValLysArgProLeuAsnIleIleAspLeuLeuAlaIleThrProTyr	254
1046	Db	CAAAAGAAATTCGGAATAACCTCTGAACATCATTTGACTTGTCTATTATTCCCTTC	1105
255	QY	TyrIleSerValLeuMetThrValPheThrGlyGluAsnSerGlnLeuGlnArgAlaGly	274
1106	Db	TATGCCACGTTGCTGTAGACACCAAGGAGAGAGTGGAGTATGTGAGAAATGGGC	1165
275	QY	ValThrLeuArgValLeuArgMetMetArgIlePheTrpValIleLysLeuAlaArgHis	294
1166	Db	AAGGTGTGCAGATCCTACCGCTTATGAGGATTTTCGAAATTCATAAAGCTTGCCCGGCAC	1235
295	QY	PheIleGlyGlnThrLeuGlyLeuThrLeuLysArgCysTrpArgGluMetValMet	314
1226	Db	TCGGTAGGACTTCGGTCTCTAGTGTGCCACTGAGACACAGTACCATGAAGTTGGCGTT	1285
315	QY	LeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeuGlu	334
1286	Db	CTGCTTCTCTCTCTGTGGGCATTTCCATTTTCTCTGTGCTTATCTACTCCGTGGAG	1345
335	QY	HisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIleProAlaAlaCysTrp	354
1346	Db	AAA-----GATACCACCATCCAGC-----CTCACCAGCATCCCATCTGCTGGTGG	1393
355	QY	TrpValIleIleSerMetThrThrValGlyTyrGlyAspMetTyrProIleThrValPro	374
1394	Db	TGGGCCACCATCAGCATGACAACTGTGGGCTATGGAGACACCCACCGGTACCTTGGCG	1453
375	QY	GlyArgIleLeuGlyGlyValCysValValSerGlyIleValLeuLeuAlaLeuProIle	394
1454	Db	GGAAGCTCATGCCACACATGCATCTGTGGCATCTTGTGGTCTTGTGGTGGCCCTCCCATC	1513

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QY 395 ThrPheIleTyrHisSerPheValGlnCysTyr----- 405
Db 1514 ACCATCATCTTCAACAAGTTTTCGAAGTACTACACAGAACAAAGGACATTCATGTGGAC 1573
QY 406 -----HisGluLeuLysPheArgSerAlaArg--- 414
Db 1574 CAGTGCAGTGAGGATGCACAGAGAGAGTGTCTACGTACCTTACTTTAACTAGGAT 1633
QY 415 ---TyrSerArgSerLeuSerThr 421
Db 1634 ATATATGCACAGCGGATGCACACC 1657

RESULT 8
US-09-336-643A-5
; Sequence 5, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2293
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (330)...(1800)
; OTHER INFORMATION: K-Hnv6
US-09-336-643A-5

Alignment Scores:
Pred. No.: 3,13e-75 Length: 2293
Score: 685.00 Matches: 152
Percent Similarity: 54.94% Conservative: 87
Best Local Similarity: 34.94% Mismatches: 152
Query Match: 30.93% Indels: 44
DB: Gaps: 12

US-10-016-647-2 (1-425) x US-09-336-643A-5 (1-2293)
QY 1 MetThrPheGly-----ArgSerGlyAlaAlaSer-----ValValLeuAsn 14
Db 330 ATGGTGTGGTGAGTGTTCATCCCTCGCCACAGACAGAGAGAGTGTCACTGAT 389
QY 15 ValGlyGlyAlaArgTyrSerLeuSerArgGluLeuLeuLysAspPheProLeuArg 34
Db 390 GTGGGGGGGTTTAAAGCAGTCTGTGACCAAGACCCCTCTCGGGTTCCTCACACAGA 449
QY 35 ValSerArgLeuHisGlyCysArgSerGluArgAspValLeuGluValCysAspTyr 54
Db 450 CTGGGAAGCTGTTACTTGCATTCGACATTCGAGCGCCATCTGAGCTGTGATGATTAC 509
QY 55 AspArgGluArgAsnGluTyrPhePheAspArgHisSerGluAlaPheGlyPheIleLeu 74
Db 510 AGTGTGGCCGATAAAGAACTACTTGTGATCGGAATCCCTCTTGTTCAGATATGTTG 569
QY 75 LeuTyrValArgGlyHisGlyLysLeuArgPheAlaProArgMetCysGluLeuSerPhe 94
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Db 570 AATTTTATTAC---ACGGGAAGCTGCATGTCTATGGAGGAGCTGCGTATTCTCATTC 626
QY 95 TyrAsnGluMetIleTyrTrpGlyLeuGluGlyAlaHisLeuGluTyrCysCysGlnArg 114
Db 627 TGCAGAGAGATCGAGTACTGGGCATCAACGAGCTCTTCATTCTTCTCTCAGCAAT 686
QY 115 ArgLeu-----AspAspArgMetSerAsp 122
Db 687 CGCTACCAAGNACGCAAGGAGGAAACCCACAGAGAGCTGGGACCAAGAAACCATGAT 746
QY 123 ThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArg----- 137
Db 747 GTGAGTACCGACTCTCTGTTTGAAGAGTCTCTCTGTTTGAGAAAGAGCTGGAGAGTTT 806
QY 138 AspGluAlaArgProGlyGlyAlaGluAlaAlaProSerArgArgTrpLeuGluArgMet 157
Db 807 GACACTGCGATTGTGTAGCTCCGG-----AAGAAATCTGGATTAGA----- 851
QY 158 ArgArgThrPheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSer 177
Db 852 -----ATGGAGAAATCCAGCGTACTGCTGCTGCGCTAAGCTTATCGTATCTCCTCC 902
QY 178 ValValPheValIleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArg 197
Db 903 TTGAGCGTGTGTGGCTCCATCGTGGCCATGTGCTTCACAGCAATGCGGAGTTCCAG 962
QY 198 AsnAlaAlaAlaAspAsnArgSerLeuAspAspArgSerArgIleIleGluAlaIle--- 216
Db 963 AAT-----GAGGATGGAGAGTGGATGAT-----CCGGTGTGGAAGAGTGGAG 1007
QY 217 -----CysIleGlyTrpPheThrAlaGluCysIleValArgPheIleValSerLysAsn 234
Db 1008 ATCGCGTGCATTGCTGCTGCTTCACCGGGAGCTTCGCGTCCGCTGCGCTCCTTGT 1067
QY 235 LysCysGluPheValLysArgProLeuAsnIleIleAspLeuLeuAlaIleThrProTyr 254
Db 1068 CAAAGAAATCTGGAAAAACCTCTGAACATCATTTGCTCTCTATTATTCCTTC 1127
QY 255 TyrIleSerValLeuMetThrValPheThrGlyGluAsnSerGlnLeuGlnArgAlaGly 274
Db 1128 TATGCCAGTTGGCTGTAGACACCAAGGAGAGAGTGGAGATATTGAGAACATGGGC 1187
QY 275 ValThrLeuArgValLeuArgMetMetArgIlePheTrpValIleLysLeuAlaArgHis 294
Db 1188 AAGTGTCTCAGATCTTACCGCTTATGAGGATTTTCCGAATTCGAAGCTTGCCTGGC 1247
QY 295 PheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMet 314
Db 1248 TCGGTAGGACTTCGGTCTCTAGGTGCCACACTGAGACACACAGCTACCATGAAGTTGG 1307
QY 315 LeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuGlu 334
Db 1308 CTGCTTCTCTCTCTGTTGGCAATTTCCATTTCTCTGTGCTTATCTACTCCGTGGAG 1367
QY 335 HisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIleProAlaAlaCysTrp 354
Db 1368 AAA-----GATGACCACACATCCAGC-----CTCACCAGCATCCCATCTCGTGG 1415
QY 355 TrpValIleIleSerMetThrThrValGlyTyrGlyAspMetTyrProIleThrValPro 374
Db 1416 TGGGCCACCATCAGCATGACAACTGGGGCTATGGAGACACCCACCCGGTCACTTGGGG 1475
QY 375 GlyArgIleLeuGlyGlyValCysValValSerGlyIleValLeuLeuAlaLeuProIle 394
Db 1476 GGAAGCTATCGCCAGCACATGCATCATCTGTGGCATCTTGTGTGGTGGCCCTTCCATC 1535
QY 395 ThrPheIleTyrHisSerPheValGlnCysTyrHisGluLeuLys 409
Db 1536 ACCATCATCTTCAACAAGTTTTCGAAGTACTACACAGAACAAAG 1580

RESULT 9
US-09-336-643A-17
; Sequence 17, Application US/09336643A

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LOCATION: (154)....(1647)

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)....(2799)

OTHER INFORMATION: n = A,T,C or G

US-09-181-339-2

Alignment Scores:

Pred. No.: 8,02e-72 Length: 2799
Score: 659.00 Matches: 157
Percent Similarity: 51.58% Conservative: 72
Best Local Similarity: 35.36% Mismatches: 169
Query Match: 29.75% Indels: 46
DB: 4 Gaps: 10

US-10-016-647-2 (1-425) x US-09-181-339-2 (1-2799)

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QY 13 LeuAsnValGlyAlaArgTyrSerLeuSerArgGluLeuLeuLysAspPheProLeu 32
Db 220 GTGACGTGGCGAGTGGCGGCTGCTGAGCGCGCGCCCTTCGCGCTTCGCGGC 279
QY 33 ArgArgValSerArgLeuHisGlyCysArgSerGluArgAspValLeuValCysAsp 52
Db 280 ACGCGCTGGCGCGCTACAGCGCGCGGCTCGAGGAGCAGCGCGCGCTGTGCGAC 339
QY 53 AspTyrAspArgGluArgAsnGluTyrPhePheAspArgHisSerGluAlaPhe--Gly 71
Db 340 GACTACAGCAGCGCGCGGACAGAGTCTACTTTGATCGGCATCCGGGCTTCTTTCGCGC 399
QY 72 PheileLeuLeuTyrValArgGlyHisGlyLysLeuArgPheAlaProArgMetCysGlu 91
Db 400 GTCCATACACTTACCGCACCGGCGAC-----CTGCACGTCTAGACGAGCTGTGCGTC 453
QY 92 LeuSerPheTyrAsnGluMetIleTyrTrpGlyLeuGluGlyAlaHisLeuGluTyrCys 111
Db 454 TTCGCTTTCGCGCAGGAGCTGACTACTGGGCGCTGGCGGAGACGCGCTGCGCCACGTCG 513
QY 112 CysGlnArgArgLeuAspArgMet-----Ser 121
Db 514 TGCGCGCGCGGATCTGGAGCGCGTGGCGGCGCTCGCGCGCTGGGACGAGCAGCAGC 573
QY 122 AspThrTyrThrPheTyrSer-----AlaAspGluProGlyValLeuGlyArgAspGlu 139
Db 574 GACGCGCGCAGCGAGCGTGGACCGCTGCCGACGAGATCTCGAGCTGCGAGCGGAGCTG 633
QY 140 AlaArgProGlyGlyAlaGluAlaAlaProSerArgArg-----TrpLeuGluArgMet 157
Db 634 GCGCGTATGGTGGCGCTCGCTGGCGCGCTGGCGCGCTCGTCTGCTGCTC-----684
QY 158 ArgArgThrPheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSer 177
Db 685 -----ACCATGAGAGATCCAGCTACTCGCTGCCAGCAAGCTCTTCAGCTGCGTATCC 738
QY 178 ValValPheValIleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArg 197
Db 739 ATCGCGGTGGTCTCGCTCCATCGCTGCATGTGCATCCACAGCTGCGCGAGTACCAA 798
QY 198 -----AsnAlaAlaAspAsnArgSerLeu-----206
Db 799 GCTCGGAGCGCGCGCGCTGGCTGCTGCGCGCTGGCGCGCTGGCGCGCGAGGAGGTG 858
QY 207 -----AspAspArgSerArgIleGluAlaIleCysIleGlyTrpPheThrAlaGlu 224
Db 859 CGGAGCACCGGTGCTGCGCGCTGGAGTACTTCTGTCATCGCTGGTTCAGTTCGAG 918
QY 225 CysIleValArgPheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsn 244
Db 919 GTGTCGTCGCGCTGCTGCTGCCAGCAGCGCAACTTCTTCTGCCACCGCTCAAC 978
QY 245 IleIleAspLeuAlaIleThrProTyrTyrIleSerValLeuMetThrValPheThr 264
Db 979 CTCATTGACATCGTGTGGTGTGCGCTTCTATCTACACTGCTGGTGGCGCAGCGCTT 1038
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QY 265 GlyGlu-----AsnSerGlnLeuGlnArgAlaGlyValThrLeuArgVal 279
Db 1039 GGTACACGCGCGGAGCAGCGGGGAGGAGCTCGGGACCTGGGCAAGTAGTGCAGTG 1098
QY 280 LeuArgMetMetArgIlePheTrpValIleLysLeuAlaArgHisPheIleGlyLeuGln 299
Db 1099 TTCGCGCTCATCGCACTTCGCGGTCTCAAGCTGGCGGCACCTCCACGGGCTCGT 1158
QY 300 ThrLeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuValPheIle 319
Db 1159 TCGCTGGCGCGCACGCTCAAGCACAGCTACCGTGAGTGGGCTCTTACTGCTGTACCTG 1218
QY 320 CysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeu 339
Db 1219 GCCGTGGTGTGTCAGTGTCTTCGCGGTGCTACACGCCGAGAA-----1266
QY 340 GluThrSerAsnLysAspPheThrSerIleProAlaAlaCysTrpTrpValIleIleSer 359
Db 1267 -----GAAACGAGGCTTTCACACAATCCCTGCTGCTGGTGGGCGCACAGTGAGC 1320
QY 360 MetThrThrValGlyTyrGlyAspMetTyrProIleThrValProGlyArgIleLeuGly 379
Db 1321 ATGACACAGTGGGCTATGGGATGTGGTCCAGAGACTGTGGTGGCAAGCTGGCGGCGC 1380
QY 380 GlyValCysValSerGlyIleValLeuAlaLeuProIleThrPheIleTyrHis 399
Db 1381 TCGGCTGCATCTCGGGGCGATCTGGTGGTGGCTCCCTCCCATCACCATCTTCAAC 1440
QY 400 SerPheValGlnCysTyrHisGluLeuLysPheArgSerAlaArgTyrSerArgSerLeu 419
Db 1441 AAGTTTTCCCACTTCTACCGCGCGCAGAGGCACTGGAGCGCGCGCTGGCGGCGGT 1500
QY 420 SerThrGluPhe 423
Db 1501 CAGCGCGAGTTT 1512
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RESULT 11

US-08-464-340A-3

Sequence 3, Application US/08464340A

Patent No. 5710019

GENERAL INFORMATION:

APPLICANT: LI, ET AL.

TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

STREET: 6 BECKER FARM ROAD

CITY: ROSELAND

STATE: NEW JERSEY

COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/464,340A

FILING DATE: June 5, 1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA: PCT/US94/08449

APPLICATION NUMBER: 28 JUL 1994

FILING DATE: 28 JUL 1994

ATTORNEY/AGENT INFORMATION:

NAME: FERRARO, GREGORY D.

REGISTRATION NUMBER: 36,134

REFERENCE/DOCKET NUMBER: 325800-415

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

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; LENGTH: 2483 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
US-08-464-340A-3

Alignment Scores:
Pred. No.: 6, 72e-69 Length: 2483
Score: 635.00 Matches: 150
Percent Similarity: 54.73% Conservative: 87
Best Local Similarity: 34.64% Mismatches: 171
Query Match: 28.67% Indels: 26
DB: 1 Gaps: 9

US-10-016-647-2 (1-425) x US-08-464-340A-3 (1-2483)
QY 5 ArgSerGlyAlaAlaSer-----ValValLeuAenValGlyValAlaArgTyr 20
DB 727 CAGAGTCGCGTGCAGGACGACATAGATAGTTCGCAACGTGGGGGGGTGCGGAG 786
QY 21 SerLeuSerArgGluLeuLeuLysAspPheProLeuArgArgValSerArgLeuHisGly 40
DB 787 GTGCTGTACGGGAGCTCTCTAGTCAGTACCTGAGACCGCGGTGGCGAGCTCATCAAC 846
QY 41 CysArgSer-----GluArgAspValLeuGluValCysAspAspTyrAspArgGluArg 58
DB 847 TGTCTTGGTGGGGGTACGACACCACTCTCTCCCTGTGCGACGACTACGACCCCGGCAAG 906
QY 59 AsnGluTyrPhePheAspArgHisSerGluAlaPheGlyPheIleLeuLeuTyrValArg 78
DB 907 CCGAGAGTCTTCTTTGACGAGGACCGGACCGCTTCAAGTGTGC---ATCGAGGTGTAC 963
QY 79 GlyHisGlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMet 98
DB 964 TATTTTCGGGAGGTCCACATGAAGAAGGACATCTGCCCATCTGTCTTCAAGAACGAGATG 1023
QY 99 IleTyrTrpGlyLeuGluClyAlaHisLeuGluTyrCysGlnArgArgLeuAspAsp 118
DB 1024 GACTTCTGAGAGTGGACCTCAAGTCTCTGGACGACTGTGTGCAAGGCCACCTGAGCGAG 1083
QY 119 ArgMetSerAspThrTyrThrPheTyrSer-----AlaAspGluProGlyValLeuGly 136
DB 1084 AAGCGGAGGAGCTGGAGGAGATCGC-GGGCGCGTGGCGATCATCTTGGACGACCTGGG 1142
QY 137 ArgAspGluAlaArgProGlyAlaGluAlaAlaProSerArgArg-TrpLeuGluArg 156
DB 1143 CGTGGACGCGGCGCA---GGGCGCGTGGCGCGCTGCCAGAAAGTGGCTCTGG----- 1191
QY 156 gMetArgArgThrPheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerVa 176
DB 1192 -----AAGTTCCTGGAGAACCGGAGTCGTCGCGCGCGGGTGGTGGCGAGCT 1244
QY 176 lSerValValPheValIleValSerMetValValLeuCysAlaSerThrLeuProAspTr 196
DB 1245 CTCCTCTCTGCTCATCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1304
QY 196 pArgAsnAlaAlaAlaAsp--AsnArgSerLeuAspAspArgSerArgIleIleGluAl 215
DB 1305 GCAGGTGCTGGACGCGGAGGAGGACCGCTGGAGACCGGACCGGAGACGCTGGAGAGCTG 1364
QY 215 alleCysIleGlyTrpPheThrAlaGluCysIleValArgPheIleValSerIysAsnLy 235
DB 1365 GGCGTGCANTGGTGTCTTCACTGCTGAGTACCTGCTGCGCTCTTCTGCTCACCAACAA 1424
QY 235 sCysGluPheValLysArgProLeuAsnIleLeuAspLeuLeuAlaIleThrProTyrTy 255
DB 1425 GCTGCATCTTGGCGCTCTCTTCAACATTTGGACGTGTGGCGATCTCTCCCTCTTCA 1484
QY 255 rIleSerValLeuMetThrValPheThrGlyGluAsnSerGlnLeuGlnArgAlaGlyVa 275
DB 1485 CGTGACCTTCACGCTACGCACTGGTGGTGGCGCATGTAGTGGAGCTGACCAACGTGCA 1544

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RESULT 12

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PCT-US94-08449A-3
; Sequence 3, Application PC/TUS9408449A
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Potassium Channel Protein 1 and 2
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESS: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/08449A
; FILING DATE: SUBMITTED HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2483 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA

```

PCT-US94-08449A-3

Alignment Scores:

Pred. No.: 6,72e-69
Score: 635.00
Percent Similarity: 54.73%
Best Local Similarity: 34.64%
Query Match: 26.67%
DB: 5

Length: 2483
Matches: 150
Conservative: 87
Mismatch: 171
Indels: 26
Gaps: 9

US-10-016-647-2 (1-425) x PCT-US94-08449A-3 (1-2483)

QY 5 ArgSerGlyAlaAlaSer-----ValValLeuAsnValGlyGlyAlaArgTyr 20
Db 727 CAGAGCTCCCTGCCAGCGACGACATAGATAGTCTCAACGTGGGGCGGTGGCGGAG 786
QY 21 SerLeuSerArgGluLeuLeuLysAspPheProLeuArgValSerArgLeuHisGly 40
Db 787 GTGCTGTACGGGACCTCTCAGTCAGTACCTGAGACCGCGGTGGCGGAGCTCATCAAC 846
QY 41 CysArgSer-----GluArgAspValLeuGluValCysAspAspTyrAspArgGluArg 58
Db 847 TGTTCGTGGGGGTACGACACATCTTCCTCTGCGGAGCTACACCCCGGCAAG 906
QY 59 AsnGluTyrPhePheAspArgHisSerGluAlaPheGlyPheIleLeuLeuTyrValArg 78
Db 907 CGCGAGTTCTTTCACAGGACCGCGAGCTTCAAGTGTGTC---ATCGAGGTGTAC 963
QY 79 GlyHisGlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMet 98
Db 964 TATTCGGGAGGTCCACATCAAGAGGACATCTGCCCATCTCTCAAGAACGAGATG 1023
QY 99 IleTyrTrpGlyLeuGluGlyAlaHisLeuGluTyrCysCysGlnArgArgLeuAspAsp 118
Db 1024 GACTTCTGGAGGTGACCTCAAGTTCCTGGAGACTGTTCAGAGCCACCTGAGCGGAG 1083
QY 119 ArgMetSerAspThrTyrThrPheTyrSer-----AlaAspGluProGlyValLeuGly 136
Db 1084 AAGCGGAGAGGTGGAGGAGATCGC-GCGCGCGTGCAGCTCATCTCGGACGACCTGG 1142
QY 137 ArgAspGluAlaArgProGlyAlaGluAlaAlaProSerArgArg-TripLeuGluArg 156
Db 1143 CGTGGACGGCGCGA---GGCGCGTGGCGCGCTGCCAGAGTGTCTG-----1191
QY 156 gMetArgArgThrPheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerVa 176
Db 1192 -----AAGTCTCTGAGAGCCGAGTGTCTGTCGCGCGCGGTGGTGGCGGAGCT 1244
QY 176 lSerValValPheValIleValSerMetValValLeuCysAlaSerThrLeuProAspTr 196
Db 1245 CTCCTTCCTGCTCATCTCTGTCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1304
QY 196 pArgAsnAlaAlaAlaAsp---AsnArgSerLeuAspAspArgSerArgIleIleGluAl 215
Db 1305 GCAGGTGCTGGACCGCGGAGGACCGCGTGGAGACCGCGTGGAGAGCTGGAGAC 1364
QY 215 alleCysIleGlyTrpPheThrAlaGluCysIleValArgPheIleValSerLysAsnLy 235
Db 1365 GCGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1424
QY 235 sCysGluPheValLysArgProLeuAsnIleIleAspLeuLeuAlaIleThrProTyrTy 255
Db 1425 GCTGCATCTGGCGCTCTCTCTCATGACATTTGGAGCTGTGGGACATCTCTCTCTCT 1484
QY 255 rIleSerValLeuMetThrValPheThrGluAsnSerGlnLeuGlnArgAlaGlyVa 275
Db 1485 CGTGAAGCTCAAGCTCAGCAGCTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGG 1544
QY 275 lThrLeuArgValLeuArgMetMetArgIlePheTrpValIleLysLeuAlaArgHisph 295
Db 1545 GCGCGTGGAGGCTCGGATTCAGGATTCGCGGATTCAGGATTCAGGATTCAGGATTCAG 1604
QY 295 eIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLe 315

Db 1605 CTCGGGGCTGCAGACCCCTCACCTATGCCCTCAAGCGAGCTTCAAGGAACTGGGGCTGCT 1664
QY 315 uLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeuGluHi 335
Db 1665 GCTCATGTACCTGCAGTGGGTATCTTCTGCTCTCTGCTCTG-----1707
QY 335 sGlyLeuAspLeuGluThrSerAsnLysAsp-----PheThrSerIleProAlaAlaCy 353
Db 1708 -GGTACACCATGAGCAGAGCAGCATCCAGAGACCTCTTTAAGAAACATCCCCAGTCTT 1766
QY 353 sTrpTrpValIleIleSerMetThrThrValGlyTyrGlyAspMetTyrProIleThrVa 373
Db 1767 CTGTGGGCCATCATCACCACCGTCCGCTGCGGACATCTACCCCAAGACCAC 1826
QY 373 lProGlyArgIleLeuGlyValCysValSerGlyIleValSerGlyIleValLeuLeuAlaLeuPr 393
Db 1827 GCTGAGCAAGCTCAACGCGGCCATCAGCTTCTGTGTGTGTGTGTGTGTGTGTGTGT 1886
QY 393 oIleThrPheIleTyrHisSerPheValGlnCysTyrHisGluLeuLysPheArgSerAl 413
Db 1887 CATCCACCCCATCATCAACAACTTTGTGAGTACTACAAAGCAGCGCGCTCTCTGGAGAC 1946
QY 413 aArgTyrSerArgSerLeuSerThrGluPheLeuAsn 425
Db 1947 CGCGGCCAAGCAGCAGCTGGAGCTGTGATGGAACCTCAAC 1983
RESULT 13
US-10-162-012-7
; Sequence 7, Application US/10162012
; Patent No. 6682597
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Rory A.J.
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
; FILE REFERENCE: 10448-190001
; CURRENT APPLICATION NUMBER: US/10/162,012
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/875,321
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18398
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,238
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,363
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18247
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/227,068
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 09/928,530
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/25475
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: US 60/226,770
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/934,421
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US01/26096
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/279,281
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 10/109,029
; PRIOR FILING DATE: 2002-03-28

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 19, 2004, 14:00:02 ; Search time 576 Seconds
(without alignments)
3301.557 Million cell updates/sec

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Perfect score: 2215
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 2890132 seqs, 2237290429 residues

Total number of hits satisfying chosen parameters: 5780264

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq*
17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq*
18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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ALIGNMENTS

RESULT 1
US-10-016-647-1
; Sequence 1, Application US/10016647
; Publication No. US20020160475A1
; GENERAL INFORMATION:
; APPLICANT: Fridde, Carl Johan
; APPLICANT: Hilbun, Erin
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20020160475A1 Human Ion Channel Protein and Polynucleotide
; FILE REFERENCE: LEX-0284-USA
; CURRENT APPLICATION NUMBER: US/10/016,647
; PRIORITY FILING DATE: 2001-12-10
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1278
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-016-647-1
Alignment Scores:

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2	2215	100.0	1844	14	US-10-016-647-3	Sequence 3, Appli
3	2209	99.7	3215	15	US-10-199-869-1	Sequence 1, Appli
4	2035.5	94.6	1651	13	US-10-114-270-45	Sequence 45, Appli
5	2076.5	93.7	2235	16	US-10-415-378-39	Sequence 39, Appli
6	1028	46.4	594	15	US-10-199-869-26	Sequence 139, App
7	864.5	39.0	2370	10	US-09-971-392-139	Sequence 1, Appli
8	835.5	38.6	2127	14	US-10-143-003-1	Sequence 1, Appli
9	835.5	38.6	2127	15	US-10-325-891-1	Sequence 628, App
10	839.5	37.4	2499	15	US-10-101-510-628	Sequence 10, Appli
11	780.5	35.2	2565	13	US-10-435-935-10	Sequence 27, Appli
12	723.5	32.7	417	15	US-10-199-869-27	Sequence 7, Appli
13	715.5	32.3	3080	15	US-10-121-746-7	Sequence 2, Appli
14	685.5	30.9	1476	13	US-10-435-935-2	Sequence 1, Appli
15	685.5	30.9	2421	13	US-10-435-935-1	Sequence 5, Appli
16	685	30.9	2293	15	US-10-121-746-5	Sequence 17, Appli
17	683	30.8	3102	15	US-10-121-746-17	Sequence 439, App
18	683	30.8	5027	15	US-10-101-510-439	Sequence 827, App
19	667	30.1	3032	13	US-10-276-774-827	Sequence 25, Appli
20	661	29.8	461	13	US-09-852-386-25	Sequence 43, Appli
21	636.5	28.7	1455	13	US-10-114-270-43	Sequence 1, Appli
22	636.5	28.7	1638	13	US-09-833-466-2	Sequence 2, Appli
23	636.5	28.7	1638	13	US-09-918-359-1	Sequence 35, Appli
24	636.5	28.7	1871	10	US-09-999-220B-35	Sequence 5, Appli
25	636.5	28.7	2103	13	US-09-833-466-1	Sequence 3, Appli
26	636.5	28.7	2310	13	US-09-918-359-5	Sequence 119, App
27	635	28.7	2483	14	US-10-325-891-3	Sequence 115, App
28	635	28.7	2483	15	US-10-143-003-3	Sequence 7, Appli
29	632.5	28.6	1871	10	US-09-999-220B-119	Sequence 1, Appli
30	632.5	28.6	2850	10	US-09-999-220B-1	Sequence 33, Appli
31	632.5	28.6	2850	10	US-09-999-220B-115	Sequence 1, Appli
32	600.5	27.1	1747	13	US-09-804-014A-7	Sequence 16, Appli
33	599.5	27.1	1871	10	US-09-999-220B-33	Sequence 7, Appli
34	599.5	27.1	1871	10	US-09-999-220B-117	Sequence 1, Appli
35	599	27.0	1371	9	US-09-974-712-1	Sequence 3, Appli
36	599	27.0	1792	9	US-09-974-712-3	Sequence 1, Appli
37	599	27.0	4372	9	US-09-993-811-1	Sequence 3, Appli
38	599	27.0	4372	15	US-10-254-010-3	Sequence 16, Appli
39	599	27.0	6823	9	US-09-989-920-16	Sequence 7, Appli
40	597	27.0	1341	10	US-09-875-321-7	Sequence 7, Appli
41	597	27.0	1341	15	US-10-162-012-7	Sequence 7, Appli
42	597	27.0	1341	16	US-10-162-102-7	Sequence 20260, A
c 43	596	26.9	1408	15	US-10-029-386-20260	Sequence 1, Appli
c 44	594	26.8	5089	15	US-10-254-008-1	Sequence 7, Appli
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Pred. No.: 2,71e-277 Length: 1278
 Score: 2215.00 Matches: 425
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14 Gaps: 0

US-10-016-647-2 (1-425) x US-10-016-647-1 (1-1278)

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 Db 1 ATGACCTTCGGGCGCAGCGGGCGGCTCGGTGCTGCTGAACTGGCGCGCGCCCGGTAT 60
 QY 21 SerLeuSerArgGluLeuLeuLysAspPheProLeuArgValSerArgLeuHisGly 40
 Db 61 TCGCTGTCGGGAGCTGCTGAAGGACTTCGGCTGCGCGCGGTGAGCGCGGTGACCGGC 120
 QY 41 CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgGlnGlu 60
 Db 121 TCGCGCTCCGAGCGCGACGCTGTCGAGGTGTCGACGACTACGACCGCGAGCGCAACGAG 180
 QY 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheIleLeuLeuTyrValArgGlyHis 80
 Db 181 TACTTCTTCGACCGGCACTCGAGGGCTTCGGCTTCATCTGCTCTACGTGCGCGCCAC 240
 QY 81 GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100
 Db 241 GGCACGCTCGGCTTCGCGCGCGGATGTGCGAGCTCTCTCTTACACGAGATGATCTAC 300
 QY 101 TrpGlyLeuGluGlyAlaHisLeuGluTyrCysGlnArgArgLeuAspArgMet 120
 Db 301 TGGGCGCTGAGGCGCGGACCTCGAGTACTGCTGCAGCGCGCGCTCGACCGCGCATG 360
 QY 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140
 Db 361 TCCGACACCTACACCTTCTACTCGCGCGAGCGCGGCTGCTGCGCGCGCGCGCGGCG 420
 QY 141 ArgProGlyGlyAlaGluAlaProSerArgArgTyrLeuGluArgMetArgArgThr 160
 Db 421 CGCGCGCGCGCGCGCGCGCGCTCCCTCCAGCGCTGCTGAGCGCATGCGCGGAC 480
 QY 161 PheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValPhe 180
 Db 481 TTCGAGGAGCCACGCTGCTGCTGCGCGCGAGCATCTGCTAGCGTGTGCTGTGTC 540
 QY 181 ValIleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArgAsnAlaAla 200
 Db 541 GTGATCGTGTCATGTTGTTGCTGTCGCGCGAGCAGCTTGGCGACGCGCGCGCGCG 600
 QY 201 AlaAspAsnArgSerLeuAspAspArgArgIleIleGluAlaIleCysIleGlyTrp 220
 Db 601 GCGGACNACCGGAGCTGGATGACCGGAGCAGGATTAATGAGCTATCTGATAGTTGG 660
 QY 221 PheThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGluPheValLys 240
 Db 661 TTCACCTGCCAGTGATCGTGAGGTTCAATGTCTCCAAAACAAGTGTGAGTTGTCAG 720
 QY 241 ArgProLeuAsnIleIleAspLeuAlaIleThrProTyrTyrIleSerValLeuMet 260
 Db 721 AGACCCCTCGAACATCATTTCTGCGGATTCAGCCGATTAACATCTCTGTGTGATG 780
 QY 261 ThrValPheThrGlyGluAsnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLeu 280
 Db 781 ACAGTGTTCACGGCGAGAACTCTCAACTCCAGAGGGCTGGAGTCACTTGGGGTACTT 840
 QY 281 ArgMetMetArgIlePheTrpValIleLysLeuAlaArgHisPheIleGlyLeuGlnThr 300
 Db 841 AGAATGATGAGGATTTTTTGGGTGATTAAGCTTGGCCGCTTCACTTGTCTTCAGACA 900
 QY 301 LeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuValPheIleCys 320
 Db 901 CTCGGTTTGACTCTCAACCGTGTCTACCGAGAGATGGTTATGTTACTTGTCTTCTTGT 960

QY 321 ValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeuGlu 340
 Db 961 GTTGCCATGCGCAATCTTTAGTGACATTTCTCAGCTTTCTTAACATGGCTGGACCTGGAA 1020
 QY 341 ThrSerAsnLysAspPheThrSerIleProAlaAlaCysTrpTrpValIleIleSerMet 360
 Db 1021 ACATCCAAACAGGACTTTACAGCATTCCTGCTGCTGCTGGTGGGTATTCTCTATG 1080
 QY 361 ThrThrValGlyTyrGlyAspMetTyrProIleThrValProGlyArgIleLeuGlyGly 380
 Db 1081 ACTACAGTTCGCTATGAGATATGTATCTCTATCAGCTGCTGGAAGAAATCTTGGAGGA 1140
 QY 381 ValCysValValSerGlyIleValLeuLeuAlaLeuProIleThrPheIleTyrHisSer 400
 Db 1141 GTTTGTGTTGTCAGTGAATTTCTATTGCGCATTAACCTATCACTTTTATCTACCATAGC 1200
 QY 401 PheValGlnCysTyrHisGluLeuLysPheArgSerAlaArgTyrSerArgSerLeuSer 420
 Db 1201 TTTGTGAGTGTATCATGAGCTCAAGTTTATGATCTGCTAGGTATAGTAGGAGCTCTCC 1260
 QY 421 ThrGluPheLeuAsn 425
 Db 1261 ACTGAATTCCTGAAT 1275

RESULT 2
 US-10-016-647-3
 ; Sequence 3, Application US/10016647
 ; Publication No. US20020160475A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fiddle, Carl Johan
 ; APPLICANT: Hilbun, Erin
 ; APPLICANT: Turner, C. Alexander Jr.
 ; TITLE OF INVENTION: No. US20020160475A1 Human Ion Channel Protein and Polynucleotide
 ; FILE REFERENCE: LEX-0284-USA
 ; CURRENT APPLICATION NUMBER: US/10/016,647
 ; CURRENT FILING DATE: 2001-12-10
 ; PRIOR APPLICATION NUMBER: US 60/257,932
 ; PRIOR FILING DATE: 2000-12-20
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 1844
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 ; US-10-016-647-3

Alignment Scores:
 Pred. No.: 5e-277 Length: 1844
 Score: 2215.00 Matches: 425
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14 Gaps: 0

US-10-016-647-2 (1-425) x US-10-016-647-3 (1-1844)

QY 1 MetThrPheGlyArgSerGlyAlaAlaSerValValLeuAsnValGlyGlyAlaArgTyr 20
 Db 457 ATGACCTTCGGGCGCAGCGGGCGGCTCGGTGCTGTAACGTGGCGCGCGCGGTAT 516
 QY 21 SerLeuSerArgGluLeuLeuLysAspPheProLeuArgArgValSerArgLeuHisGly 40
 Db 517 TCGTGTCCCCGGGAGCTGTGAAGACTTCCCGCTGCGCGCGGTGAGCCGGGTGCACGGC 576
 QY 41 CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu 60
 Db 577 TGCCGCTCCGAGCGCGAGCTGCTGAGGTGTCGACGACTACGACCGCGAGCGCAACGAG 636
 QY 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheIleLeuLeuTyrValArgGlyHis 80
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 QY 81 GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100

Db 697 GGCAAGCTGGCTTCGCGCGGGAGTGTGCGAGCTCTCTTACAAAGAGATGATCTAC 756
QY 101 TrpGlyLeuGluAlaHisLeuGluTyrCysGlnArgArgLeuAspArgMet 120
Db 757 TGGGGCTTGAGGGCGCGCACTCGAGTACTGCTGCCAGCGCGCTCGACACCGCATG 816
QY 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140
Db 817 TCGACACCTACACCTTCTACTCGCGCGAGCGGGCTGCTGGCGCGCGAGCGG 876
QY 141 ArgProGlyGlyAlaGluAlaProSerArgArgTyrTrpLeuGluArgMetArgThr 160
Db 877 CGCCCCGGGGCGCGAGCGGCTCCCTCCAGCGCTGGCTGAGCGCATGGGGGAC 936
QY 161 PheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValPhe 180
Db 937 TTCGAGAGCCACGTCGTCGTCGGCGCGAGATCTGCTAGCGTTCGGTGTGTC 996
QY 181 ValIleValSerMetValValLeuGluCysAlaSerThrLeuProAspTrpArgAsnAlaAla 200
Db 997 GTGATCGTGTCCATGGTGTGTGTGCGCGAGCAGCTTCCCGAGCTGGCGCAACGAGCC 1056
QY 201 AlaAspAsnArgSerLeuAspArgSerArgIleIleGluAlaIleCysIleGlyTrp 220
Db 1057 GCGCAACCGGAGCTGGATACCGGAGCAGGAGTAATGAAGCTATCTGCATAGTTGG 1116
QY 221 PheThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGluPheValLys 240
Db 1117 TTCACCTGCGAGTGCATCGTGTGAGTTCAITGCTCCAAAACAAGTGTGAGTTTGTCAAG 1176
QY 241 ArgProLeuAsnIleIleAspLeuAlaIleThrProTyrTyrIleSerValLeuMet 260
Db 1177 AGACCCCTGAAATCATTAATTTACTGGCAATCAGCCCGATATACATCTCTGTGTGATG 1236
QY 261 ThrValPheThrGlyGluAsnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLeu 280
Db 1237 ACAGTGTTTACAGCGAGAACTCTCACTCCAGAGGCTGGAGTCACTTGGAGGTACTT 1296
QY 281 ArgMetMetArgIlePheTrpValIleLysLeuAlaArgHisPheIleGlyLeuGlnThr 300
Db 1297 AGAATGATGAGGATTTTTGGGTGATTAAGCTTGGCCGCTCACTTCACTTGGTCTTCAGACA 1356
QY 301 LeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuValPheIleCys 320
Db 1357 CTCGGTTTGACTCTCAACGTTGCTACCAGAGATGGTTATGTTACTTCTTCATTGT 1416
QY 321 ValAlaMetAlaIlePheSerAlaLeuSerGlnLeuGluHisGlyLeuAspLeuGlu 340
Db 1417 GTTGCCATGGCAATCTTTAGTGCACCTTCTCAGCTTCTTGAACATGGGCTGGACCTGGAA 1476
QY 341 ThrSerAsnLysAspPheThrSerIleProAlaAlaCysTyrTrpValIleIleSerMet 360
Db 1477 ACATCCAAACAGGACTTTACCAAGCATTCCTGCTGCTGCTGCTGGTGTATATCTCTATG 1536
QY 361 ThrThrValGlyTyrGlyAspMetTyrProIleThrValProGlyArgIleLeuGlyGly 380
Db 1537 ACTACAGTTGGCTATGAGATATGATCTATATCAGTGCCTGGAGAAATCTTGGAGGA 1596
QY 381 ValCysValValSerGlyIleValLeuLeuAlaLeuProIleThrPheIleTyrHisSer 400
Db 1597 GTTGTGTGTGTGAGTGAATTTGCTATTGGCATTTACCTATCACCTTTTATCTACCATAGC 1656
QY 401 PheValGlnCysTyrHisGluLeuLysPheArgSerAlaArgTyrSerArgSerLeuSer 420
Db 1657 TTTGTGCACTGTATCATGAGCTCAAGTTTAGATCTGCTAGGTATAGTAGGAGCCTCTCC 1716
QY 421 ThrGluPheLeuAsn 425
Db 1717 ACTGAATTCCTGAAT 1731

RESULT 3

US-10-199-869-1

; Sequence 1, Application US/10199869
; Publication No. US20030152953A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUB
; FILE REFERENCE: D0161 NP
; CURRENT APPLICATION NUMBER: US/10/199,869
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/306,577
; PRIOR FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 3215
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1275)
; OTHER INFORMATION:
US-10-199-869-1
Alignment Scores:
Pred. No.: 7,67e-276 Length: 3215
Score: 2209.00 Matches: 424
Percent Similarity: 99.76% Conservative: 0
Best Local Similarity: 99.76% Mismatches: 1
Query Match: 99.73% Indels: 0
DB: 15 Gaps: 0

US-10-016-647-2 (1-425) x US-10-199-869-1 (1-3215)

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QY 21 SerLeuSerArgGluLeuLeuLysAspPheProLeuArgValSerArgLeuHisGly 40
Db 61 TCGCTGTCCCGGAGCTGTGAGGACTTCCCGCTGCGCGCGTGAAGCCCGCTCAGCGC 120
QY 41 CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu 60
Db 121 TGGCGCTCCGAGCGCGAGCTGCTCGAGGTGTGCGACGACTACGACCGCGAGCGCAACGAG 180
QY 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheIleLeuLeuTyrValArgGlyHis 80
Db 181 TACTTCTTCGACCGCGACTCGGAGGCTTCGGCTTCTATCCTGCTCTACGTGCGCGCAC 240
QY 81 GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100
Db 241 GGCAGCTGGCTTCGCGCGCGGATGTGCGAGCTCTCTTCTACACGAGATGATCTAC 300
QY 101 TrpGlyLeuGluGlyAlaHisLeuGluTyrCysCysGlnArgArgLeuAspArgMet 120
Db 301 TGGGGCTGGAGGGCGCGACCTCGAGTACTGTGCTGCCAGCGCGCTCGACACCGCATG 360
QY 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140
Db 361 TCCGACACCTACACCTTCTACTCGCGCGAGCGCGGCTGTGGCGCGCGAGCGGCG 420
QY 141 ArgProGlyGlyAlaGluAlaAlaProSerArgArgTrpLeuGluArgMetArgArgThr 160
Db 421 CGCCCCGGGGCGCGAGCGGCTCCCTCCAGCGCTGGTGGAGCGCATGCGCGGAC 480
QY 161 PheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValPhe 180
Db 481 TTCGAGAGCGCGAGCTCGCTGGCGCGCAGATCTCTGGCTAGCGTGTGGTGTTC 540
QY 181 ValIleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArgAsnAlaAla 200
Db 541 GTGATGTGTCCATGGTGTGTGTGCGCGCAGCAGCTTTCGCCGACTGGCGCAACGCGAC 600

QY 201 AlaAspAsnArgSerLeuAspArgSerArgIleleuAlaileCysleGlyTyr 220
 Db 601 GCCGACACCGCAGCTGGATGACCGGAGCAGGATTAATGAAGCTATCTGCATAGTTGG 660
 QY 221 PheThrAlaGluCysleValArgPheIleValSerLysAsnLysCysGluPheVallys 240
 Db 661 TTCACGTCCGAGTGCATCGTGGGTTTCATGTCTCCAAAACAAAGGTGAGTTGCAAG 720
 QY 241 ArgProLeuAsnIleleAspLeuLeuAlaIleThrProTyrTyrIleSerValLeuMet 260
 Db 721 AGACCCCTGACATCATTTACTTGGCAATCACGCGGATTTACATCTCTGTGTTGATG 780
 QY 261 ThrValPheThrGlyGluLeuSerGlnLeuArgAlaGlyValThrLeuArgValLeu 280
 Db 781 ACAGTGTTCACGCGGAGAACTCTCAACTCCAGAGGGCTGGAGTCACTTGAGGGTACTT 840
 QY 281 ArgMetMetArgIlePheTTPValIleLysLeuAlaArgHisPheIleGlyLeuGlnThr 300
 Db 841 AGAATGATGAGGATTTTGGGTGATTAAGCTTGGCCGCTCACTTCATTCGTTTCAGATA 900
 QY 301 LeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuValPheIleCys 320
 Db 901 CTCGGTTGACTCTCAACGCTTCTACCGAGAGATGGTTATGTACTTGTCTCTCATTTGT 960
 QY 321 ValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeuGlu 340
 Db 961 GTTGCCATGCAATCTTTAGTGCACTTTCAGCTTCTTGAACATGGCTGGACCTGGAA 1020
 QY 341 ThrSerAsnLysAspPheThrSerIleProAlaAlaCysTrpTrpValIleIleSerMet 360
 Db 1021 ACATCCCAAGACATTACCAACATTCCTGCTGCTGCTGGTGGGTGATTAATCTCTATG 1080
 QY 361 ThrThrValGlyTyrGlyAspMetTyrProIleThrValProGlyArgIleLeuGlyGly 380
 Db 1081 ACTACAGTTCGCTATGAGATATGTATCTCATCACAGTGCCTGGAAGAAATCTTGAGGA 1140
 QY 381 ValCysValValSerGlyIleValLeuLeuAlaLeuProIleThrPheIleTyrHisSer 400
 Db 1141 GTTTGTGTTGTCAGTGGAAATGTTCTATTGGCATTACCTATCATCTTTATCATCATAC 1200
 QY 401 PheValGlnCysTyrHisGluLeuLysPheArgSerAlaArgTyrSerArgSerLeuSer 420
 Db 1201 TTTGTGAGTGTATTATCATGAGTCAAGTTTAGATCTGCTAGGTATATAGTAGGACCTCTCC 1260
 QY 421 ThrGluPheLeuAsn 425
 Db 1261 ACTGAATTCCTGAAT 1275

RESULT 4

US-10-114-270-45
 ; Sequence 45, Application US/10114270
 ; Publication No. US20040030110A1
 ; GENERAL INFORMATION:

; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Miller, Charles E.
 ; APPLICANT: Malyankar, Uriel M.
 ; APPLICANT: Spytek, Kimberly A.
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Liu, Ziaohong
 ; APPLICANT: Gusev, Vladimir Y.
 ; APPLICANT: Li, Li
 ; APPLICANT: Vernet, Corine
 ; APPLICANT: Zerkhusen, Bryan D.
 ; APPLICANT: Gorman, Linda
 ; APPLICANT: Shenoy, Suresh G.
 ; APPLICANT: Pena, Carol E.A.
 ; APPLICANT: Smithson, Glenda
 ; APPLICANT: Burgess, Catherine E.
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Shimkets, Richard A.
 ; APPLICANT: Gangolli, Esha A.

; APPLICANT: Taupier Jr., Raymond J.
 ; APPLICANT: Caeman, Stacie J.
 ; APPLICANT: Ji, Weizhen
 ; APPLICANT: Anderson, David W.
 ; APPLICANT: Liette, Mario W.
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Edinger, Shlomit R.
 ; APPLICANT: Stone, David J.
 ; APPLICANT: MacDougall, John R.
 ; APPLICANT: Rothenberg, Mark E.
 ; TITLE OF INVENTION: No. US20040030110A1e1 Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 21402-322C
 ; CURRENT APPLICATION NUMBER: US/10/114,270
 ; CURRENT FILING DATE: 2002-11-27
 ; PRIOR APPLICATION NUMBER: 60/281,086
 ; PRIOR FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: 60/281,136
 ; PRIOR FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: 60/281,863
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/281,906
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/282,020
 ; PRIOR FILING DATE: 2001-04-06
 ; PRIOR APPLICATION NUMBER: 60/282,930
 ; PRIOR FILING DATE: 2001-04-10
 ; PRIOR APPLICATION NUMBER: 60/282,934
 ; PRIOR FILING DATE: 2001-04-10
 ; PRIOR APPLICATION NUMBER: 60/283,512
 ; PRIOR FILING DATE: 2001-04-12
 ; PRIOR APPLICATION NUMBER: 60/283,710
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/284,234
 ; PRIOR FILING DATE: 2001-04-17
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 470
 ; SEQ ID NO 45
 ; LENGTH: 1651
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1642)
 ; US-10-114-270-45

Alignment Scores:

Pred. No.: 1,48e-261 Length: 1651
 Score: 2095.50 Matches: 411
 Percent Similarity: 91.54% Conservative: 0
 Best Local Similarity: 91.54% Mismatches: 35
 Query Match: 94.60% Indels: 35
 DB: 13 Gaps: 3
 US-10-016-647-2 (1-425) x US-10-114-270-45 (1-1651)

QY 1 MetThrPheGlyArgSerGlyAlaAlaSerValValLeuAsnValGlyGlyAlaArgTyr 20
 Db 58 ATGACCTTCGGGCGCAGCGGGCGGCTCGGTGTGTCTGAACGTGGGCGGCCCGGTAT 117
 QY 21 SerLeuSerArgGluLeuLeuLysAspPheProLeuArgArgValSerArgLeuHisGly 40
 Db 118 TCGCTGTCCCGGAGCTGCTGAAGACTTCCTCGCTGCGCGCTGAGCGGCTGACGGC 177
 QY 41 CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu 60
 Db 178 TGCCGCTCCGAGCGCAGCTGCTGAGGTGTGCGACCACTACGACCGCGCGCAACGAG 237
 QY 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheIleLeuLeuTyrValArgGlyHis 80
 Db 238 TACTTCTTCGACCGGCACTCGAGGCGCTTCGGCTTCATCTGCTCTACGTGGCGGCCAC 297
 QY 81 GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100

Db 298 GCAAGCTGCGCTTCGCGCGCGGATGTGCGAGCTCTCTTCTTCAACAGAGATGATCTAC 357
Qy 101 TTPGLYLeuGluGluValAlaHisLeuGluTyrCysGlnArgArgLeuAspArgMet 120
Db 358 TGGGCGCTGGAGGGCGCGCACTCGAGTACTGCTGCCAGCGCGCTCGACACCGCATG 417
Qy 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140
Db 418 TCCGACACTACCTTCTACTCGCCGCGAGCGCGCGTCTGGCGCGCGAGCGCG 477
Qy 141 ArgProGly-----GlyValGluAlaAlaPro--- 149
Db 478 CGCCCCGCGCGCGAGCGCGCTCCCTCAGCGCTGGCTGGAGCGCATCGCGCGACCTT 537
Qy 150 -----SerArgArgTrpLeuGluArgMetArgArgThrPhe 161
Db 538 CGAGGAGCCACGTCGTCGCTGGCGCGCGCGCTGGCTGGAGCGCATCGCGCGACCTTC 597
Qy 162 GluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValValPheVal 181
Db 598 GAGGAGCCACGTCGTCGCTGGCGCGCGAGATCTCGGTAGCGTGTGCGTGTGTCGTG 657
Qy 182 IleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArgAsnAlaAla 201
Db 658 ATCGTGTCCATGTTGCTGTGCGCCAGCACGTTGCCGACTGCGCGCAACGCGCGCC 717
Qy 202 AspAsnArgSerLeuAspArgSer----- 210
Db 718 GACAAACCGAGCGCTGGATGACCGGAGCAGGACTCCGCGCGCCCTGGGAGGAGCCCTCC 777
Qy 211 -----ArgIleIleGluAlaIleCysIleGlyTrpPheThrAlaGluCys 225
Db 778 GGGTGTCTCTTGACAGAGTAATTCAGCATATCTGCATAGTTGGTTCACCTGCCGAGTGC 837
Qy 226 IleValArgPheIleValSerIleAsnLysCysGluPheValLysArgProLeuAsnIle 245
Db 838 ATCGTGAGGTTCAATGTCTCAAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGAACATC 897
Qy 246 IleAspLeuLeuAlaIleThrProTyrTyrIleSerValLeuMetThrValPheThrGly 265
Db 898 ATTGATTTACTGGCAATCAGCCGTTATCATCTCTGTGTGTGATGACAGTGTTCACAGGC 957
Qy 266 GluAsnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIle 285
Db 958 GAGAACTCTCAACTCCAGAGGCTGAGTCACTTCACTTGGTGTGATGACAGTGTTCACAGGC 1017
Qy 286 PheTrpValIleLysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrIleu 305
Db 1018 TTTTGGGTGATTAGCTTGGCCGTCACCTTCACTTGTGTCTTCAGACACTCGGTTTGACTCTC 1077
Qy 306 LysArgCysTyrArgGluMetValMetLeuLeuValPheIleCysValAlaMetAlaIle 325
Db 1078 AAACGTTGCTACCGAGAGATGTTATGTTACTTGTCTTCAATTTGTTGCCATGCAATC 1137
Qy 326 PheSerAlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAsp 345
Db 1138 TTTAGTGCACTTTCTCAGCTCTTGAACATGGCTGGACCTCGAAACATCCAAACAGGAC 1197
Qy 346 PheThrSerIleProAlaAlaCysTrpTrpValIleIleSerMetThrThrValGlyTyr 365
Db 1198 TTTTACAGCATCTCTGCTGCTGCTGGTGGTGTATATCTCTATGACTACAGTTGGCTAT 1257
Qy 366 GlyAspMetTyrProIleThrValProGlyArgIleLeuGlyValCysValValSer 385
Db 1258 GGAGATATGATATCTATCAGTGGCTCGAAGAAATCTTGGAGAGATTTGTGTGTGTCAGT 1317
Qy 386 GlyIleValLeuLeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCysTyr 405
Db 1318 GGAATGTTCTATTGGCATATCACTTTTATCTTACCATAGCTTTTGTGAGTGTAT 1377
Qy 406 HisGluLeuLysPheArgSerAlaArg 414
Db 1378 CATGAGCTCAAGTTTAGATCTGCTAGG 1404

RESULT 5

US-10-415-378-39
; Sequence 39, Application US/10415378
; Publication No. US20040014945A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; TANG, Y. Tom
; APPLICANT: YUE, Henry; NGUYEN, Danniell B.;
; APPLICANT: HAFALIA, April J.A.; ELLIOTT, Vicki S.;
; APPLICANT: LU, Yan; CHAWLA, Narinder K.;
; APPLICANT: YAO, Monique G.; BAUGHN, Mariah R.;
; APPLICANT: SANDHI, Ameena R.; DING, Li;
; APPLICANT: SANJANWALA, Madhusudan M.; RAMKUMAR, Jayalaxmi;
; APPLICANT: ARVIZU, Chandra S.; GIETZEN, Kimberly J.;
; APPLICANT: LAL, Preeti G.; AZIMZAI, Raica;
; APPLICANT: KHAN, Farrah A.; THANGAVELU, Kavitha;
; APPLICANT: THORNTON, Michael B.; LU, Dyoung Aina M.;
; APPLICANT: TRIBOULEY, Catherine M.; WARREN, Bridget A.;
; APPLICANT: ISON, H. Craig; DAS, Debopriya;
; APPLICANT: RAUMANN, Brigitte E.; POLICKY, Jennifer L.;
; APPLICANT: KEARNEY, Liam
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PI-0270 USN
; CURRENT APPLICATION NUMBER: US/10/415,378
; CURRENT FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: PCT/US01/46055
; PRIOR FILING DATE: 2001-10-27
; PRIOR APPLICATION NUMBER: US 60/250,790
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/252,232
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/249,661
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/247,673
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/245,904
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/243,989
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PERL Program
; SEQ ID NO 39
; LENGTH: 2235
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040014945A1 7482060CB1
US-10-415-378-39

Alignment Scores:

Pred. No.:	7,28e-259	Length:	2235
Score:	2076.50	Matches:	406
Percent Similarity:	97.83%	Conservative:	0
Best Local Similarity:	97.83%	Mismatches:	1
Query Match:	93.75%	Indels:	9
DB:	16	Gaps:	2

US-10-016-647-2 (1-425) x US-10-415-378-39 (1-2235)

Qy	1	MetThrPheGlyArgSerGlyAlaAlaSerValValLeuAsnValGlyGlyAlaArgTyr	20
Db	428	ATGACCTTCGGGCGCAGCGGGCGGCTCGTGGTGTCTGAACTGGCGCGCCCGGTAT	487
Qy	21	SerLeuSerArgGluLeuLeuLysAspPheProLeuArgArgValSerArgLeuHisGly	40
Db	488	TCGCTGTCCCGGAGCTGCTGAAGGACTTCCGCTGCGCGCGTGAAGCGGCTGCACGGC	547
Qy	41	CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu	60
Db	548	TGCCGCTCCGAGCGCGCAGCTGCTCGAGGTTGTCGACGACTACGACCGGAGCGCAACGAG	607
Qy	61	TyrPhePheAspArgHisSerGluAlaPheGlyPheIleLeuLeuTyrValArgGlyHis	80

608 TACTTCTTCAGCGGACCTCGAGGCGCTTCGGCTTCATCTCTCTACGTGCGCGCCAC 667
 Qy 81 GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100
 Db 668 GCGAAGCTGCGCTTCGCGCGGATGTGCGAGCTCTCTCTACACGAGATGATCTAC 727
 Qy 101 TrpGlyLeuGluGlyAlaHisLeuGluTyrCysGlnArgArgLeuAspArgMet 120
 Db 728 TGGGGCTGGAGCGCGGACCTCGAGTACTGCTGCCAGCGCGCTCGACACCGCATG 787
 Qy 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140
 Db 788 TCCGACACCTACACCTTCTACTCGCGCGAGCGCGCGGCTGCTGGCGCGCAGCGGCG 847
 Qy 141 ArgProGlyGlyAla-GluAlaAlaProSerArgTyrLeuGluArgMetArgArgTh 160
 Db 848 CGCCCC--GGCGCGGAGCGGCTCTCCAGCGCGCTGGAGCGCATCGCGCGGAC 904
 Qy 160 rPheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValValPh 180
 Db 905 CTTCGAGGAGCCACATC-----CTGGCTAGCGTGTGCGTGTGT 945
 Qy 180 eValIleValSerMetValValLeuGluCysAlaSerThrLeuProAspTrpArgAsnAla 200
 Db 946 CGTGATCGTGTCCATCGTGTGTGTGCGCCAGCAGCTGCGCGGCTGCGCGCAACGCGAGC 1005
 Qy 200 aAlaAspAsnArgSerLeuAspArgSerArgIleLeuAlaAlaCysIleGlyTr 220
 Db 1006 CGCGGACACCGGAGCTGTGATGACCGGAGCAGGATAATTGAAGTACTATCTGATAGTGTG 1065
 Qy 220 pPheThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGluPheVal 240
 Db 1066 GTTCACTGCGGAGTGTGATGAGTGTGATGCTCTCAAAAAACAAGTGTGAGTGTGTCAA 1125
 Qy 240 sArgProLeuAsnIleAlaSerLeuAlaIleThrProTyrTyrIleSerValLeuMe 260
 Db 1126 GAGACCCCTGAACATCATTTACTGCAATACCGCGATGATGATGATGATGATGAT 1185
 Qy 260 tThrValPheThrGlyGluAsnSerGlnLeuGlnArgAlaGlyValThrLeuArgVal 280
 Db 1186 GACAGTGTTTACAGGCGGAGACTCTCACTCCAGAGGCTGAGTCACTTGGAGGTACT 1245
 Qy 280 uArgMetMetArgIlePheThrValIleLysLeuAlaArgHisPheIleGlyLeuGluTh 300
 Db 1246 TAGAATGATGAGATTTTGGGTGATTAAGCTTGGCGGTCACTTCACTTGGTTCCTCAGAC 1305
 Qy 300 rLeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuValPheIleCy 320
 Db 1306 ACTCGGTTTGACTCTCAACAGTTGCTACCGAGAGATGTTATGTTACTTGTCTTCATTGT 1365
 Qy 320 sValAlaMetAlaIlePheSerAlaLeuSerGlnLeuGluHisGlyLeuAspLeuGl 340
 Db 1366 TGTGCGCATGGCAATCTTTAGTGCACTTTCTCAGCTTCTGAACATGGGCTGGAGCTGGA 1425
 Qy 340 uThrSerAsnLysAspPheThrSerIleProAlaAlaCysTrpTrpValIleIleSerMe 360
 Db 1426 AACATCCACACAGGACTTTTACCAGCATCTCTGCTGCTGCTGCTGGTGGTATATCTCTAT 1485
 Qy 360 tThrThrValGlyTyrGlyAspMetTyrProIleThrValProGlyArgIleLeuGlyGl 380
 Db 1486 GACTACAGTGGGTATGAGAGATATGATCTATCATCAGTGCCTGGAAGAATCTTGGAGG 1545
 Qy 380 yValCysValValSerGlyIleValLeuLeuAlaLeuProIleThrPheIleTyrHis 400
 Db 1546 AGTTTGTGTGTGAGTGAATGTTCTATTGGCATTACCTATCATCTTTATCTACCATAG 1605
 Qy 400 rPheValGlnCysTyrHisGluLeuLysPheArgSerAlaArg 414
 Db 1606 CTTTGTGAGTGTATCATGAGCTCAAGTTTATGATCTGCTAGG 1648

; Sequence 26, Application US/10199869
 ; Publication No. US20030152953A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUB
 ; FILE REFERENCE: D0161 NP
 ; CURRENT APPLICATION NUMBER: US/10/199,869
 ; CURRENT FILING DATE: 2002-07-19
 ; PRIOR APPLICATION NUMBER: US 60/306,577
 ; PRIOR FILING DATE: 2001-07-19
 ; NUMBER OF SEQ ID NOS: 90
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 26
 ; LENGTH: 594
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-199-869-26
 Alignment Scores:
 Pred. No.: 2,18e-123 Length: 594
 Score: 1028.00 Matches: 198
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 46.41% Indels: 0
 DB: 15 Gaps: 0
 US-10-016-647-2 (1-425) x US-10-199-869-26 (1-594)
 Qy 212 IleIleGluAlaIleCysIleGlyTyrPheThrAlaGluCysIleValArgPheIleVal 231
 Db 1 ATAAATTGAACCTATCTCCATGAGTGTGTTGCTTCACTCCGAGTGCATCTGAGTTCATGTC 60
 Qy 232 SerLysAsnLysCysGluPheValLysArgProLeuAsnIleLeuAspLeuLeuAlaIle 251
 Db 61 TCCAAAAACAAGTGTGAGTGTGTCAAGAGACCCCTCAACATCATCTGATTACTTGGCAATC 120
 Qy 252 ThrProTyrTyrIleSerValLeuMetThrValPheThrGlyGluAsnSerGlnLeuGln 271
 Db 121 ACGCCGTGATTACATCTCTGTGTGATGACAGTGTTCACGGCGAGAACTCTCAACTCCAG 180
 Qy 272 ArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTrpValIleLysLeu 291
 Db 181 AGGCTCGAGTCACTTGGAGTGTGTTAGATCATGAGGATTTTGGGTGATTAAAGCTT 240
 Qy 292 AlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyrArgGlu 311
 Db 241 GCCCGTCACTTCATTTGCTCTTCAGACACTCGGTTTGACTCTCAACAGCTTGTCTACCGAGAG 300
 Qy 312 MetValMetLeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeuSerGln 331
 Db 301 ATGGTTATGTTACTTGTCTTCTTATTTGTTGCCATGGCAATCTTTAGTGCACATTTCTCAG 360
 Qy 332 LeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIleProAla 351
 Db 361 CTTCTTGACATGGCTGGACCTCGAAACATCCAAACAGGACTTTTACAGCATTTCTCTGCT 420
 Qy 352 AlaCysTrpTrpValIleIleSerMetThrThrValGlyTyrGlyAspMetTyrProIle 371
 Db 421 GCCTGCTGGTGGTGTATATCTCTATGACTACAGTGGCTATGGAGATATGATATCTATC 480
 Qy 372 ThrValProGlyArgIleLeuGlyGlyValCysValValSerGlyIleValLeuLeuAla 391
 Db 481 ACAGTGCCTGGAAGAATCTTGGAGGAGTGTGTTGTGTCAGTGAATTTGTTCTATTGGCA 540
 Qy 392 LeuProIleThrPheIleTyrHisSerPheValGlnCysTyrHisGluLeuLys 409
 Db 541 TTACCTATCATCTTTATCTACCATAGCTTTGTGCGAGTGTATCATGAGCTCAAG 594
 RESULT 7
 US-09-971-392-139
 ; Sequence 139, Application US/09971392
 ; Publication No. US20030134283A1

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/009,492
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: 08/464,340
 ; FILING DATE: June 5,1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: FERRARO, GREGORY D.
 ; REGISTRATION NUMBER: 36,134
 ; REFERENCE/DOCKET NUMBER: 325800-415
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-994-1700
 ; TELEFAX: 201-994-1744
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2127 BASE PAIRS
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: SINGLE
 ; TOPOLOGY: LINEAR
 ; MOLECULE TYPE: cDNA
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-10-325-891-1

Alignment Scores:
 Pred. No.: 5,18e-100 Length: 2127
 Score: 855.50 Matches: 178
 Percent Similarity: 60.94% Conservative: 81
 Best Local Similarity: 41.88% Mismatches: 141
 Query Match: 38.62% Indels: 25
 DB: 15 Gaps: 8

US-10-016-647-2 (1-425) x US-10-325-891-1 (1-2127)

Qy 11 ValValLeuAsnValGlyGlyAlaArgTyrSerLeuSerArgGluLeuLeuLeuAspPhe 30
 Db 474 ATCATCATCAAGTACAGGCGGCACTCAAGTACTCGCTCGCTGGACACACGAGATTC 533
 Qy 31 ProLeuArgArgValSerArgLeuHisGlyCysArgSerGluArgAspValLeuVal 50
 Db 534 CGCTGACGCGCTGGCGGCGCTCAAGCGCTCAAGCTTCGACGACATCTCAACGTG 593
 Qy 51 CysAspAspTyrAspArgGluArgAsnGluTyrPhePheAspArgHisSerGluAlaPhe 70
 Db 594 TCGGATGACTACGACGTACCTGCAACGAGTCTTCCTCGACCGCAACCGGGGCGCTTC 653
 Qy 71 GlyPheLeuLeuTyrValArgGlyHisGlyLysLeuArgPheAlaProArgMetCys 90
 Db 654 GGCACATATCTGACCTTCTGCGCGCG--GGCAAGCTGCGGCTGCTGCGGAGATGTGC 710
 Qy 91 GluLeuSerPheTyrAsnGluMetIleTyrTrpGlyLeuGluGlyAlaHisLeuGluTyr 110
 Db 711 GCGCTGTCTTCCAGGAGGAGTGTGTACTGGGCGATCGCGGAGACACCTGGACGCGC 770
 Qy 111 CysCysGlnArgArgLeuAspAspArgMetSerAspThrTyrThrPheTyrSerAlaAsp 130
 Db 771 TGCTGCAAGCGCGCTACCTGCAGAGAATTGAGGAGTTGCGGAGATGTTGGAGCGGAG 830
 Qy 131 GluProGlyValLeu-----GlyArgAspGluAlaArgProGlyGlyAlaGlu 146
 Db 831 GAAGAGGACGACGCGCTGACAGCGAGGCGCCGACACGAGGCGCCGCGGAGCGGCGAG 890
 Qy 147 AlaAlaProSerArgArgTrpLeuGluArgMetArgArgThrPheGluGluProThrSer 166
 Db 891 GCGCCGCTGGGG--CGCTGATCGCGGCGACTGCGGACATGTTGGAGAGGCGGCACTCG 947
 Qy 167 SerLeuAlaAlaGlnIleLeuAlaSerValSerValPheValIleValSerMetVal 186
 Db 948 GGGCTGCTCGGCAAGGTGTTCGCTGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1007
 Qy 187 ValLeuCysAlaSerThrLeuProAspTrpArgAsnAlaAlaAlaAspAsnArg----- 204
 Db 1008 AACCTTCGCTCAGACACTTGCACGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1067
 Qy 205 SerLeuAspAspArgSerArgIleIleGluAlaIleCysIleGlyTrpPheThrAlaGlu 224

Db 1068 CAGATGTGCCAACACGCTTTCATCGTGGAGTCGCTGTGGTGGCTGGTTCCTCCCTGGAG 1127
 Qy 225 CysIleValArgPheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsn 244
 Db 1128 TTCCTCTCGGCTCATTCAGGCGCCAGCAAGTTCGCTTCTCTGGGAGCCGCTGACG 1187
 Qy 245 IleIleAspLeuLeuAlaIleThrProTyrTyrIleSerValLeuMetThr---ValPhe 263
 Db 1188 CTGATCGACCTGGTGGCCATCTCGCTACTATACAGCTGTCTGTGGAGCGGCGGCC 1247
 Qy 264 ThrGlyGlu-----AsnSerGlnLeuGlnArgAlaGlyValThrLeu 277
 Db 1248 GCAGGCGCTGCGAAGCCCGCGCGGCAACAGCTACTCTGGACAAGTGGGGCTGCTG 1307
 Qy 278 ArgValLeuArgMetMetArgIlePheTrpValIleLysLeuAlaArgHisPheIleGly 297
 Db 1308 CGCTGCTCGGCGCTGCGCACTCTGTAGTGTGCGCTGCGGCGGCACTCTCCCTGGGG 1367
 Qy 298 LeuGlnThrLeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuVal 317
 Db 1368 CTGCAGACGCTGGGCTCACGGCCGCGCTGCACCGCGAGTTCGGGCTCTCTGCTGCTC 1427
 Qy 318 PheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuGluHisGlyLeu 337
 Db 1428 TTCCTGCTGGCGCATCGCCCTTTCGCGCCCTGCTTACGTCATCGAAGACGAGATG 1487
 Qy 338 AspLeuGluThrSerAsnLysAspPheThrSerIleProAlaAlaCysTrpTrpValIle 357
 Db 1488 -----GCCGACAGCCCGAGTTCACCGACATCTCTCCCTGCTACTGCTGGGCTGTC 1538
 Qy 358 IleSerMetThrThrValGlyTyrGlyAspMetTy-ProIleThrValProGlyArgIle 377
 Db 1539 ATCACCATGACGCGGTGAGTATGGCGACATGTCCTCCAGGAGCACCCCGGCGCAGGTA 1598
 Qy 378 LeuGlyGlyValCysValValSerGlyIleValLeuLeuAlaLeuProIleThrPheIle 397
 Db 1599 GTGGCCCTGAGCAGCATCTCGAGCGCATCTCTGCTATGSCCTTCCAGTACCTCCATC 1658
 Qy 398 TyrHisSerPheValGlnCysTyrHisGluLeuLys-----Phe 410
 Db 1659 TTCACACCTTCTCCCGCTCTACCTGGAGCTCAACAGGAGCAAGAGAGGCTGATGTTTC 1718
 Qy 411 ArgSerAlaArgTyr 415
 Db 1719 CGGAGCGCGCAGTTC 1733
 RESULT 10
 US-10-101-510-628
 ; Sequence 628 Application US/10101510
 ; Publication No US20030148295A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WAN, JACKSON
 ; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
 ; FILE REFERENCE: 15117.0012
 ; CURRENT APPLICATION NUMBER: US/10/101,510
 ; PRIOR FILING DATE: 2002-03-20
 ; PRIOR FILING DATE: 2001-03-20
 ; NUMBER OF SEQ ID NOS: 805
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 628
 ; LENGTH: 2499
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-101-510-628
 Alignment Scores:
 Pred. No.: 1.64e-96 Length: 2499
 Score: 829.50 Matches: 181
 Percent Similarity: 57.49% Conservative: 80
 Best Local Similarity: 39.87% Mismatches: 138

Score: 780.50 Matches: 172
 Percent Similarity: 60.00% Conservative: 83
 Best Local Similarity: 40.47% Mismatches: 160
 Query Match: 35.24% Indels: 12
 DB: 13 Gaps: 5

US-10-016-647-2 (1-425) x US-10-435-935-10 (1-2565)

QY 1 MetThrPheGlyArgSerGlyAlaAlaSer-----ValValLeuAsnValGlyGlyAla 18
 DB 49 ATGGAGATCGTCGGCAGCAAGCGGTCTCTGGCGGGTCCGCCCTCAACGTCGGGGGGCTG 108
 QY 19 ArgTyrSerLeuSerArgGluLeuLeuLysAspPheProLeuArgArgValSerArgLeu 38
 DB 109 GCGCAGGAGGTACTCTGGGTACCTCGACCGCCCTGCCCGCCCGCAGCGCTGGCAAGCTC 168
 QY 39 HisGlyCysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArg 58
 DB 169 CGCGACTCAACACACGACGATCGTCTCGAGGTGCGGATGACTACAGCCTCGACGAC 228
 QY 59 AsnGluTyrPhePheAspArgHisSerGluAlaPheGlyPheLeuLeuTyrValArg 78
 DB 229 AACGAGTACTTCTTGACCGCCACCGCGCGCTTCACCTCCATCTCAACTTCTACCGC 288
 QY 79 GlyHisGlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMet 98
 DB 289 ---ACTGGCGGACTCCACATGATGGAGGAGATGTGCGCGCTCAGCTTCAGCCAAAGAGCTC 345
 QY 99 IleTyrTrpGlyLeuGluGlyAlaHisLeuGluTyrCysGlnArgArgLeuAspAsp 118
 DB 346 GACTACTGGGCATCGACGAGATCTACTTGGAGTCTCTGCCAGCGCCGTACACACG 405
 QY 119 ArgMetSerAspThrTyrPheTyrSerAlaAspGluProGlyValLeuGlyArgAsp 138
 DB 406 AAGAAAGACGATGA--ACGAGGAGCTCAAGCGTGAGCGCGAGACTCTACGGGAGCGG 463
 QY 139 GluAlaArgProGlyGlyAlaGluAlaProSerArgArgTyrLeuGluArgMetArg 158
 DB 464 AAGCGGAGGTTGGATTAACAGTCTCGCA--GAGAAGAGG-----AAAAAATCTCGG 516
 QY 159 ArgThrPheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerVal 178
 DB 517 GACCTACTGGAGAACCCCAATTCCTCTGTGGTGCCAAAGATCCTTGCCATAATTCACATC 576
 QY 179 ValPheValIleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArgAsn 198
 DB 577 ATGTTTCATCGTCTCTCCACCATTCCTCTGCTGCTGCTCAACACGCTGCCCTGAGCTACAGAGC 636
 QY 199 AlaAlaAlaAspAsnArgSerLeuAspAsp---ArgSerArgIleIleGluAlaIleCys 217
 DB 637 CTCGATGAGTTCGGCCAGTCCACACACACCCCAAGCTGGCCAGCTGGCGCGGTGTGC 696
 QY 218 IleGlyTrpPheThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGlu 237
 DB 697 ATCGCATGTTTCCACATGAGTACCTGTGTGAGTTCTCTCTCTCCCAAGAAAGTGAAG 756
 QY 238 PheValLysArgProLeuAsnIleIleAspLeuLeuAlaIleThrProTyrTyrIleSer 257
 DB 757 TTCCTCAAGGCCCACTCAATGCCATGACTGTGTGGCCATCTGCCATATATGTACCC 816
 QY 258 ValLeuMetThrValPheThrGlyGluAsnSerGlnLeuGlnArgAlaGlyValThrLeu 277
 DB 817 ATTTTCTCACCGAATCAACAAGAGCGTGTGTGCAATTCAGAAATGTCCGCGCGGTGTGC 876
 QY 278 ArgValLeuArgMetMetArgIlePheTrpValIleLysLeuAlaArgHisPheIleGly 297
 DB 877 CAGATCTTCGCGCATCATCGCAATTCGCGCATCTTAAGCTTGACGCGCATTCACACTGC 936
 QY 298 LeuGlnThrLeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuVal 317
 DB 937 CTCAGTCTCTGGGTCTTCACTTGGGAGGAGCTACATGAGTTGGGTCTGCTCATCCTC 996
 QY 318 PheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeuGluHisGlyLeu 337

DB 997 TTCCTTGCCATGGGCATTATGATCTTCTCAGCCTTGTCTTCTTGTGAGAAGGATGAG 1056
 QY 338 AspLeuGluThrSerAsnLysAspPheThrSerIleProAlaAlaCysTrpTrpValIle 357
 DB 1057 GAC-----GACACCAAGTTCAAAGCATCCAGCCCTCTTCTGTGGTGGGCACC 1104
 QY 358 IleSerMetThrThrValGlyTyrGlyAspMetTyrProIleThrValProGlyArgIle 377
 DB 1105 ATCACCATGACTACTGTTGGTATGGAGACATCTACCCCAAGACTCTCTCTGGGGAAAT 1164
 QY 378 LeuGlyGlyValCysValValSerGlyIleValLeuLeuAlaLeuProIleThrPheIle 397
 DB 1165 GTTGGGGAGCTGCTGCATTCGAGGATGCTGATGCTCTTCCCATCCCATCATC 1224
 QY 398 TyrHisSerPheValGlnCysTyrHisGluLeuLysPheArgSerAlaArgTyrSerArg 417
 DB 1225 GTCAATTAATCTCTAGTTCTATAAGGACGACAGAGACAGGAAAGCAATCAACCG 1284
 QY 418 SerLeuSerThrGlu 422
 DB 1285 CGAGAGGCTCTGGAG 1299

RESULT 12
 US-10-199-869-27
 ; Sequence 27, Application US/10199869
 ; Publication No. US20030152953A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUB
 ; FILE REFERENCE: D0161 NP
 ; CURRENT APPLICATION NUMBER: US/10/199,869
 ; CURRENT FILING DATE: 2002-07-19
 ; PRIOR APPLICATION NUMBER: US 60/306,577
 ; PRIOR FILING DATE: 2001-07-19
 ; NUMBER OF SEQ ID NOS: 90
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 27
 ; LENGTH: 417
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-199-869-27

Alignment Scores:
 Pred. No.: 5,06e-84 Length: 417
 Score: 723.50 Matches: 138
 Percent Similarity: 98.57% Conservative: 0
 Best Local Similarity: 98.57% Mismatches: 0
 Query Match: 32.66% Indels: 2
 DB: 15 Gaps: 1

US-10-016-647-2 (1-425) x US-10-199-869-27 (1-417)

QY 11 ValValLeuAsnValGlyGlyAlaArgTyrSerLeuSerArgGluLeuLysAspPhe 30
 DB 1 GTGGTGTGAACGTGGCGCGCGCGGTATTCGTCTCCCGGAGCTGCTGAAGGACTTC 60
 QY 31 ProLeuArgArgValSerArgLeuHisGlyCysArgSerGluArgAspValLeuGluVal 50
 DB 61 CCCTGCGCGCGGTGAGCGCGCTGCACGCGCTCCGCTCCGAGCGCAGCTGCTCGAGGTG 120
 QY 51 CysAspAspTyrAspArgGluArgAsnGluTyrPhePheAspArgHisSerGluAlaPhe 70
 DB 121 TGGGACGACTACGACCGCGAGCGCAACGAGTACTTCTCGACCGGCACTCGGAGGCTTC 180
 QY 71 GlyPheIleLeuLeuTyrValArgGlyHisGlyLysLeuArgPheAlaProArgMetCys 90
 DB 181 GGCTTTCATCTGCTACGTGCGCGCGCCACGCAAGCTGCGCTTCGCGCGCGCATGTGC 240
 QY 91 GluLeuSerPheTyrAsnGluMetIleTyrTrpGlyLeuGluGlyAlaHisLeuGluTyr 110
 DB 241 GAGCTCTCTTACAAACGAGATGATCTACTGGGGCTTGAGGCGCGGACCTCGAGTAC 300

US-10-435-935-2
 ; Sequence 2, Application US/10435935
 ; Publication No. US20040038890A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aiyar, Jayashree
 ; Kang, Jiesheng
 ; TITLE OF INVENTION: HUMAN VOLTAGE-GATED POTASSIUM
 ; CHANNEL SUBUNIT
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ZENECA Pharmaceuticals, Inc.
 ; STREET: 1800 Concord Pike
 ; CITY: Wilmington
 ; STATE: DE
 ; COUNTRY: USA
 ; ZIP: 19850-5437
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/435,935
 ; FILING DATE: 12-May-2003
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/074,878
 ; FILING DATE: 08-MAY-1998
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Higgins, Patrick H
 ; REGISTRATION NUMBER: 39,709
 ; REFERENCE/DOCKET NUMBER: PHM.70310
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 302.886.4889
 ; TELEFAX: 302.886.8221
 ; TELEX: <Unknown>
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1476 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: cDNA
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-435-935-2

Alignment Scores:
 Pred. No.: 3,71e-78 Length: 1476
 Score: 685.50 Matches: 157
 Percent Similarity: 52.9% Conservative: 91
 Best Local Similarity: 33.5% Mismatches: 155
 Query Match: 30.9% Indels: 65
 DB: 13 Gaps: 14

US-10-016-647-2 (1-425) x US-10-435-935-2 (1-1476)

QY 1 MetThrPheGly-----ArgSerGlyAlaAlaSer-----ValValLeuAsn 14
 DB 1 ATGGTGTTGGTGAGTTTTCATCGCCCTGGACAGACGAGGAACCTGTCAACCTGAT 60
 QY 15 ValGlyGlyAlaArgTyrSerLeuSerArgGluLeuLeuLysAspPheProLeuArg 34
 DB 61 GTGGGGGGCTTTAAGCAGTCTGTGACCAAAAGCACCCTCCTCGGTTTCCTCACACCAGA 120
 QY 35 ValSerArgLeuHisGlyCysArgSerGluArgAspValLeuGluValCysAspTyr 54
 DB 121 CTGGGAAGCTGCTTACTTGGCAATCTGAAGAGGCCATTCTGGAGCTGTGATATTAC 180
 QY 55 AspArgGluArgAsnGluTyrPhePheAspArgHisSerGluAlaPheGlyPheLeu 74
 DB 181 AGTGTGGCCGATAAGGAATACTACTTGTATCGAATCCCTCCTTGTTCAGATATGTTTG 240
 QY 75 LeuTyrValArgGlyHisGlyLysLeuArgPheAlaProArgMetCysGluLeuSerPhe 94

DB 241 AATTTTATTAC---ACGGGGAAGCTGCATGTATGGAGGAGCTGTGCGTATTCTCATTC 297
 QY 95 TyrAsnGluMetIleTyrTrpGlyLeuGluGlyAlaHisLeuGluTyrCysCysGlnArg 114
 DB 298 TGCAGGAGATCAGTACTGGGCGATCAACAGAGCTTTCATTGATTCCTGCTGCACCAAT 357
 QY 115 ArgLeu-----AspAspArgMetSerAsp 122
 DB 358 CGCTACAGGAACGCAAGGAGGAAACACACAGAGGAGCTGGGACCCAGAAAGCCATGAT 417
 QY 123 ThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArg----- 137
 DB 418 GTGAGTACCGACTCCCTCGTTTGAAGAGTCTCTCTGTTTGAAGAAGAGCTGGAGAAGTTT 477
 QY 138 AspGluAlaArgProGlyGlyAlaGluAlaAlaProSerArgArgTrpLeuGluArgMet 157
 DB 478 GACACACTCGGATTGTGTGCTCAGCTCGG-----AAGAAATCTGGATTAGA----- 522
 QY 158 ArgArgThrPheGluGluProThrSerSerLeuAlaAlaGluLeuLeuAlaSerValSer 177
 DB 523 -----ATGGAGAATCCAGCGTACTCGCTGCTGCTAAGCTTATCGCTATCTCCTCC 573
 QY 178 ValValPheValIleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArg 197
 DB 574 TTGAGCGTGTGCTGGCTCCATCGTGGCCATGTGCTTACAGCATGTCCGAGTTCACG 633
 QY 198 AsnAlaAlaAlaAspAsnArgSerLeuAspAspArgSerArgIleleGluAlaIle--- 216
 DB 634 AAT-----GAGGATGAGAGAAGTGATGAT-----CCGGTGTGGAAGAGGTGGAG 678
 QY 217 -----CysIleGlyTrpPheThrAlaGluCysIleValArgPheIleValSerLysAsn 234
 DB 679 ATCGGTGTCATTCCCTGTTTACCGGGGAGCTGCGCTCGCGTGGCTCGCTCCTTGT 738
 QY 235 LysCysGluPheValLysArgProLeuAsnIleIleAspLeuLeuAlaIleThrProTyr 254
 DB 739 CAAAGAAGATTCTGGAAACCCCTCGAACATCATTTGACTTCTCTATTATTCCTTC 798
 QY 255 TyrIleSerValLeuMetThrValPheThrGlyGluAsnSerGlnLeuGluArgAlaGly 274
 DB 799 TATGCCACGTTGCTGTAGACACCAAGGAGGAGAGAGTGGATATTGAGAACATGGGC 858
 QY 275 ValThrLeuArgValLeuArgMetMetArgIlePheTrpValIleLysLeuAlaArgHis 294
 DB 859 AAGGTGTCAGATCTACGGCTTATGAGGATTTTCGGAATTTCTAAAGCTTGCCTGCGCAC 918
 QY 295 PheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMet 314
 DB 919 TCGGTAGGACTTCGGTCTCTAGTGCACACTGACACACAGCTACCATGAAGTTGGCGCT 978
 QY 315 LeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuGlu 334
 DB 979 CTGCTTCTCTCTCTCTGTCGTCATTTCCATTTTCTCTGCTTATCTACTCCGTGGAG 1038
 QY 335 HisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIleProAlaAlaCysTrp 354
 DB 1039 AAA-----GATGACACACATCCAGC-----CTCACCAGCATCCCATCTGCTGTGG 1086
 QY 355 TrpValIleIleSerMetThrThrValGlyTyrGlyAspMetTyrProIleThrValPro 374
 DB 1087 TGGGCCACCATCAGCATGACAATCTGGGTATGGAGACACCCACCCCGCTCACCTTGGCG 1146
 QY 375 GlyArgIleLeuGlyGlyValCysValValSerGlyIleValLeuLeuAlaLeuProIle 394
 DB 1147 GGAAAGCTCATCGCCAGCACATCATCTGTGGCATCTTGTGGTGGCGCTTCCCATC 1206
 QY 395 ThrPheIleTyrHisSerPheValGlnCysTyr----- 405
 DB 1207 ACCATCATCTTCAACAAGTTTCCAACTACTACAGAAAGCAAGGACATGATGTGGAC 1266
 QY 406 -----HisGluLeuLysPheArgSerAlaArg--- 414


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QY 395 ThrPheIleTyrHisSerPheValGlnCysTyr----- 405
Db ||| |||:|:|:| |||:|:| |||:|:|
1659 ACCATCATCTTCACACAAGTTTCCAAAGTACTACCAAGCAAAAGGACATTGATGTGGAC 1718
QY 406 -----HisGluLeuLysPheArgSerAlaArg--- 414
Db ||| |||:|:|:| |||:|:| |||:|:|
1719 CAGTGCAGTGAGGATGCCACGAGAGAGTGTCTATGAGCTACCTTACTTTACATTAGGAT 1778
QY 415 ---TyrSerArgSerLeuSerThr 421
Db ||| |||:|:|:| |||:|:| |||:|:|
1779 ATATATGCACAGCGGATGCACACC 1802
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Search completed: April 19, 2004, 16:57:04
Job time : 640 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 19, 2004, 12:51:52 ; Search time 4330 Seconds
(without alignments)
3453.603 Million cell updates/sec

Title: US-10-016-647-2

Perfect score: 22.15

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Delop 6.0 , Delext 7.0	

Searched: 37577330 seqs, 17593059518 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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84:	/cgn2_6/ptodata/2/pna/US6028 COMB.seq:
85:	/cgn2_6/ptodata/2/pna/US6029 COMB.seq:
86:	/cgn2_6/ptodata/2/pna/US6030 COMB.seq:
87:	/cgn2_6/ptodata/2/pna/US6031 COMB.seq:
88:	/cgn2_6/ptodata/2/pna/US6032 COMB.seq:
89:	/cgn2_6/ptodata/2/pna/US6033 COMB.seq:
90:	/cgn2_6/ptodata/2/pna/US6034 COMB.seq:
91:	/cgn2_6/ptodata/2/pna/US6035 COMB.seq:
92:	/cgn2_6/ptodata/2/pna/US6036 COMB.seq:
93:	/cgn2_6/ptodata/2/pna/US6037 COMB.seq:
94:	/cgn2_6/ptodata/2/pna/US6038 COMB.seq:
95:	/cgn2_6/ptodata/2/pna/US6039 COMB.seq:
96:	/cgn2_6/ptodata/2/pna/US6040 COMB.seq:
97:	/cgn2_6/ptodata/2/pna/US6041 COMB.seq:
98:	/cgn2_6/ptodata/2/pna/US6042 COMB.seq:
99:	/cgn2_6/ptodata/2/pna/US6043 COMB.seq:
100:	/cgn2_6/ptodata/2/pna/US6044 COMB.seq:
101:	/cgn2_6/ptodata/2/pna/US6045 COMB.seq:

Qy	241	ArgProLeuAsnIleIleAspLeuLeuAlaIleThrProTyrTyrIleSerValLeuMet	260
Db	721	AGACCCCTGAACATCATTTGATTTACTGGCAATCAAGCGTATTACATCTCTGTGTGATG	780
Qy	261	ThrValPheThrGlyGluAsnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLeu	280
Db	781	ACAGTGTTTACAGCGGAGAACTCTCACTCCAGAGGCTGGAGTCACCTTGAGGGTACTT	840
Qy	281	ArgMetMetArgIlePheTrpValIleIleLysLeuAlaArgHisPheIleGlyLeuGlnThr	300
Db	841	AGAATGATGAGGATTTTGTGGTGATTAAGCTTCGCCGTCACTTCATTGGTCTTCAGACA	900
Qy	301	LeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuValPheIleCys	320
Db	901	CTCGTTTGACTCTCAACAGTTGCTACCGAGAGATGGTATGTATTACTTGTCTTCATTGT	960
Qy	321	ValAlaMetAlaIlePheSerAlaLeuSerGlnLeuGluHisGlyLeuAspLeuGlu	340
Db	961	GTTCCCATGGCAATCTTTAGTGCACATTTCTCAGCTTCTTGAAACATGGGCTGGACCTGGAA	1020
Qy	341	ThrSerAsnLysAspPheThrSerIleProAlaAlaCysTrpValIleIleSerMet	360
Db	1021	ACATCCAAACAGACTTTACAGCATTCCTGCTGCTGGTGGGTGATTATCTCTATG	1080
Qy	361	ThrThrValGlyTyrGlyAspMetTyrProIleThrValProGlyArgIleLeuGlyCly	380
Db	1081	ACTACAGTTGGCTATGGAGATATGATCTCTATCAGTCGCTGGAAGAATTCCTGGAGGA	1140
Qy	381	ValCysValValSerGlyVileValLeuLeuAlaLeuProIleThrPheIleTyrHisSer	400
Db	1141	GTITGTGTTGTCACTGGNAITGTTCTATTGGCATTACCTATCATCTTTTATCTACCATAGC	1200
Qy	401	PheValGlnCysTyrHisGluLeuLysPheArgSerAlaArgTyrSerArgSerLeuSer	420
Db	1201	TTTGTGCAGTGTTATCATGAGCTCAAGTTTAGATCTGCTAGCTATAGGAGGCTCTCC	1260
Qy	421	ThrGluPheLeuAsn	425
Db	1261	ACTGAATTCCTGAAT	1275

RESULT 2
 US-10-016-647-3
 ; Sequence 3, Application US/10016647
 ; GENERAL INFORMATION:
 ; APPLICANT: Friddle, Carl Johan
 ; APPLICANT: Hilbun, Erin
 ; APPLICANT: Turner, C. Alexander Jr.
 ; TITLE OF INVENTION: Novel Human Ion Channel Protein and Polynucleotides Encoding the
 ; FILE OF INVENTION: LEX-0284-USA
 ; CURRENT APPLICATION NUMBER: US/10/016,647
 ; CURRENT FILING DATE: 2001-12-10
 ; PRIOR APPLICATION NUMBER: US 60/257,932
 ; PRIOR FILING DATE: 2000-12-20
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 1844
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 ; US-10-016-647-3

457	Db	ATGACCTTCGGGCGCAGCGGGCGGCTCGGTGGTCTGAACGTGGCGCGCCCGGTAT	516
21	Qy	SerieserArgGluLeuLeuLysAspPheProLeuArgArgValSerArgLeuHisGly	40
517	Db	TGCGTCTCCGGGAGCTGCTGAAGGACTTCCCGCTGCGCGCGGTGAGCCGGCTGCACGGC	576
41	Qy	CysArgSerGluArqAspValLeuGluValCysAspAspTyrAspArgGluArqAsnGlu	60
577	Db	TGCGGCTCCAGCGCGACGTGCTCGAGGTGTGCAGAGCTACGACCGCGAGCGGACGAG	636
61	Qy	TyrPhePheAspArgHisSerGluAlaPheGlyPheIleLeuLeuTyrValArgGlyHis	80
637	Db	TACTTCTTCGACGGCAGCTCGGAGGCTTCGGCTTCATCTGCTCTACGTGCGCGGCAC	696
81	Qy	GlyLysLeuArgPheAlaProArqMetCysGluLeuSerPheTyrAsnGluMetIleTyr	100
697	Db	GGCAAGCTGGCTTCGCGCGCGGAGTGTGCGAGCTTCCTTCTACAACGAGATGATCTAC	756
101	Qy	TrpGlyLeuGluGlyAlaHisLeuLeuGluTyrCysCysGlnArgArgLeuAspArgMet	120
757	Db	TGGGGCTTGAGGGCGCGCACCTCGAGTACTGTGTCAGCGCGGCTCGACGACGGCATG	816
121	Qy	SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArcAspGluAla	140
817	Db	TCCGACACCTTACACCTTCTACTCGGCGCAGCGCGGGCGTGTGGGCCCGCGAGGCG	876
141	Qy	ArgProGlyGlyAlaGluAlaAlaProSerArgTrpLeuGluArqMetArgThr	160
877	Db	CGCCCCGGCGGCGGAGGCGGCTCCCTCCAGGCGCTGGTGGAGCGCATGCGGCGGACC	936
161	Qy	PheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValValPhe	180
937	Db	TTCGAGAGCGCCACGCTGCTGCGTCGCGCGCGCAGATCTGTGCTAGCTGTGCGTGGTTC	996
181	Qy	ValIleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArgAsnAlaAla	200
997	Db	GTGATCGTGTCATGGTGGTGTGTGCGCGCAGCACGTTGCGCGACTGGCGCAACGCGACC	1056
201	Qy	AlaAspAsnArgSerLeuAspAspArgSerArgIleIleGluAlaIleCysIleGlyTrp	220
1057	Db	GCGCAACACCGCAGCTTGAGTATCGGAGCAGAGATAATTGAAGCTATCTGCTAGGTGG	1116
221	Qy	PheThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGluPheValLys	240
1117	Db	TTCACTGCCGAGTGTCATGTCGTGAGTTCAATGTCTCCAAAAACAAGTGTAGTTTGTCAAG	1176
241	Qy	ArgProLeuAsnIleIleAspLeuLeuAlaIleThrProTyrTyrIleSerValLeuMet	260
1177	Db	AGACCCCTGAACATCATTGATTTACTTGGCAATCAGCGCGTATTACATCTCTGTGTGATG	1236
261	Qy	ThrValPheThrGlyGluAsnSerGlnLeuGluArgAlaGlyValThrLeuArgValLeu	280
1237	Db	ACAGTGTTTACGGCGAGAACTCTCACTCCAGAGGCTGGAGTCACCTTGAGGTCATT	1296
281	Qy	ArgMetMetArgIlePheTrpValIleLysLeuAlaArgHisPheIleGlyLeuGlnThr	300
1297	Db	AGAATGATGAGGATTTTTCGGTGATTAAAGCTTCGCCGTCACTTCATTTGTGCTTCAGACA	1356
301	Qy	LeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuValPheIleCys	320
1357	Db	CTCGTGTGACTCTCAACAGTTGCTACCGAGAGATGGTTATGTATTCTTCTTCATTGT	1416
321	Qy	ValAlaMetAlaIlePheSerAlaLeuSerSerGlnLeuLeuGluHisGlyLeuAspLeuGlu	340
1417	Db	GTTCGCATGCAATCTTTAGTGACCTTTCTCAGCTTCTTGAAACATGGGCTGGACCTGAA	1476
341	Qy	ThrSerAsnLysAspPheThrSerIleProAlaAlaCysTrpTrpValIleIleSerMet	360
1477	Db	ACATCCACAGAGACTTACACAGATTCTCTGCTGCTGCTGGTGGGTGATTACTCTATG	1536
361	Qy	ThrThrValGlyTyrGlyAspMetTyrProIleThrValProGlyArgIleLeuGlyGly	380

; PRIOR APPLICATION NUMBER: US 60/306,577
; PRIOR FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 3215
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1275)
; OTHER INFORMATION:
US-10-199-869-1

Alignment Scores:

Pred. No.: 5,62e-218 Length: 3215
Score: 2209.00 Matches: 424
Percent Similarity: 99.76% Conservative: 0
Best Local Similarity: 99.76% Mismatches: 1
Query Match: 99.73% Indels: 0
DB: 46 Gaps: 0

US-10-016-647-2 (1-425) x US-10-199-869-1 (1-3215)

QY 1 MetThrPheGlyArgSerGlyAlaAlaSerValValLeuAsnValGlyAlaArgTyr 20
Db 1 ATGACCTTCGGCGGAGCGGGCGGCTCGGTGGTGTCTGAACGTGGCGGCGCCGGTAT 60
QY 21 SerLeuSerArgGluLeuLeuLysaspPheProLeuArgArgValSerArgLeuHisGly 40
Db 61 TCGCTGTCCGGGAGCTGTGAAGACTTCCCGCTGCGCGGCTGAGCGGCTGACCGGC 120
QY 41 CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu 60
Db 121 TCCCGCTCCAGCGGAGCGCTGTCTGAGGTGTGCGAGCTACGACCGGAGCGCAACGAG 180
QY 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheLeuLeuTyrValArgGlyHis 80
Db 181 TACTTCTTCGACCGGCACCTCGGAGGCTTCGGGCTTCATCTCTCTAGCTGCGCGCCAC 240
QY 81 GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100
Db 241 GGCAGCTCGGCTTCGCGCGGAGTGTGCGAGCTCTCTCTTCAACGAGATGATCTAC 300
QY 101 TrpGlyLeuGluGlyAlaHisLeuGluTyrCysGlnArgArgLeuAspArgMet 120
Db 301 TGGGGCTCGAGGCGCGCACCTCGAGTACTGCTGCCAGCGCGCTCGACGACGCGATG 360
QY 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140
Db 361 TCCGACACCTACACCTTCTACTCGGCGGAGCGCGGCGTCTGGCGCGGAGCGG 420
QY 141 ArgProGlyGlyAlaGluAlaProSerArgArgTyrLeuGluArgMetArgArgTyr 160
Db 421 CGCCCGCGGCGGCGGAGCGGCTCCCTCCAGCGCGCTGGCTGAGCGCATCGCGCGGACC 480
QY 161 PheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValPhe 180
Db 481 TTCGAGGACCCACCGTCTGCTGCGCGGAGCGGAGTCTGGTGTGTGCTGCTGTTTC 540
QY 181 ValIleValSerMetValValLeuCysAlaSerThrLeuProAspTyrArgAsnAlaAla 200
Db 541 GTGATCGTCTCATGTTGTTGTGCGGACGACAGTGTGCCGACTGGCGCAGCCAGCC 600
QY 201 AlaAspAsnArgSerLeuAspArgSerArgIleIleGluAlaIleCysIleGlyTyr 220
Db 601 GCCGACACCGGAGCGCTGATGACCGGAGCAGGATAATGAAGCTATCTGCATAGTTGG 660
QY 221 PheThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGluPheValLys 240
Db 661 TTCACGCGGAGTGCATGCTGAGGTTCATGTCTCCAAAAACAAGTGTGAGTTGTCAAG 720
QY 241 ArgProLeuAsnIleIleAspLeuLeuAlaIleThrProTyrTyrIleSerValLeuMet 260

Db 721 AGACCCCTGAACATCATTTACTGCAATCAAGCGGTATTACATCTCTGTGTGATG 780
QY 261 ThrValPheThrGlyGluAsnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLeu 280
Db 781 ACAGTGTTCACAGCGGAGAACTCTCACTCCAGAGGCTGGAGTCACTTGAGGCTACTT 840
QY 281 ArgMetMetArgIlePheTyrValIleLysLeuAlaArgHisPheIleGlyLeuGlnThr 300
Db 841 AGAATGATGAGGATTTTGGGTGATTAAAGCTTGGCGTCACTTCATTTGCTTCAGATA 900
QY 301 LeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuValPheIleCys 320
Db 901 CTCGGTTTGACTCTCAACCGTTGCTACCGAGAGATGGTATTGTTACTTGTCTTCATTGT 960
QY 321 ValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeuGlu 340
Db 961 GTTCCCATGGCAATCTTTAGTGCACTTCTCAGCTTCTTGAACATGGCTGGACCTGAA 1020
QY 341 ThrSerAsnLysAspPheThrSerIleProAlaAlaCysTrpTrpValIleIleSerMet 360
Db 1021 ACATCCAAACAGGACTTTACAGCATTCCTGCTGCTGCTGGTGGTATTATCTCTATG 1080
QY 361 ThrThrValGlyTyrGlyAspMetTyrProIleThrValProGlyArgIleLeuGlyGly 380
Db 1081 ACTACAGTTGGCTATGGAGATATGTACTCTATCACAGTGCCTGGAAGAAATCTTGGAGGA 1140
QY 381 ValCysValValSerGlyIleValLeuLeuAlaLeuProIleThrPheIleTyrHisSer 400
Db 1141 GTTTGTGTGTGAGTGGAAATGTTTCTATTGGCAATACCTATCACTTTTATCTACCATAGC 1200
QY 401 PheValGlnCysTyrHisGluLeuLysPheArgSerAlaArgTyrSerArgSerLeuSer 420
Db 1201 TTTGTGAGTGTATCATGAGCTCAAGTTAGATCTGCTAGGTATAGTAGGAGCTCTCC 1260
QY 421 ThrGluPheLeuAsn 425
Db 1261 ACTGAATTCCTGAAT 1275
RESULT 5
US-60-306-577-1
; Sequence 1, Application US/60306577
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUB
; FILE REFERENCE: K+alpha2
; CURRENT APPLICATION NUMBER: US/60/306,577
; CURRENT FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3215
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1275)
US-60-306-577-1
Alignment Scores:
Pred. No.: 5,62e-218 Length: 3215
Score: 2209.00 Matches: 424
Percent Similarity: 99.76% Conservative: 0
Best Local Similarity: 99.76% Mismatches: 1
Query Match: 99.73% Indels: 0
DB: 87 Gaps: 0
US-10-016-647-2 (1-425) x US-60-306-577-1 (1-3215)
QY 1 MetThrPheGlyArgSerGlyAlaAlaSerValValLeuAsnValGlyAlaArgTyr 20
Db 1 ATGACCTTCGGCGGAGCGGGCGGCTCGGTGGTGTCTGAACGTGGCGGCGCCGGTAT 60

Qy 41 CysArgSerGluArgAspValLeuGluValCysAspTyrAspArgGluArgAsnGlu 60
 Db 547 TCGCGCTCGAGCGGCGAGCTGCTCGAGGTGTGCGAGCTACGACCGCGAGCGAAGCAG 606
 Qy 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheLeuLeuTyrValArgGlyHis 80
 Db 607 TACTTCTTCGACCGGCGACTCGAGGCGCTTCGCTCTTCCTGCTCTAGCTGCGGCGCAC 666
 Qy 81 GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100
 Db 667 GSCAAGCTGCGCTTCGCGCGCGAGTGTGCGAGCTCTCTTCTACAACAGATGATCTAC 726
 Qy 101 TrpGlyLeuGluGlyAlaHisLeuGluTyrCysGlnArgArgLeuAspArgMet 120
 Db 727 TGGGCGCTGAGGCGCGCGACCTCGAGTACTGCTGCCAGCGCGCTCGACGCGCATG 786
 Qy 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140
 Db 787 TCCGACACCTACCTTCTACTTCGCGCGAGCGCGGCTGCTGGGCGCGAGCGCG 846
 Qy 141 ArgProGlyGlyAlaGluAlaProSerArgArgTyrLeuGluArgMetArgThr 160
 Db 847 CGCGCGCGCGCGCGCGCTCCCTCCAGGCGCTGCTGGAGCGATCGCGCGGAC 906
 Qy 161 PheGluGluProThrSerSerLeuAlaGlnIleLeuAlaSerValSerValValPhe 180
 Db 907 TTCGAGGAGCGCGCGCTGCTGCTGCGCGCGAGATCTTGGCTAGCGTGTGCTGTG 966
 Qy 181 ValIleValSerMetValValLeuCysAlaSerThrLeuProAspTyrArgAsnAlaAla 200
 Db 967 GTGATCGTGTCCATGCTGTGTGTGCGCGAGACGTTGCGCGACTGCGCGCAAGCGAC 1026
 Qy 201 AlaAspAsnArgSerLeuAspAspArgSerArg----- 211
 Db 1027 GCGCAACCGCGAGCTGTGATACCGAGCGAGGTACTCGCGCGCGCTGGAGGAGCGCC 1086
 Qy 212 -----IleIleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleValArgPhe 229
 Db 1087 TCCGGGATAATTGAAGCTATCTGCATAGTTGGTTCACTGCCGAGTGCTGTCGAGGTTC 1146
 Qy 230 IleValSerLysAsnLysCysGluPheValLysArgProLeuAsnIleIleAspLeuLeu 249
 Db 1147 ATTGTCTCCAAACAAAGTGTGAGTTGTCAAGAGACCCCTGAACATCATGATTACTG 1206
 Qy 250 AlaIleThrProTyrTyrIleSerValLeuMetThrValPheThrGlyGluAsnSerGln 269
 Db 1207 GCAATCACGCGGTATATCATCTCTGTGTGATGACAGTGTTCAGGCGAGACTCTCAA 1266
 Qy 270 LeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTrpValIle 289
 Db 1267 CTCAGAGGCGTGGAGTCACCTTGAGGTACTTAGAATGATGAGGATTTTGGGTGATT 1326
 Qy 290 LysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyr 309
 Db 1327 AAGCTTGCGCGTCACTTCATTTGGTCTTCAGACACTCGGTTTGACTCTCAACAGTGTCTAC 1386
 Qy 310 ArgGluMetValMetLeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeu 329
 Db 1387 CGAGAGATGGTTATGTTACTTCTTCTTCTTCTTGTGTTGCTGCAATCTTTAGTGCATT 1446
 Qy 330 SerGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIle 349
 Db 1447 TCTAGCTTCTTGAACATGGGTGACCTGGAACATCCAAACAGAGCTTTTACCAGCAT 1506
 Qy 350 ProAlaAlaCysTyrTrpValIleIleSerMetThrThrValGlyTyrGlyAspMetTyr 369
 Db 1507 CTGTCTGCTGCTGTGGTGGTATATCTATGATCATCAGTTGGCTATGGAGATATGAT 1566
 Qy 370 ProfileThrValProGlyArgIleLeuGlyValCysValValSerGlyIleValLeu 389
 Db 1567 CCTATCACAGTCCCTCGAAGATTTCTTGAGGAGTTTGTGTGTGTCAGTGAATTTGTTCTA 1626

Qy 390 LeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCysTyrHisGluLeuLys 409
 Db 1627 TTGGCATTACTATCACTTTTATCTACCATAGCTTTGTGCGAGTGTATCATGAGCTCAAG 1686
 Qy 410 PheArgSerAlaArgTyrSerArgSerLeuSerThrGluPheLeuAsn 425
 Db 1687 TTTAGATCTCTAGTATAGTAGAGCCTCTCCACTGAAATTCCTGAAT 1734
 RESULT 7
 PCT-US03-28227-1172
 ; Sequence 1172, Application PC/TUS0328227
 ; GENERAL INFORMATION:
 ; APPLICANT: INCYTE CORPORATION; SCHMIDT, Jeanette P.;
 ; APPLICANT: WRIGHT, Rachel J.; BRUNS, Christopher M.;
 ; APPLICANT: MARJANOVIC, Mirjana M.; SHEN, Fan;
 ; APPLICANT: HARTSHORNE, Toinette A.; SUCHOROLSKI, Martin;
 ; APPLICANT: ALTUS, Christina M.; PITTS, Steven J.;
 ; APPLICANT: ELDER, Linda V.; MOONEY, Elizabeth M.;
 ; APPLICANT: DELEGANE, Angelo M.; PANESAR, Iqbal S.;
 ; APPLICANT: BANVILLE, Steven C.; REDDY, Thirupathi P.;
 ; APPLICANT: STEVENS, Kristian A.; BLANCHARD, John L.;
 ; APPLICANT: PANZER, Scott R.; WANG, Xinhao;
 ; APPLICANT: AU, Alan P.; GERSTIN, Edward H., Jr.;
 ; APPLICANT: PERALTA, Careyna H.; ANDERSON, Scott E.;
 ; APPLICANT: RIAUX, Pierre; SHEN, Edward J.;
 ; APPLICANT: WU, Mingham C.; STUVE, Laura L.;
 ; APPLICANT: LAGACE, Robert E.; SPIRO, Peter A.;
 ; APPLICANT: STEWART, Elizabeth A.; WINGROVE, James A.;
 ; APPLICANT: VITT, Ursula A.; KIRTON, Edward;
 ; APPLICANT: XU, Yuming; KWONG, Mary;
 ; APPLICANT: POLICKY, Jennifer L.; HURWITZ, Bonnie L.;
 ; APPLICANT: MA, Yan; JACKSON, Jennifer L.;
 ; APPLICANT: GIETZEN, Darryl; PATURY, Srikanth;
 ; APPLICANT: SHI, Xiaobing; SUAREZ, Charlyn J.
 ; TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: PN-0100 PCT
 ; CURRENT APPLICATION NUMBER: PCT/US03/28227
 ; CURRENT FILING DATE: 2003-09-12
 ; PRIOR APPLICATION NUMBER: US 60/410,260
 ; PRIOR FILING DATE: 2002-09-12
 ; PRIOR APPLICATION NUMBER: US 60/410,259
 ; PRIOR FILING DATE: 2002-09-12
 ; NUMBER OF SEQ ID NOS: 5444
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 1172
 ; LENGTH: 2405
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Incyte ID No: 937585.PT34
 PCT-US03-28227-1172
 Alignment Scores:
 Pred. No.: 1,94e-207 Length: 2405
 Score: 2106.00 Matches: 407
 Percent Similarity: 98.31% Conservative: 0
 Best Local Similarity: 98.31% Mismatches: 1
 Query Match: 95.08% Indels: 7
 DB: 1 Gaps: 1
 US-10-016-647-2 (1-425) x PCT-US03-28227-1172 (1-2405)
 Qy 1 MetThrPheGlyArgSerGlyAlaAlaSerValValLeuAsnValGlyAlaArgTyr 20
 Db 597 ATGACCTTCGGCGCAGCGGCGGCTCGGTGGTGTGAACGTGGCGCGCGCGGTAT 656
 Qy 21 SerLeuSerArgGluLeuLeuLysAspPheProLeuArgValSerArgLeuHisGly 40
 Db 657 TCGCTGCCGCGAGCTGCTGAAGGACTTCCCTCGCGCGCTGAGCGCGCTGCACGGC 716
 Qy 41 CysArgSerGluArgAspValLeuGluValCysAspTyrAspArgGluArgAsnGlu 60

Db 717 TGCGCTCCGAGCGGACGCTGCTCGAGGTGTCGACGACTACGACCGCGAGCGCAACGAG 776
 Qy 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheLeuLeuTyrValArgGlyHis 80
 Db 777 TACTTTCTTGACCGGACCTCGAGGGCTTCGGGCTTCATCTGCTCTAGTGGCGGCCAC 836
 Qy 81 GlyLeuLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100
 Db 837 GCGAAGCTGCGCTTCGCGCGCGGATGTCGAGCTCTCTCTACAAAGAGATGATCTAC 896
 Qy 101 TrpGlyLeuGluAlaHisIleGluTyrCysGlnArgArgLeuAspArgMet 120
 Db 897 TGGGGCTGAGGGCGGCGACCTCGAGTACTGTCGCGCGGCTTCGACGACCGCATG 956
 Qy 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140
 Db 957 TCCGACACCTACACCTTCTACTCGGCGGACGCGCGGCTGCTGGCGCGCACGAGCG 1016
 Qy 141 ArgProGlyGlyAlaGluAlaProSerArgArgTyrLeuGluArgMetArgThr 160
 Db 1017 CGCCCGCGGGCGGCGGCTCCCTCCAGCGCTGCTGGAGCGCATCGCGCGGACC 1076
 Qy 161 PheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValPhe 180
 Db 1077 TTCGAGGAGCCACATC-----CTGCTAGCGTGTGCTGGTGTTC 1117
 Qy 181 ValIleValSerMetValValLeuCysAlaSerThrLeuProAspTyrArgAsnAlaAla 200
 Db 1118 GTGATCGTGTCCATGCTGTGTCGCGCAGCACGCTTCCCGGACTGGCGCAACGACGC 1177
 Qy 201 AlaAspAsnArgSerLeuAspArgSerArgIleIleGluAlaIleCysIleGlyTrp 220
 Db 1178 GCCCAACCGCGAGCTGATGATCCGAGCAGAGATTAATGAAGCTATCTGCATAGTTGG 1237
 Qy 221 PheThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGluPheVallys 240
 Db 1238 TTCACCTGCGAGTGCATCGTAGTTCATTTGCTCCAAAAACAAGTGTGAGTTTCAAG 1297
 Qy 241 ArgProLeuAsnIleIleAspLeuAlaIleThrProTyrTyrIleSerValLeuMet 260
 Db 1298 AGACCCCTGAACATCATTTACTGGCAATCACGCCGTATATACATCTCTGTGTGATG 1357
 Qy 261 ThrValPheThrGlyGluAsnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLeu 280
 Db 1358 ACAGTGTTTACAGCGGAGAACTCTCACTCCAGAGCGCTGGAGTCACTTGAGGTACTT 1417
 Qy 281 ArgMetMetArgIlePheThrValIleLysLeuAlaArgHisPheIleGlyLeuGlnThr 300
 Db 1418 AGAATGATGAGGATTTTGGGTGATTAAGCTTGCCCGTCATTCATTGGTCTTCAGACA 1477
 Qy 301 LeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuValPheIleCys 320
 Db 1478 CTGGTTTGACTCTCAACGTTGCTACCGAGAGATGTTATGTTACTTGTCTTCAATTGT 1537
 Qy 321 ValAlaMetAlaIlePheSerAlaLeuSerGlnLeuGluHisGlyLeuAspLeuGlu 340
 Db 1538 GTTGCCATGCGCATCTTTATGTCACCTTCTCAGCTTCTTGAACATGGGCTGACCTGGA 1597
 Qy 341 ThrSerAsnLysAspPheThrSerIleProAlaAlaCysTyrTyrValIleIleSerMet 360
 Db 1598 ACATCCACACAGACCTTACAGCANTCTGCTGCGCTGCTGGGTGATATCTCTATG 1657
 Qy 361 ThrThrValGlyTyrGlyAspMetTyrProIleThrValProGlyArgIleLeuGly 380
 Db 1658 ACTACAGTTGGCTATGAGATATGATCTCTATCACAGTGCCTGGAAGAAATCTTCGAGA 1717
 Qy 381 ValCysValValSerGlyIleValLeuLeuAlaLeuProIleThrPheIleTyrHisSer 400
 Db 1718 GTTGTGTGTAGTGGAAATTTTATTGGCAATTTACCTATCACCTTTTATCTACCATAGC 1777
 Qy 401 PheValGlnCysTyrHisGluLeuLysPheArgSerAlaArg 414
 Db 1778 TTGTGCGAGTGTATCATGAGCTCAAGTTTAGATCTGCTAGG 1819

RESULT 8

PCT-US02-10780-45
 ; Sequence 45, Application PC/TUS0210780
 ; GENERAL INFORMATION:
 ; APPLICANT: Curagen Corporation
 ; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Miller, Charles E.
 ; APPLICANT: Malyankar, Uriel M.
 ; APPLICANT: Spyttek, Kimberly A.
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Liu, Ziaohong
 ; APPLICANT: Gusev, Vladimir Y.
 ; APPLICANT: Li, Li
 ; APPLICANT: Vernet, Corine
 ; APPLICANT: Zerhusen, Bryan D.
 ; APPLICANT: Gorman, Linda
 ; APPLICANT: Shenoy, Sureesh G.
 ; APPLICANT: Pena, Carol E.A.
 ; APPLICANT: Smithson, Glenda
 ; APPLICANT: Burgess, Catherine E.
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Shimkets, Richard A.
 ; APPLICANT: Gangolli, Esha A.
 ; APPLICANT: Taupier Jr., Raymond J.
 ; APPLICANT: Casman, Stacie J.
 ; APPLICANT: Ji, Weizhen
 ; APPLICANT: Anderson, David W.
 ; APPLICANT: Liete, Mario W.
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Edinger, Shomit R.
 ; APPLICANT: Stone, David J.
 ; APPLICANT: MacDougall, John R.
 ; APPLICANT: Rothenberg, Mark E.
 ; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 21402-322C-061
 ; CURRENT APPLICATION NUMBER: PCT/US02/10780
 ; CURRENT FILING DATE: 2002-04-03
 ; PRIOR APPLICATION NUMBER: 10/114,270
 ; PRIOR FILING DATE: 2002-04-02
 ; PRIOR APPLICATION NUMBER: 60/281,086
 ; PRIOR FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: 60/281,136
 ; PRIOR FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: 60/281,863
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/281,906
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/282,020
 ; PRIOR FILING DATE: 2001-04-06
 ; PRIOR APPLICATION NUMBER: 60/282,930
 ; PRIOR FILING DATE: 2001-04-10
 ; PRIOR APPLICATION NUMBER: 60/282,934
 ; PRIOR FILING DATE: 2001-04-10
 ; PRIOR APPLICATION NUMBER: 60/283,512
 ; PRIOR FILING DATE: 2001-04-12
 ; PRIOR APPLICATION NUMBER: 60/283,710
 ; PRIOR FILING DATE: 2001-04-13
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 470
 ; SEQ ID NO 45
 ; LENGTH: 1651
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1642)
 PCT-US02-10780-45
 Alignment Scores:
 Pred. No.: 1.46e-206 Length: 1651

Score: 2095.50 Matches: 411
Percent Similarity: 91.54% Conservative: 0
Best Local Similarity: 92.54% Mismatches: 3
Query Match: 94.60% Indels: 35
DB: 1 Gaps: 3

US-10-016-647-2 (1-425) x PCT-US02-10780-45 (1-1651)

QY 1 MetThrPheGlyArgSerGlyAlaAlaSerValValLeuAsnValGlyGlyAlaArgTyr 20
DB 58 ATGACCTTCGGCGGAGCGGGCGGCGCTCGGTGGTCTGAAGCTGGGCGGCGCGGTAT 117
QY 21 SerLeuSerArgGluLeuLeuLysAspPheProLeuArgArgValSerArgLeuHisGly 40
DB 118 TCGCTGTCCGGAGAGCTGCTGAAGACTTCCTCGCTGCGCGCGGTGAGCGGCTGCACGCG 177
QY 41 CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu 60
DB 178 TCCCGCTCCGAGCGGAGCGTGTCTGAGGTGTCTGAGCTAGACCGCGAGCGCAACGAG 237
QY 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheLeuLeuLeuTyrValArgGlyHis 80
DB 238 TACTTCTTCGAGCGGCACTCGAGGCTTCGGCTTCCTCTAGCTGCGCGGCGCAC 297
QY 81 GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100
DB 298 GGCAGAGCTCGCTTCGCGCGCGGATGTGCGAGCTCTCTCTACACGAGATGATCTAC 357
QY 101 TrpGlyLeuGluGlyAlaHisLeuGluTyrCysGlnArgArgLeuAspAspArgMet 120
DB 358 TGGGCGCTGGAGGCGGCGGCACTCGAGTACTGCTCCAGCGCGGCTCTGACGCGCATG 417
QY 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140
DB 418 TCCGACACCTACACTTCTACTCGCGCGAGCGGCGGCTGCTGGCGCGGAGCGG 477
QY 141 ArgProGly-----GlyAlaGluAlaPro--- 149
DB 478 CGCCCCGCGCGGAGCGGCTCCCTCCAGGCGCTGGTGGAGCGCATGCGCGCGACCTT 537
QY 150 -----SerArgArgTyrLeuGluArgMetArgArgThrPhe 161
DB 538 CGAGGAGCGCCAGCTCGTCTGCGCGCGAGCGCTGCTGCGAGCGCATGCGCGGACCTTC 597
QY 162 GluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValPheVal 181
DB 598 GAGGAGCGCCAGCTCGTCTGCGCGCGAGATCTCGGTAGCGTCTGCGGTGTGTCTG 657
QY 182 IleValSerMetValValLeuCysAlaSerThrLeuProAspTyrArgAsnAlaAla 201
DB 658 ATCTGTTCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 717
QY 202 AspAsnArgSerLeuAspAspArgSer----- 210
DB 718 GACAAACCGAGCGCTGGATCCGCGAGCAGGTACTCCGCGCGGCGCTGGAGGAGCGCTTC 777
QY 211 -----ArgIleLeuGluAlaIleCysIleGlyTyrPheThrAlaGluCys 225
DB 778 GGGTGTCTCTTCAGAGGATAATTGAAGCTATCTGCATAGGTGTGTCTCAGCGAGTGC 837
QY 226 IleValArgPheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsnIle 245
DB 838 ATCTGTGAGTTCATTGTCTCTCAAAACAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 897
QY 246 IleAspLeuLeuAlaIleThrProTyrTyrIleSerValLeuMetThrValPheThrGly 265
DB 898 ATTGATTTACTGGCAATCACGCGGATTTACATCTCTGTGTGTGTGTGTGTGTGTGTGT 957
QY 266 GluAsnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIle 285
DB 958 GAGAACTCTCACTCCAGAGGCTGGAGTCCACTTGGAGGTACTTAGAATGATGAGGATT 1017
QY 286 PheTrpValIleLysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeu 305

DB 1018 TTTTGGTGATTAAGCTTGCCTGCTCACTTTCATTTGGTCTTCAGACACTCGGTTGACTCTC 1077
QY 306 LysArgCysTyrArgGluMetValMetLeuLeuValPheIleCysValAlaMetAlaIle 325
DB 1078 AAACGTTGCTACCGAGAGATGTTATGTTACTTGTCTTCTTCTTGTGTGCAATGGCAATC 1137
QY 326 PheSerAlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAsp 345
DB 1138 TTTAGTGCACCTTTCTCAGCTTCTTGAACATGGGCTGGACCTGGAAACATCCAAACAGAC 1197
QY 346 PheThrSerIleProAlaAlaCysTyrTrpValIleIleSerMetThrThrValGlyTyr 365
DB 1198 TTTACACGACTTCTCTGCTGCTGCTGGTGGTGAATATCTATGATACAGTTGGCTAT 1257
QY 366 GlyAspMetTyrProIleThrValProGlyArgIleLeuGlyValCysValValSer 385
DB 1258 GGAGATATGATCTCTATCACAGTGCCTGGAGAAATCTTGGAGGAGTTTGTGTGTGCT 1317
QY 386 GlyIleValLeuLeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCysTyr 405
DB 1318 GGAATCTTCTATTTGGCATTACCTATCATTCTATCTACCATAGCTTTGTGCGAGTGTAT 1377
QY 406 HisGluLeuLysPheArgSerAlaArg 414
DB 1378 CATGAGCTCAAGTTTAGATCTGCTAGG 1404

RESULT 9
US-10-114-270-45
; Sequence 45, Application US/10114270
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Miller, Charles E.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Patturajan, Meera
; APPLICANT: Liu, Zhaozhong
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Li, Li
; APPLICANT: Vernet, Corine
; APPLICANT: Zertusen, Bryan D.
; APPLICANT: Gorman, Linda
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Smithson, Glennda
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Gangolli, Bsha A.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Ji, Weizhen
; APPLICANT: Anderson, David W.
; APPLICANT: Lieta, Mario W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Stone, David J.
; APPLICANT: MacDougall, John R.
; APPLICANT: Rothenberg, Mark E.
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-322C
; CURRENT APPLICATION NUMBER: US/10/114,270
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/281,086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/282,020
 ; PRIOR FILING DATE: 2001-04-06
 ; PRIOR APPLICATION NUMBER: 60/282,930
 ; PRIOR FILING DATE: 2001-04-10
 ; PRIOR APPLICATION NUMBER: 60/282,934
 ; PRIOR FILING DATE: 2001-04-10
 ; PRIOR APPLICATION NUMBER: 60/283,512
 ; PRIOR FILING DATE: 2001-04-12
 ; PRIOR APPLICATION NUMBER: 60/283,710
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/284,234
 ; PRIOR FILING DATE: 2001-04-17
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 470
 ; SEQ ID NO 45
 ; LENGTH: 1651
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1642)
 ; US-10-114-270-45

Alignment Scores:

Prec. No.: 1,46e-206 Length: 1651
 Score: 2095.50 Matches: 411
 Percent Similarity: 91.54% Conservative: 0
 Best Local Similarity: 91.54% Mismatches: 3
 Query Match: 94.60% Indels: 35
 DB: 45 Gaps: 3

US-10-016-647-2 (1-425) x US-10-114-270-45 (1-1651)

QY 1 MetThrPheGlyArgSerGlyAlaAlaSerValValLeuAsnValGlyGlyAlaArgTyr 20
 DB 58 ATGACCTTCGGGCGCAGCGGGGGGCTCGTGGTGTCTGAACTGGGCGGCGCCGGTAT 117
 QY 21 SerLeuSerArgGluLeuLeuLeuAspPheProLeuArgArgValSerArgLeuHisGly 40
 DB 118 TCCTGTCTCCGGGAGCTGCTGAAGGACTTCGGCTCGCGCTGAGCGCGCTGCACGCG 177
 QY 41 CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgGlu 60
 DB 178 TGGCGCTCCGAGCGCGACGCTCGAGGTGTGGAGCTACGACCGCGCGCGACACGAG 237
 QY 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheLeuLeuLeuTyrValArgGlyHis 80
 DB 238 TACTTCTCGACCGGCACCTCGAGGCTTCGGCTTCATCTGCTACGTGCGCGCCAC 297
 QY 81 GlyIysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100
 DB 298 GGCAAGCTGGCTTCGCGCGCGGATGTGGAGCTCTCCTCTTACACGAGATGATCTAC 357
 QY 101 TrpGlyLeuGluGlyAlaHisLeuGluTyrCysGlnArgArgLeuAspArgMet 120
 DB 358 TGGGCGCTGAGGCGCGGACCTCGAGTACTGTGCGCGCGCTCGACGCGCATG 417
 QY 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140
 DB 418 TCGGACACCTTACACCTTCTACTCGGCGCGAGCGCGGGGTGTGGCGCGCGAGCGGG 477
 QY 141 ArgProGly-----GlyValGluAlaPro--- 149
 DB 478 CGCGCGCGCGCGGCGGCTCCCTCCAGGCGCTGGTGGAGCGCATCGCGGACCTT 537
 QY 150 -----SerArgArgTyrLeuGluArgValArgValArgThrPhe 161
 DB 538 CGAGGAGCCACCGCTGCTGGTGGCGCGCGCTGGTGGAGCGCATCGCGGCGACCTTC 597
 QY 162 GluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValPheVal 181
 DB 598 GAGGAGCCACGCTGCTGCTGGCGCGCGAGATCTGGCTAGCGTGTGGTGTGTGGT 657

QY 182 IleValSerMetValValLeuCysAlaSerThrLeuProAspTyrArgAsnAlaAla 201
 DB 658 ATCGTGTCATGGTGGTGTCTGGCGCAGCACGTTGCCGACATGGCGCAGCGCGCC 717
 QY 202 AspAsnArgSerLeuAspArgSer----- 210
 DB 718 GACAAACCGCAGCTGGATGACCGGAGCAGGTACTCGCGCGCCCTGGAGGAGCCCTCC 777
 QY 211 -----ArgIleIleGluAlaIleCysIleGlyTyrPheThrAlaGluCys 225
 DB 778 GGGGTCTCTTACAGAGATAATTGAAGCTATCTGCATAGCTTGGTCTACTGCCGAGTGC 837
 QY 226 IleValArgPheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsnIle 245
 DB 838 ATCGTAGGTTCAITGTCTCCAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGAACATC 897
 QY 246 IleAspLeuLeuAlaIleThrProTyrTyrIleSerValLeuMetThrValPheThrGly 265
 DB 898 ATTGAITTTACTGGCAATCAGCGCGTATTACATCTCTGTGTGATGACAGTGTATTACGGC 957
 QY 266 GluAsnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIle 285
 DB 958 GAGAACTCTCACTCCAGAGGGCTGGAGTCACCTTGAGGGTACTTAGAATGATGAGGATT 1017
 QY 286 PheTrpValIleLysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeu 305
 DB 1018 TTTTGGGTGATTAAGCTTGCCCGTCACTTCATTGGTCTTCAGACACATCGGTTTGACTCTC 1077
 QY 306 LysArgCysTyrArgGluMetValMetLeuLeuValPheIleCysValAlaMetAlaIle 325
 DB 1078 AAGCTTGTCTACCGAGAGATGTTATGTTACTTGTCTCATTTGTGTGCGCATCGCAATC 1137
 QY 326 PheSerAlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAsp 345
 DB 1138 TTTAGTCACCTTCTCAGCTTCTTGAACATGGCTGGACCTGGAAACATCCAAACAAGGAC 1197
 QY 346 PheThrSerIleProAlaAlaCysTyrTrpValIleIleSerMetThrThrValGlyTyr 365
 DB 1198 TTTACCAGCATCTCTGCTGCTGCTGGTGGTGATTAATCTCTATGACTACAGTTGGCTAT 1257
 QY 366 GlyAspMetTyrProIleThrValProGlyArgIleLeuGlyValCysValValSer 385
 DB 1258 GGAGATATGATCTCTATCAGATGCTCGTGAAGAATCTTGGAGGAGTTTGTGTTCAGT 1317
 QY 386 GlyIleValLeuLeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCysTyr 405
 DB 1318 GGAATTTCTTATTGGCAATTACCTATCATTCTTATCATTATCATTATGCTAGTGTGTTAT 1377
 QY 406 HisGluLeuLysPheArgSerAlaArg 414
 DB 1378 CATGAGCTCAAGTTAGATCTGCTAGG 1404

RESULT 10

US-10-415-378-39
 ; Sequence 39, Application US/10415378
 ; GENERAL INFORMATION:
 ; APPLICANT: INCYTE CORPORATION; TANG, Y. Tom
 ; APPLICANT: YUE, Henry; NGUYEN, Daniel B.;
 ; APPLICANT: HAFALIA, April J.A.; ELLIOTT, Vicki S.;
 ; APPLICANT: LU, Yan; CHAWLA, Narinder K.;
 ; APPLICANT: YAO, Monique G.; BAUGHN, Mariah R.;
 ; APPLICANT: GANDHI, Ameera R.; DING, Li;
 ; APPLICANT: SANJANWALA, Madhusudan M.; RAMKUMAR, Jayalaxmi;
 ; APPLICANT: ARVIZU, Chandra S.; GIETZEN, Kimberly J.;
 ; APPLICANT: LAL, Preeti G.; AZIMZAI, Yalda;
 ; APPLICANT: KEHAN, Farrar A.; THANGAVELU, Kavitha;
 ; APPLICANT: THORNTON, Michael B.; LU, Dying Aina M.;
 ; APPLICANT: TRIBOULEY, Catherine M.; WARREN, Bridget A.;
 ; APPLICANT: ISON, H. Craig; DAS, Debopriya;
 ; APPLICANT: RAUMANN, Brigitte E.; POLICKY, Jennifer L.;
 ; APPLICANT: KEARNEY, Liam
 ; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
 ; FILE REFERENCE: PI-0270 USN

```

; CURRENT APPLICATION NUMBER: US/10/415,378
; CURRENT FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: PCT/US01/46055
; PRIOR FILING DATE: 2001-10-27
; PRIOR APPLICATION NUMBER: US 60/250,790
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/252,232
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/249,561
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/247,673
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/245,904
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/243,989
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PERL Program
; SEQ ID NO 39
; LENGTH: 2235
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7482060CB1
US-10-415-378-39

Alignment Scores:
Pred. No.: 2,056-204 Length: 2235
Score: 2076.50 Matches: 406
Percent Similarity: 97.83% Conservative: 0
Best Local Similarity: 97.83% Mismatches: 1
Query Match: 93.75% Indels: 9
DB: 51 Gaps: 2

US-10-016-647-2 (1-425) x US-10-415-378-39 (1-2235)

QY 1 MetThrPheGlyArgSerGlyAlaAlaSerValValLeuAsnValGlyGlyAlaArgTyr 20
Db 428 ATGACCTTCGGCGGAGCGGGCGGCTCGGTGCTGAACGTGGCGGCGCCGGTAT 487

QY 21 SerLeuSerArgGluLeuLeuLysAspPheProLeuArgArgValSerArgLeuHisGly 40
Db 488 TGGCTGTCCGGAGCTGCTGAAGACTTCCCGCTGCGCGCGGTGAGCGCGCTGCACGCG 547

QY 41 CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu 60
Db 548 TGGCGCTCCGAGCGGACGCTGCTCGAGGTGTGCGAGCACTACGACCGGCGGCGCAACGAG 607

QY 61 TyrPhePheAspArgHisSerGluAlaPheGlyPheLeuLeuTyrValArgGlyHis 80
Db 608 TACTTCTTCGACCGGCACCTCGAGGCGCTTCGGCTTCATCTCTCTACGTGCGCGGCGCAC 667

QY 81 GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100
Db 668 GCGAAGCTCGCTTCGGCGCGGAGTGTGCGAGCTCTCTCTTCAACGAGATGATCTAC 727

QY 101 TrpGlyLeuGluGlyAlaHisLeuGluTyrCysGlnArgArgLeuAspAspArgMet 120
Db 728 TGGGCGCTGGAGGCGGCGGACCTCGAGTACTCTGCTGCCAGCGCGGCTCGACGCGCATG 787

QY 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla 140
Db 788 TCGACACCTACACCTTCTTACCTGCGCGGAGCGGCGGCTGCTGGCGGCGGAGCGGCG 847

QY 141 ArgProGlyGlyAla-GluAlaAlaProSerArgArgTrpLeuGluArgMetArgArgTh 160
Db 848 CGCCCC---GGCGCGGAGGCGGCTCCCTCCAGGCGCTGGCTGGAGCGCATGCGGCGGAC 904

QY 160 rPheGluGluProThrSerSerLeuAlaAlaClnleuAlaSerValSerValValph 180
Db 905 CTTGAGGAGGCCACATC-----CTGGCTAGCGGTGCGGTGGTGT 945

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QY 180 eValileValSerMetValValLeuCysAlaSerThrLeuProAspTrpArgAsnAlaAl 200
Db 946 CGTGATCGTGCCATGGTGGTGTGTCGCCGAGCAGCGTGGCCGACTGGCGCAACGCGAGC 1005

QY 200 aAlaAspAsnArgSerLeuAspArgSerArgIleleGluAlaIleCysIleGlyTr 220
Db 1006 CGCGGACCAACCGACCGCTGGATGACCGGAGGAGGATATTTGAAGCTATCTGCATAGGTTG 1065

QY 220 pPheThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGluPheVally 240
Db 1066 GTTCACCTGCCAGTGCATCGTGAGGTTCATGTCTCCAAAAACAAGTGTGAGTTGTCTCA 1125

QY 240 sArgProLeuAsnIleleAspLeuAlaIleThrProTyrTyrIleSerValLeuMe 260
Db 1126 GAGACCCCTGAACATCATTTACTGGCAATCACGCCGATTACATCTCTGTGTGTAT 1185

QY 260 tThrValPheThrGlyGluAsnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLe 280
Db 1186 GACAGTGTTTACAGCGGAGAACTCTCAACTCCAGAGGCTGGAGTCACTTGGAGGTACT 1245

QY 280 uArgMetMetArgIlePheTrpValIleLysLeuAlaArgHisPheIleGlyLeuGlnTh 300
Db 1246 TAGAATGATGAGGATTTTGGGTGATTAAGCTTGGCCGTCACCTTCATTGCTTCAGAC 1305

QY 300 rLeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuValPheIleCy 320
Db 1306 ACTCGGTTTGACTCTCAACGCTTGTACCGAGAGATGGTATGTATTCTTCTTCATTG 1365

QY 320 sValAlaMetAlaIlePheSerAlaLeuSerGlnLeuGluHisGlyLeuAspLeuGl 340
Db 1366 TGTGGCCATGGCAATCTTTAGTGACATTTCTCAGCTTCTTGAACATGGGTGGACCTGGA 1425

QY 340 uThrSerAsnLysAspPheThrSerIleProAlaAlaCysTrpPrpValIleIleSerMe 360
Db 1426 AACATCCAAACAGGACTTACCAAGATTCCTGCTGCTGCTGGGTGGGTATTCTCTAT 1485

QY 360 tThrThrValGlyTyrGlyAspMetTyrProIleThrValProGlyArgIleLeuGlyGl 380
Db 1486 GACTACAGTTGGCTATGGAGATATGTATCTCTATCACAGTGCCTGGAAGATTTCTTGAGG 1545

QY 380 yValCysValValSerGlyIleValLeuLeuAlaLeuProIleThrPheIleTyrHisSe 400
Db 1546 AGTTTGTGTGTCAGTGAATTTGTTATTGGCAATTACCTATCATTCTTTATCTACCATAG 1605

QY 400 rPheValGlnCysTyrHisGluLeuLysPheArgSerAlaArg 414
Db 1606 CTTTGTGCGAGTTTATCATGAGCTCAAGTTTAGATCTGCTAGG 1648

RESULT 11
US-10-343-903-47
; Sequence 47, Application US/10343903
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; YUE, Henry;
; APPLICANT: THORNTON, Michael; RAMKUMAR, Jayalaxmi;
; APPLICANT: TANG, Y. Tom; AZIMZAI, Yalda;
; APPLICANT: BAUGHN, Mariah R.; YANG, Junming;
; APPLICANT: YAO, Monique G.; LAL, Preeti G.;
; APPLICANT: CHAWLA, Narinder K.; GANDHI, Ameena R.;
; APPLICANT: HAPALIA, April J.A.; NGUYEN, Danielle B.;
; APPLICANT: ARVIZU, Chandra S.; ELLIOTT, Vicki S.;
; APPLICANT: TRIBOULEY, Catherine M.; LU, Dyung Aina M.;
; APPLICANT: XU, Yuning; REDDY, Roopa;
; APPLICANT: HERNANDEZ, Roberto; BOROWSKY, Mark L.;
; APPLICANT: LO, Terence P.; LU, Yan;
; APPLICANT: POLICKY, Jennifer L.; GREENE, Barrie D.;
; APPLICANT: SANJANWALA, Madhusudan M.; RAUMANN, Brigitte E.;
; APPLICANT: BURFORD, Neil; ISON, Craig H.;
; APPLICANT: LEE, Brnestine A.; DING, Li;
; APPLICANT: DAS, Debopriya; KALLICK, Deborah A.;
; APPLICANT: KEAN, Farrah A.; SEILHAMER, Jeffrey J.;
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PI-0183 USN
; CURRENT APPLICATION NUMBER: US/10/343,903

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CURRENT FILING DATE: 2003-02-03		PCT/US01/24217	
PRIOR APPLICATION NUMBER: 60/231,434		60/231,434	
PRIOR FILING DATE: 2000-09-08		2000-09-08	
PRIOR APPLICATION NUMBER: 60/230,067		60/230,067	
PRIOR FILING DATE: 2000-08-31		2000-08-31	
PRIOR APPLICATION NUMBER: 60/228,140		60/228,140	
PRIOR FILING DATE: 2000-08-25		2000-08-25	
PRIOR APPLICATION NUMBER: 60/226,410		60/226,410	
PRIOR FILING DATE: 2000-08-18		2000-08-18	
PRIOR APPLICATION NUMBER: 60/224,456		60/224,456	
PRIOR FILING DATE: 2000-08-10		2000-08-10	
PRIOR APPLICATION NUMBER: 60/223,269		60/223,269	
PRIOR FILING DATE: 2000-08-03		2000-08-03	
NUMBER OF SEQ ID NOS: 60		60	
SOFTWARE: PERL Program		PERL Program	
SEQ ID NO 47		47	
LENGTH: 2312		2312	
TYPE: DNA		DNA	
ORGANISM: Homo sapiens		Homo sapiens	
FEATURE:			
NAME/KEY: misc feature		misc feature	
OTHER INFORMATION: Incyte ID No: 7474111CB1		Incyte ID No: 7474111CB1	
US-10-343-903-47			
Alignment Scores:			
Pred. No.:	2,698-171	Length:	2312
Score:	1758.00	Matches:	351
Percent Similarity:	83.37%	Conservative:	0
Best Local Similarity:	83.37%	Mismatches:	70
Query Match:	79.37%	Indels:	1
DB:	49	Gaps:	1
US-10-016-647-2 (1-425) x US-10-343-903-47 (1-2312)			
Qy	5	ArgSerGlyAlaAlaSerValValLeuAsnValGlyGlyAlaAlaArgTyrSerLeuSerArg	24
Db	790	CGAGCGGGCGCGCTCGGTGGTGGTGAACGTGGGGCGCGCGGTATTCGCTGTCGGG	849
Qy	25	GluLeuLeuValAspPheProLeuArgArgValSerArgLeuHisGlyCysArgSerGlu	44
Db	850	GAGCTGCTGAAGACTTCCCGCTGGCGGCTGAGCGGCTGACCGCTGCGGCTCCGAG	909
Qy	45	ArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGluTyrPhePheAsp	64
Db	910	CGGACGTGCTCGAGGTGTCGACGACTACGACCGGCGAGCAACGAGTACTTCTTCGAC	969
Qy	65	ArgHisSerGluAlaPheGlyPheLeuLeuTyrValArgGlyHisGlyLysLeuArg	84
Db	970	CGGACCTCGAGGCTTCGCGCTTCATCTCTCTAC	1005
Qy	85	PheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyrTrpGlyLeuGlu	104
Db	1005	-----	1005
Qy	105	GlyAlaHisLeuGluTyrCysGlnArgArgLeuAspAspArgMetSerAspThrTyr	124
Db	1005	-----	1005
Qy	125	ThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAlaArgProGlyGly	144
Db	1005	-----	1005
Qy	145	AlaGluAlaProSerArgArgTrpLeuGluArgMetArgArgPheGluGluPro	164
Db	1006	-----CGGCGTCCCTCCAGCGCTGCGAGCGATGCGCGGACCTTCGAGGAGCCC	1059
Qy	165	ThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValPheValIleValSer	184
Db	1060	ACGTGCTGCTGGCGCGGAGATCTCGCTAGCGGTGCTGGTGTGCTGATCGTGTC	1119
Qy	185	MetValValLeuCysAlaSerThrLeuProAspTrpArgAsnAlaAlaAspAsnArg	204

Db	1120	ATGGTGGTGTGTGGCGCAGCAGTGTGGCGAATGGCGAAGCAGCGCGCGCAACCCG	1179
Qy	205	SerLeuAspAspArgSerArgIleGluAlaIleCysIleGlyTrpPheThrAlaGlu	224
Db	1180	AGCCTGGATACCGGAGCAGGATAATGAAGCTATCTGCATAGTTGGTTCACCTGCGGAG	1239
Qy	225	CysIleValArgPheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsn	244
Db	1240	TGCATCGTGAAGTTCATTTGCTCCAAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGAAC	1299
Qy	245	IleIleAspLeuLeuAlaIleThrProTyrTyrIleSerValLeuMetThrValPheThr	264
Db	1300	ATCATTGATTACTGGCAATCAGCCCGTATTACATCTCTGTGTGATGACAGTGTTTACA	1359
Qy	265	GlyGluAsnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArg	284
Db	1360	GGCGAGAACTCTCACTCCAGAGGGCTGGAGTCACTTGGAGGTACTTAGAATGATGAGG	1419
Qy	285	IlePheTrpValIleLysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThr	304
Db	1420	ATTTTGGGTGATTAAAGCTTGCCCGTCACTTATTGGTCTTCAGACACTCGGTTTGA	1479
Qy	305	LeuLysArgCysTyrArgGluMetValMetLeuLeuValPheIleCysValAlaMetAla	324
Db	1480	CTCAACGTTGCTACCGAGAGATGGTTATGTTTCTTCTTCTTCTTCTTCTTCTTCTT	1539
Qy	325	IlePheSerAlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLys	344
Db	1540	ATCTTTAGTCACATTTCTCAGCTTCTTGAACATGGGTGGACCTGGAACATCAACAAG	1599
Qy	345	AspPheThrSerIleProAlaAlaCysTrpTrpValIleIleSerMetThrValGly	364
Db	1600	GACTTTACCAAGCATTCCTGCTGCTGCTGGTGGTGAATATCTCTATGACTACAGTTGGC	1659
Qy	365	TyrGlyAspMetTyrProIleThrValProGlyArgIleLeuGlyValCysValVal	384
Db	1660	TATGGAGATATGATCTATCATCAGAGTCCCTGGAAGAATTTCTGGAGGAGTTTGTGTGTC	1719
Qy	385	SerGlyIleValLeuLeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCys	404
Db	1720	AGTGAATTTGTTTATTTGGCATACCTATCATTATCTATACCATAGCTTTGTGCACTGT	1779
Qy	405	TyrHisGluLeuLysPheArgSerAlaArgTyrSerArgSerLeuSerThrGluPheLeu	424
Db	1780	TATCATGAGCTCAAGTTAGTCTGCTAGTATAGTAGGAGCTCTCCACTGAATTCCTG	1839
Qy	425	Asn 425	
Db	1840	AAT 1842	

RESULT 12

US-10-170-235-1828

Sequence 1828, Application US/10170235

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig

TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN

TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF

FILE REFERENCE: CL001380

CURRENT APPLICATION NUMBER: US/10/170,235

CURRENT FILING DATE: 2003-03-17

NUMBER OF SEQ ID NOS: 42514

SEQ ID NO 1828

LENGTH: 1416

TYPE: DNA

ORGANISM: HUMAN

US-10-170-235-1828

Alignment Scores:

Se-169 Length: 1416

Pred. No.: 1731.50

Score: 340

Percent Similarity: 91.05%

Conservative: 6

Best Local Similarity: 89.47%

Mismatches: 5

Query Match: 78.17% Indels: 29
DB: 46 Gaps: 3
US-10-016-647-2 (1-425) x US-10-170-235-1828 (1-1416)
QY 1 MetThrPheGlyArgSerGlyAlaAlaSerValValLeuAsnValGlyGlyAlaArgTyr 20
DB 1 ATGACCTTCGGGCGGAGCGGCGGCGCTCGGTGGTGTGAACGTCGTGGGCGGCGCGGTAT 60
QY 21 SerLeuSerArgGluLeuLeuLysAspPheProLeuArgArgValSerArgLeuHisGly 40
DB 61 TCGCTGTCCGGGAGCTGCTGAGAGCTTCGCGCTGCGCGCGGTGAGCGCGCTGCACGCG 120
QY 41 CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu 60
DB 121 TCGCGCTCCGAGCGGAGCGTGTCTGAGGTGTGCGAGGACTACGACCGCGGAGCGAACGAG 180
QY 61 TyrPhePheAspArgHisSerClnAlaPheGlyPheLeuLeuLeuTyrValArgGlyHis 80
DB 181 TACTTCTTCGACCGGACCTCGGAGGCGCTTCGCGCTTCATCTCTACGTGCGGCGCAC 240
QY 81 GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100
DB 241 GCGAAGCTGGCTTCGCGCGCGGATGTGCGAGCTCTCTCTCAACAGATGATCTAC 300
QY 101 TrpGlyLeuGluGlyAlaHisLeuGluTyrCysGlnArgArgLeuAspArgMet 120
DB 301 TGGGCGCTGGAGGCGGCGACCTCGAGTACTGCTGCCAGCGCGCTCGACGCGCATG 360
QY 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyValArgAspGluAla 140
DB 361 TCCGACACTACACTTCTACTCGCGCGAGCGCGGCGGTGCTGGCGCGGAGCGCG 420
QY 141 ArgProGlyGlyAlaGluAlaAlaProSerArgArgTyrLeuGluArgMetArgThr 160
DB 421 CCGCCCGCGGCGGCGAGCGGCTCCCTCCAGCGCTGCTGCGAGCGCATCGCGCGGACC 480
QY 161 PheGluGluProThrSerSerLeuAlaAlaGlnLeuLeuAlaSerValSerValPhe 180
DB 481 TTCGAGGAGCGCCACCTGCTGCTGCGCGCGAGATCCCTGGGTAGCGTGTGCGGTGTC 540
QY 181 ValIleValSerMetValValLeuCysAlaSerThrLeuProAspTyrArgAsnAlaAla 200
DB 541 GTGATCGTGCATGCTGCTGCTGCGCGCGAGCGTTCGCGCGCATCGCGCAACGCGACC 600
QY 201 AlaAspAsnArgSerLeuAspAspArgSerArgIleLeuGluAlaIleCysIleGlyTrp 220
DB 601 GCGGCAACCGCGCGCTGGATGACCGGAGCGAGGATAATTGAAGCTATCTGCATAGGTGG 660
QY 221 PheThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGluPheValLys 240
DB 661 TTCACCTGCGGAGTGCATGCTGAGGTTCATTGCTCCAAAACAGTGTGAGTTGTCAAG 720
QY 241 ArgProLeuAsnIleLeuAspLeuLeuAlaIleThrProTyrTyrIleSerValLeuMet 260
DB 721 AGACCCCTGAACATCATTTACTTGGCAATCAGCGCGTATTACATCTCTGTGTGATG 780
QY 261 ThrValPheThrGlyGluAsnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLeu 280
DB 781 ACAGTGTTTACAGGCGAGAACTCTCACTCCAGGCGGTGAGTCACTTGAAGG----- 834
QY 281 ArgMetMetArgIlePheTrpValIleLysLeuAlaArgHisPheIleGlyLeuGlnThr 300
DB 835 -----ACA 837
QY 301 LeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuValPheIleCys 320
DB 838 CTCGGTTTGACCTCAACAGTGTGACCGAGAGATGGTTATGTACTTGTCTTATTGT 897
QY 321 ValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeuGlu 340
DB 898 GTTGCCATGGCAATCTTTAGTGCACTTTCTCAGCTTCTTTGAACATGGGCTGAGCTGAA 957

QY 341 ThrSerAsnLysAspPheThrSerIleProAlaAlaCysTrpTrpValIleIleSer--- 359
DB 958 ACATCCAAACAGGACTTTACGACCATCTCTGCTGCTGCTGGAGCATTTCCCTTAACAAGT 1017
QY 360 -----MetThrThrValGlyTyrGlyAspMetTyrProIleThrValProGly 375
DB 1018 GTCACCTTCTGTGCTGGGCACTGTGGGTATACAGATG-----ACCATCAACGGG 1068
RESULT 13
US-10-144-771-10588 Application US/10144771
; Sequence 10588
; GENERAL INFORMATION: US/10144771
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/10/144, 771
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 10588
; LENGTH: 1005
; TYPE: DNA
; ORGANISM: HUMAN
US-10-144-771-10588
Alignment Scores:
Pred. No.: 2,89e-162 Length: 1005
Score: 1666.50 Matches: 322
Percent Similarity: 97.03% Conservative: 5
Best Local Similarity: 95.55% Mismatches: 7
Query Match: 75.24% Indels: 3
DB: 45 Gaps: 1
US-10-016-647-2 (1-425) x US-10-144-771-10588 (1-1005)
QY 89 MetCysGluLeuSerPheTyrAsnGluMetIleTyrTrpGlyLeuGluGlyAlaHisLeu 108
DB 1 ATGTGGGAGCTCTCTTCTACACAGATGATCTACTGGGCGCTGGAGGCTGGCACCTG 60
QY 109 GluTyrCysCysGlnArgArgLeuAspAspArgMetSerAspThrTyrThrPheTyrSer 128
DB 61 GAGTACTGTCTGCGAGCGCGCTAGACGCGCATGTCGACACCCACACCTTTCAGCGG 120
QY 129 AlaAspGluProGlyValLeuGlyArgAspGluAlaArgProGlyGlyAlaGluAlaAla 148
DB 121 GCAGACGAG-----CTGGGCGCGGAGCAGCCTCTCCCGCGGACCCGAGCGGCG 171
QY 149 ProSerArgArgTrpLeuGluArgMetArgArgThrPheGluGluProThrSerSerLeu 168
DB 172 CCCTCCCGGCGCTGGCTGGAGCGCATCGGCGGACCTTCGAGGAGCGCCACGCTGCTG 231
QY 169 AlaAlaGlnIleLeuAlaSerValSerValPheValIleValSerMetValValLeu 188
DB 232 GCGCGCGAGATCTCGCCAGCGTGTGCGTGGTGTTCGTGATCTGTCCTGTTGGTGTG 291
QY 189 CysAlaSerThrLeuProAspTrpArgAsnAlaAlaAlaAspAsnArgSerLeuAspAsp 208
DB 292 TGGCGCAGCAGCGCTGCGGCGGCGGCGGTGCTGACAAACCGCGAGCTGTGGATGAC 351
QY 209 ArgSerArgIleLeuGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleValArg 228
DB 352 CGGAGCAGGAGATAATTGAAGCTATCTCATAGGTGGTTCACCGCGGAGTGCATCTGCGG 411
QY 229 PheIleValSerLysAsnLysCysGluPheValIleArgProLeuAsnIleIleAspLeu 248
DB 412 TTCATCTCTCCAAAACAGTGTGAGTTGTCAAGAGACCCCTGAACATCATTTACTTGA 471
QY 249 LeuAlaIleThrProTyrTyrIleSerValLeuMetThrValPheThrGlyGluAsnSer 268
DB 472 CTGGCAATCAGCGCTATTACATCTCTGTCTATGACAGTGTGTTACAGCGGAGAACTCT 531
QY 269 GlnLeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTrpVal 288
DB 532 CAACCTCCAGAGGCGCTGGGCTCACCTTGAGGCTCTCTCGAATGATGCGGATCTTCTGG 591

QY 289 IleLysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCys 308
 Db 592 ATCAAGCTTGGCCGAGCACTTCAATGGTCTGCGAGACACTGGGCTTGACTCTCAAGCGGTGC 651
 QY 309 TyrArgGluMetValMetLeuLeuValPheIleCysValAlaMetAlaIlePheSerAla 328
 Db 652 TACCGAGAGATGTCATGTTACTTGTCTTCACTGTGTGTGGCCATGCGCAATCTTTAGTGCA 711
 QY 329 LeuSerGluLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSer 348
 Db 712 CTCTCTCAGCTCTTGGACATGGGCTGGACCTTGGAAACATCCCAACAGGATTTCCCCAGC 771
 QY 349 IleProAlaAlaCysTrpTrpValIleSerMetThrThrValGlyTyrGlyAspMet 368
 Db 772 ATCCCCGCTGCCTGTGGTGGGTGATATCTCTATGACTACAGTTGGCTATGGAGATATG 831
 QY 369 TyrProIleThrValProGlyArgIleLeuGlyValCysValValSerClyIleVal 388
 Db 832 TATCTTATCAGCGTGCCTGGAAAGATTTCTGGAGGAGTTTGTGTGAGTGGGATTTGT 891
 QY 389 LeuLeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCysTyrHisGluLeu 408
 Db 892 CTGTTGGCATTACCCATCACTTTCTATCATTACATAGCTTTGTGSCAGTGTCTACCCAGGCTC 951
 QY 409 LysPheArgSerAlaArgTyrSerArgSerLeuSerThrGluPheLeuAsn 425
 Db 952 AAGTTTAGATCGGCTAGATATAGTAGGAGCCTCTCAGCTGAGTTCTCTGAAT 1002
 RESULT 14
 US-60-360-207-10588
 ; Sequence 10588, Application US/60360207
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig
 ; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
 ; FILE REFERENCE: CL001321
 ; CURRENT APPLICATION NUMBER: US/60/360,207
 ; CURRENT FILING DATE: 2002-03-01
 ; NUMBER OF SEQ ID NOS: 47235
 ; SEQ ID NO 10588
 ; LENGTH: 1005
 ; TYPE: DNA
 ; ORGANISM: HUMAN
 US-60-360-207-10588
 Alignment Scores:
 Pred. No.: 2,89e-162 Length: 1005
 Score: 1666.50 Matches: 322
 Percent Similarity: 97.03% Conservativity: 5
 Best Local Similarity: 95.55% Mismatches: 7
 Query Match: 75.24% Indels: 3
 DB: 93 Gaps: 1
 US-10-016-647-2 (1-425) x US-60-360-207-10588 (1-1005)
 QY 89 MetCysGluLeuSerPheTyrAsnGluMetIleTyrTrpGlyLeuGluGlyAlaHisLeu 108
 Db 1 ATGTGGAGCTCTCTTCTTCAACAGAGATGATCTACTGGGCTGGAGGTGGCGACCTG 60
 QY 109 GluTyrCysGlnArgLeuAspArgMetSerAspThrTyrThrPheTyrSer 128
 Db 61 GAGTACTGTGCGAGCGCGCTAGACCGCATGTCGACACCCACACCTTTCCACCG 120
 QY 129 AlaAspGluProGlyValLeuGlyArgAspGluAlaArgProGlyGlyAlaGluAla 148
 Db 121 GCAGACGAG-----CTGGGCGCGAGACGCTCGTCCCGCGGACCCGAGCGGCC 171
 QY 149 ProSerArgArgTrpLeuGluArgMetArgArgThrPheGluGluProThrSerSerLeu 168
 Db 172 CCTTCCCGCGCTGGCTGAGCGCATGCGCGGACCTTCGAGAGCCCGACCGTCGCGCTG 231
 QY 169 AlaAlaGlnIleLeuAlaSerValSerValPheValIleValSerMetValValLeu 188

Db 232 GCCCGCAGATCTCGCCAGCGGTCCGTGGTGTTCGTGATCGTCCATGGTGGTGGCTG 291
 QY 189 CysAlaSerThrLeuProAspTrpArgAsnAlaAlaAlaAspAsnArgSerLeuAspAsp 208
 Db 292 TGGCCAGCAGCGTGGCCGACTGGCGTGGCGCGGTGCTGACAAACCGCAGTCTGGATGAC 351
 QY 209 ArgSerArgIleIleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleValArg 228
 Db 352 CGGAGCAGGAGTAATGAAGCTATCTCATAGGTGGTTCCCGCGGAGTGCATCGTGGCG 411
 QY 229 PheIleValSerLysLysAsnLysCysGluPheValLysArgProLeuAsnIleIleAspLeu 248
 Db 412 TTATCTGCTTCCAAAACAGTGTGAGTTGTCAAGAGACCCCTGACCATCATTTGACTTA 471
 QY 249 LeuAlaIleThrProTyrTyrIleSerValLeuMetThrValPheThrGlyGluAsnSer 268
 Db 472 CTGGCAATCAAGCCCTATTACATCTCTGTGCTAATGACAGTGTTCACAGCGCAGAACTCT 531
 QY 269 GlnLeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTyrVal 288
 Db 532 CAATCTCAGAGGGCTGGGGTCACTTGGAGGTCTCCGAATGATGCGGATCTTCUGGGTG 591
 QY 289 IleLysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCys 308
 Db 592 ATCAAGCTTGGCCGCACTTCAATGGTCTGCAGACACTGGGCTTGACTCTCAAGCGGTGC 651
 QY 309 TyrArgGluMetValMetLeuLeuValPheIleCysValAlaMetAlaIlePheSerAla 328
 Db 652 TACCGAGAGATGTCATGTTACTTGTCTTCACTGTGTGGTGGCCATGCAATCTTTAGTGCA 711
 QY 329 LeuSerGlnLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSer 348
 Db 712 CTCTCTCAGCTCTTGGACATGGGCTGGACCTGGAAACATCCCAACAGGATTTCCGACG 771
 QY 349 IleProAlaAlaCysTrpTrpValIleSerMetThrThrValGlyTyrGlyAspMet 368
 Db 772 ATCCCCGCTGCCTGTGGTGGTGAATATCTCTATGACTACAGTTGGCTATGGAGATATG 831
 QY 369 TyrProIleThrValProGlyArgIleLeuGlyGlyValCysValValSerGlyIleVal 388
 Db 832 TATCTTATCAGCGTGCCTGGAAATTTCTTGGAGGAGTTTGTGTGTCAGTGGGATTTGT 891
 QY 389 LeuLeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCysTyrHisGluLeu 408
 Db 892 CTGTTGGCATTACCCATCACTTTCTATCATTACATAGCTTTGTGSCAGTGTCTACCCAGGCTC 951
 QY 409 LysPheArgSerAlaArgTyrSerArgSerLeuSerThrGluPheLeuAsn 425
 Db 952 AAGTTTAGATCGGCTAGATATAGTAGGAGCCTCTCAGCTGAGTTCTCTGAAT 1002
 RESULT 15
 US-60-196-712-1268
 ; Sequence 1268, Application US/60196712
 ; GENERAL INFORMATION:
 ; APPLICANT: Bonazzi, Vivien
 ; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
 ; TITLE OF INVENTION: AND USES THEREOF
 ; FILE REFERENCE: CL000451
 ; CURRENT APPLICATION NUMBER: US/60/196,712
 ; CURRENT FILING DATE: 2000-04-13
 ; NUMBER OF SEQ ID NOS: 3846
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1268
 ; LENGTH: 695
 ; TYPE: DNA
 ; ORGANISM: HUMAN
 US-60-196-712-1268
 Alignment Scores:
 Pred. No.: 5,24e-105 Length: 695
 Score: 1113.50 Matches: 218
 Percent Similarity: 98.64% Conservativity: 0

Best Local Similarity: 98.64% Mismatches: 0
Query Match: 50.27% Indels: 3
DB: 75 Gaps: 1

US-10-016-647-2 (1-425) x US-60-196-712-1268 (1-695)

QY 205 SerLeuAspArgSerArgIleGluAlaIleCysIleGlyTrpPheThrAlaGlu 224
DB 9 TCCTTTGAC-----AGGATAATTGAAGCTATCTGCATAGTTGGTTCACCTGCCGAG 59

QY 225 CysIleValArgPheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsn 244
DB 60 TGCATCGTGAGGTTCTCTCCAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGAAC 119

QY 245 IleIleAspLeuLeuAlaIleThrProTyrTyrIleSerValLeuMetThrValPheThr 264
DB 120 ATCAATTGATTTACTGGCAATCAGCCGTATTACATCTCTGTGTGATGACAGTGTTTACA 179

QY 265 GlyGluAsnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArg 284
DB 180 GCGAGAACTCTCAACTCCAGAGGGCTGGAGTCACCTTGAGGGTACTTAGAATGATGAGG 239

QY 285 IlePheTrpValIleLysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThr 304
DB 240 ATTTTGGGTGATTAAAGCTTGCCCTCACTTCATTGGTCTTCAGACACTCGGTTTGACT 299

QY 305 LeuLysArgCysTyrArgGluMetValMetLeuLeuValPheIleCysValAlaMetAla 324
DB 300 CTCAAACGTTGTACCAGAGAGATGTTATGTATTGTCTTCTATTGTGTGCCATGGCA 359

QY 325 IlePheSerAlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLys 344
DB 360 ATCTTTAGTGCACCTTCTCAGCTTCTTGAAACATGGGCTGGACCTGAAACATCCAAACAAG 419

QY 345 AspPheThrSerIleProAlaAlaCysTrpTyrValIleIleSerMetThrThrValGly 364
DB 420 GACTTTACCAGCATTCCTGCTGCTGCTGGTGGTGAATTATCTCTATGACTACAGTTGGC 479

QY 365 TyrGlyAspMetTyrProIleThrValProGlyArgIleLeuGlyGlyValCysValVal 384
DB 480 TATGGAGATATGATCTCTATCACAGTGCCTGGAAGAAATTCCTGGAGGAGTTTGTGTGTC 539

QY 385 SerGlyIleValLeuLeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCys 404
DB 540 AGTGGAAATTGTTCTATTGTGCATTACCTATCACTTTTATCTACCATAGCTTTGTGCAGTGT 599

QY 405 TyrHisGluLeuLysPheArgSerAlaArgTyrSerArgSerLeuSerThrGluPheLeu 424
DB 600 TATCATGAGCTCAAGTTTAGATCTGCTAGGTATAGTAGGAGCTCTCCACTGAATTCCTG 659

QY 425 Asn 425
DB 660 AAT 662

Search completed: April 19, 2004, 16:44:38
Job time : 4387 secs

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Db 62 CTGAGCGCATGCGCGGACCTTCGAGGAGCCACGCTCGCTGCGCGCGCAGATCCTG 121
 Qy 174 AlaserValSerValValPheValIleValSerMetValValLeuCysAlaSerThrLeu 193
 Db 122 GCTAGCGTGTGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 181
 Qy 194 ProAspTrpArgAsnAlaAlaAspAsnArgSerLeuAspAspArgSerArgIleIle 213
 Db 182 CCCGACTGGCGCAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 241
 Qy 214 GluAlaIleCysIleGlyTrpPheThrAlaGluCysIleValArgPheIleValSerLys 233
 Db 242 GAAGCTATCTGCATAGTGTGTTTCACTGCGGAGTGCATCGTGGGTTTCAATGCTCCAAA 301
 Qy 234 AsnLysCysGluPheValLysArgProLeuAsnIleIleAspLeuLeuAlaIleThrPro 253
 Db 302 AACAGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTACTGCGCAATCAGCGCG 361
 Qy 254 TyrTyrIleSerValLeuMetThrValPheThrGlyGluAsnSerGlnLeuGlnArgAla 273
 Db 362 TATTACATCTCTGTGTGATGACAGTGTTCACAGCGGAGAACTCTCAACTCCAGAGGGCT 421
 Qy 274 GlyValThrLeuArgValLeuArgMetMetArgIlePheThrValIleLysLeuAlaArg 293
 Db 422 GGAGTCACCTTGAGG----- 436
 Qy 294 HisPheIleGlyLeuGlnThrLeuGlyLeuLysArgCysTyrArgGluMetVal 313
 Db 437 -----ACACTCGGTTTGACTCTCAACGTTGTACCGAGAGATGGTT 478
 Qy 314 MetLeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeu 333
 Db 479 ATGTACTTGTCTTCATTGTGTGTCATGCGCAATCTTTAGTGCATCTTCTCAGCTTCTT 538
 Qy 334 GluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIleProAlaAlaCys 353
 Db 539 GAACATGGCTGGACCTGGAAACATCAACAGGACTTTACAGGACTTCTGCTGCTGCTGC 598

RESULT 2

US-60-545-213-4195
 ; Sequence 4195, Application US/60545213
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Mounts, William Martin
 ; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
 ; FILE OF INVENTION: Target Genes
 ; FILE REFERENCE: AM101083 (031896-042099)
 ; CURRENT APPLICATION NUMBER: US/60/545,213
 ; CURRENT FILING DATE: 2004-02-18
 ; NUMBER OF SEQ ID NOS: 303284
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 4195
 ; LENGTH: 600
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-60-545-213-4195

Alignment Scores:
 Pred. No.: 1.28e-111 Length: 600
 Score: 983.50 Matches: 199
 Percent Similarity: 90.45% Conservative: 0
 Best Local Similarity: 90.45% Mismatches: 0
 Query Match: 44.40% Indels: 21
 DB: 7 Gaps: 1

US-10-016-647-2 (1-425) x US-60-545-213-4195 (1-600)

Qy 134 ValLeuGlyArgAspGluAlaArgProGlyAlaGluAlaAlaProSerArgArgTrp 153
 Db 2 GTGCTGGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 61
 Qy 154 LeuGluArgMetArgArgThrPheGluGluProThrSerSerLeuAlaAlaGlnIleLeu 173

Db 62 CTGAGCGCATGCGCGGACCTTCGAGGAGCCACGCTCGCTGCGCGCGCAGATCCTG 121
 Qy 174 AlaserValSerValValPheValIleValSerMetValValLeuCysAlaSerThrLeu 193
 Db 122 GCTAGCGTGTGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 181
 Qy 194 ProAspTrpArgAsnAlaAlaAspAsnArgSerLeuAspAspArgSerArgIleIle 213
 Db 182 CCCGACTGGCGCAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 241
 Qy 214 GluAlaIleCysIleGlyTrpPheThrAlaGluCysIleValArgPheIleValSerLys 233
 Db 242 GAAGCTATCTGCATAGTGTGTTTCACTGCGGAGTGCATCGTGGGTTTCAATGCTCCAAA 301
 Qy 234 AsnLysCysGluPheValLysArgProLeuAsnIleIleAspLeuLeuAlaIleThrPro 253
 Db 302 AACAGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTTACTGCGCAATCAGCGCG 361
 Qy 254 TyrTyrIleSerValLeuMetThrValPheThrGlyGluAsnSerGlnLeuGlnArgAla 273
 Db 362 TATTACATCTCTGTGTGATGACAGTGTTCACAGCGGAGAACTCTCAACTCCAGAGGGCT 421
 Qy 274 GlyValThrLeuArgValLeuArgMetMetArgIlePheThrValIleLysLeuAlaArg 293
 Db 422 GGAGTCACCTTGAGG----- 436
 Qy 294 HisPheIleGlyLeuGlnThrLeuGlyLeuLysArgCysTyrArgGluMetVal 313
 Db 437 -----ACACTCGGTTTGACTCTCAACGTTGTACCGAGAGATGGTT 478
 Qy 314 MetLeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeu 333
 Db 479 ATGTACTTGTCTTCATTGTGTGTCATGCGCAATCTTTAGTGCATCTTCTCAGCTTCTT 538
 Qy 334 GluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIleProAlaAlaCys 353
 Db 539 GAACATGGCTGGACCTGGAAACATCAACAGGACTTTACAGGACTTCTGCTGCTGCTGC 598

RESULT 3

US-60-545-213-8466
 ; Sequence 8466, Application US/60545213
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Mounts, William Martin
 ; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
 ; FILE OF INVENTION: Target Genes
 ; FILE REFERENCE: AM101083 (031896-042099)
 ; CURRENT APPLICATION NUMBER: US/60/545,213
 ; CURRENT FILING DATE: 2004-02-18
 ; NUMBER OF SEQ ID NOS: 303284
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 8466
 ; LENGTH: 600
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-60-545-213-8466

Alignment Scores:
 Pred. No.: 1.28e-111 Length: 600
 Score: 983.50 Matches: 199
 Percent Similarity: 90.45% Conservative: 0
 Best Local Similarity: 90.45% Mismatches: 0
 Query Match: 44.40% Indels: 21
 DB: 7 Gaps: 1

US-10-016-647-2 (1-425) x US-60-545-213-8466 (1-600)

Qy 134 ValLeuGlyArgAspGluAlaArgProGlyAlaGluAlaAlaProSerArgArgTrp 153
 Db 2 GTGCTGGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 61
 Qy 154 LeuGluArgMetArgArgThrPheGluGluProThrSerSerLeuAlaAlaGlnIleLeu 173

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Db      62  CTGAGGCGCATCGCGGACCTTCGAGGAGCCACGTCGTCGTCGCGCGGAGATCCTG 121
Qy      174  AlaSerValSerValValPheValIleValSerMetValValLeuCysAlaSerThrLeu 193
Db      122  GCTAGCGTGTGCGTGTGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 181
Qy      194  ProAspTirArgAsnAlaAlaAspAsnArgSerLeuAspArgSerArgIleIle 213
Db      182  CCCGACTGGCGAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 241
Qy      214  GluAlaIleCysIleGlyTirPheThrAlaGluCysIleValArgPheIleValSerIys 233
Db      242  GAAGCTATCTGCATAGTGTGTTCACTGCGGAGTCGTCGTCGTCGTCGTCGTCGTCGTC 301
Qy      234  AsnLysCysGluPheValLysArgProLeuAsnIleIleAspLeuLeuAlaIleThrPro 253
Db      302  AACAGTGTGAGTGTGTGTCAGAGACCCCTGAACATCATTTGTCGCAATCAGCGG 361
Qy      254  TyrTyrIleSerValLeuMetThrValPheThrGlyGluAsnSerGlnLeuGlnAla 273
Db      362  TATTACATCTCTGTGTGTGTCAGAGTGTTCACAGCGGAGAACTCTCAACTCCAGAGG 421
Qy      274  GlyValThrLeuArgValLeuArgMetMetArgIlePheTirPheValIleLysLeuAla 293
Db      422  GGAGTCACCTTGAGG-----ACACTCGGTTTGACTCTCAACAGCTTACCAGCATTCCTGCTGCTGC 436
Qy      294  HisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyrArgGluMetVal 313
Db      437  -----ACACTCGGTTTGACTCTCAACAGCTTACCAGCATTCCTGCTGCTGC 478
Qy      314  MetLeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeu 333
Db      479  ATGTTACTTGTCTTCACTTTGTTGTCATGTCGCAATCTTTAGTGCACTTTCTCAGCTTCT 538
Qy      334  GluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIleProAlaAlaCys 353
Db      539  GAACATGGCTGACCTGGAACATCCAAACAGGACTTTACCAGCATTCCTGCTGCTGC 598

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RESULT 4

```

US-60-545-213-8457
; Sequence 8467, Application US/60545213
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042099)
; CURRENT APPLICATION NUMBER: US/60/545,213
; CURRENT FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8467
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-545-213-8467

```

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Alignment Scores:
Pred. No.: 1,28e-111 Length: 600
Score: 983.50 Matches: 199
Percent Similarity: 90.45% Conservative: 0
Best Local Similarity: 90.45% Mismatches: 0
Query Match: 44.40% Indels: 21
DB: 7 Gaps: 1

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US-10-016-647-2 (1-425) x US-60-545-213-8467 (1-600)

```

Qy      134  ValLeuGlyArgAspGluAlaArgProGlyGlyAlaGluAlaAlaProSerArgTirp 153
Db      2  GTGCTGGCGCGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 61
Qy      154  LeuGluArgMetArgThrPheGluGluProThrSerSerLeuAlaAlaGlnIleLeu 173

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Db      62  CTGAGGCGCATCGCGGACCTTCGAGGAGCCACGTCGTCGTCGTCGTCGTCGTCGTCGTCG 121
Qy      174  AlaSerValSerValValPheValIleValSerMetValValLeuCysAlaSerThrLeu 193
Db      122  GCTAGCGTGTGCGTGTGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 181
Qy      194  ProAspTirArgAsnAlaAlaAspAsnArgSerLeuAspArgSerArgIleIle 213
Db      182  CCCGACTGGCGAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 241
Qy      214  GluAlaIleCysIleGlyTirPheThrAlaGluCysIleValArgPheIleValSerIys 233
Db      242  GAAGCTATCTGCATAGTGTGTTCACTGCGGAGTCGTCGTCGTCGTCGTCGTCGTCGTC 301
Qy      234  AsnLysCysGluPheValLysArgProLeuAsnIleIleAspLeuLeuAlaIleThrPro 253
Db      302  AACAGTGTGAGTGTGTGTCAGAGACCCCTGAACATCATTTGTCGCAATCAGCGG 361
Qy      254  TyrTyrIleSerValLeuMetThrValPheThrGlyGluAsnSerGlnLeuGlnAla 273
Db      362  TATTACATCTCTGTGTGTGTCAGAGTGTTCACAGCGGAGAACTCTCAACTCCAGAGG 421
Qy      274  GlyValThrLeuArgValLeuArgMetMetArgIlePheTirPheValIleLysLeuAla 293
Db      422  GGAGTCACCTTGAGG-----ACACTCGGTTTGACTCTCAACAGCTTACCAGCATTCCTGCTGCTGC 436
Qy      294  HisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyrArgGluMetVal 313
Db      437  -----ACACTCGGTTTGACTCTCAACAGCTTACCAGCATTCCTGCTGCTGC 478
Qy      314  MetLeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeu 333
Db      479  ATGTTACTTGTCTTCACTTTGTTGTCATGTCGCAATCTTTAGTGCACTTTCTCAGCTTCT 538
Qy      334  GluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIleProAlaAlaCys 353
Db      539  GAACATGGCTGACCTGGAACATCCAAACAGGACTTTACCAGCATTCCTGCTGCTGC 598

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RESULT 5

```

US-10-796-280-586
; Sequence 586, Application US/10796280
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001510
; CURRENT APPLICATION NUMBER: US/10/796,280
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 68533
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 586
; LENGTH: 4656
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-796-280-586

```

```

Alignment Scores:
Pred. No.: 2,35e-84 Length: 4656
Score: 774.50 Matches: 171
Percent Similarity: 59.53% Conservative: 82
Best Local Similarity: 40.24% Mismatches: 162
Query Match: 34.97% Indels: 12
DB: 6 Gaps: 5

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US-10-016-647-2 (1-425) x US-10-796-280-586 (1-4656)

```

Qy      1  MetThrPheGlyArgSerGlyAlaAlaSer-----ValValLeuAsnValGlyAla 18
Db      225  ATGAGATCGTCGCGACCAAGCGGTCTCTCGCGCGGTCCGCTCAACGTCGGGGGCTG 284
Qy      19  ArgTyrSerLeuSerArgGluLeuLeuLysAspPheProLeuArgValSerArgLeu 38
Db      285  GCGCAGCAGGTACTCTGCGGTACCTTGGACCGCTGCGCGCGCGCGCGCGCGCGCGCG 344

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;
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in ver. 2.1
; SEQ ID NO 1
; LENGTH: 2103
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human alpha subunit of voltage-gated potassium
; OTHER INFORMATION: channel Kv10.1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (151)..(1788)
; OTHER INFORMATION: Kv10.1
US-10-815-297-1
Alignment Scores:
Pred. NO.: 7,27e-68 Length: 2103
Score: 636.50 Matches: 148
Percent Similarity: 53.96% Conservative: 77
Best Local Similarity: 35.49% Mismatches: 159
Query Match: 28.74% Indels: 33
DB: Gaps: 10
US-10-016-647-2 (1-425) x US-10-815-297-1 (1-2103)
Qy 13 LeuAsnValGlyGlyAlaArgTyrSerLeuSerArgGluLeuLeuLysAspPheProLeu 32
Db 451 GTGAACCTGGGTGGCCACAGCTACAGCTAGCTGAGCTGGCGGCTTCCCAAG 510
Qy 33 ArgArgValSerArgLeuHisGlyCysArgSerGluArgAspValLeuGluValCysAsp 52
Db 511 ACGCGCTAGTGTGGCTGGCCACCTCCACAGCGCGAGCCGACGCTAAGCTGTGGAC 570
Qy 53 AspTyrAspArgGluArgAsnGluTyrPhePheAspArgHisSerGluAlaPheGlyPhe 72
Db 571 GACTACAGAGAGACAGACAGATATCTTTCGACCGCCAGCCGCGCTTCCAGCTG 630
Qy 73 IleLeuLeuTyrValArgGlyHisGlyLysLeuArgPheAlaProArgMetCysGluLeu 92
Db 631 GTCTACAATTCTACCTGTCC--GGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 687
Qy 93 SerPheTyrAsnGluMetIleTyrTyrGluGluGluGluGluGluGluGluGluGluGlu 112
Db 688 CGTTCCTGGAGAGCTGGGCTACTGGGGCTGGGGCTCAAGTACAGCCACGCTGTGTG 747
Qy 113 -----GlnArgArg-----LeuAspAspArgMetSerAspThrThrThr 125
Db 748 CGCATCTGCTTCGAGGAGCGCGCGAGCTGAGCGAAGCGCTCAAGATCCACAGCAG 807
Qy 126 PheTyrSer-----AlaAspGluProGlyValLeuGlyArgAspGluAlaArgPro 142
Db 808 CTGCGCGCGAGCGCGAGGTGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 867
Qy 143 GlyGlyAlaGluAlaAlaProSerArgArgTyrLeuGluArgMetArgArgThrPheGlu 162
Db 868 GGC-----CCGACGCGCGC-----CGCCTCTGGAACCTCATGAG 903
Qy 163 GluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValPheValIle 182
Db 904 AAGCCATTCTCTCGTGGCGCGCCAGGCGCATCTCCGCGGAGGAGGAGGAGGAGGAGGAG 963
Qy 183 ValSerMetValValLeuCysAlaSerThrLeuProAspTyrArgAsnAlaAlaAsp 202
Db 964 GTCTCCGTGGTGGCGCTGGCGCTCAACAGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1023
Qy 203 AsnArgSerLeuAspAspArgSerArgIle-----IleGluAlaIleCysIleGly 219
Db 1024 GCGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1083
Qy 220 TrpPheThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGluPheVal 239
Db 1084 TTCTTACGCTCGAGTACCTGCTGCGCTAGCTTCCACGCCCGCGCGCGCGCGCGCGCGCG 1143

```

RESULT 7

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US-10-815-297-1
; Sequence 1. Application US/10815297
; GENERAL INFORMATION:
; APPLICANT: Jægla, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: Kv10.1, a Novel Voltage-Gated Potassium Channel From
; TITLE OF INVENTION: Human Brain
; FILE REFERENCE: 018512-005910US
; CURRENT APPLICATION NUMBER: US/10/815,297
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US/03/833,466
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/197,793

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Qy 240 LysArgProLeuAsnIleLeuAspLeuLeuAlaIleThrProTyrTyrIleSerValLeu 259
Db 1144 CGAGCGCCCTCAACCTGGTGGAGCCTGGTGGCCATCTCGCGCTACCTTACGCTGGTG 1203
Qy 260 MetThrValPheThrGlyGluAenSerGln- - - - -LeuGlnArg 272
Db 1204 CTGAGTGCTTACGGCGAGGGCCACCAACGGCGGACAGCGTGGCGGAGTGGGTAAG 1263
Qy 273 AlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTrpValIleLysLeuAla 292
Db 1264 GTGGGTCAAGTGTGGCGTCAATCGCGCTCATCGCATCTTCGGCATCTCAAGCTGGCG 1323
Qy 293 ArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyrArgGluMet 312
Db 1324 CGGCATCCACCGGAGTGGCTGGCTTCACGCTGGCCAGTGTACAGCAGGTTG 1383
Qy 313 ValMetLeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeu 332
Db 1384 GGCTGCTGCTGCTTCATCGCATGGCATCTTCATCTTCCTCGGCTGCTACTCT 1443
Qy 333 LeuGluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIleProAlaAla 352
Db 1444 GTGGAGCAC- - - - -GATGGCCAGCAGCAAC- - - - -TTCACTACCATCCCTCC 1491
Qy 353 CysTrpTrpValIleIleSerMetThrThrValGlyTyrGlyAspMetTyrProIleThr 372
Db 1492 TGGTGGTGGCGCGGAGCATCTCCACGCTGGGTGCTAGGAGACATGTACCCAGAGACC 1551
Qy 373 ValProGlyArgIleLeuGlyGlyValCysValValSerGlyIleValLeuLeuAlaLeu 392
Db 1552 CACCTGGCGAGGTTTGGCTTCCTCTGCTGCTGCTTTGGGATCATCTTCAACGGGATG 1611
Qy 393 ProIleThrPheIleTyrHisSerPheValGlnCysTyrHisGluLeuLys 409
Db 1612 CCCATTCATCTCTACAAAGTTTTCGTATTACTACAGCAAGCTGAAG 1662

RESULT 8
PCT-US04-03417-9
; Sequence 9, Application PC/TUS0403417
; GENERAL INFORMATION:
; APPLICANT: Kelly, Louise M.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Farlow, Deborah
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 9118, 990, 17662, 81982, 630,
; TITLE OF INVENTION: 21472, 17692, 19290, 21620, 21689, 28859, 53659, 64549,
; TITLE OF INVENTION: 9455, 23544, 7366, 27417, 57259, 21844, 943, 2061, 5891,
; TITLE OF INVENTION: 9137, 13908, 14310, 17600, 25584, 27824, 28469, 38947,
; TITLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 12405 OR
; FILE REFERENCE: MPI03-015
; CURRENT APPLICATION NUMBER: PCT/US04/03417
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US 60/445,241
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/448,389
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/456,320
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/460,279
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/465,924
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/470,052
; PRIOR FILING DATE: 2003-05-13
; PRIOR APPLICATION NUMBER: US 60/498,106
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/500,179
; PRIOR FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US 60/502,909
; PRIOR FILING DATE: 2003-09-15
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; PRIOR APPLICATION NUMBER: US 60/510,351
; PRIOR FILING DATE: 2003-10-10
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 3303
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (381)...(1952)
PCT-US04-03417-9

Alignment Scores:
Pred. No.: 6.92e-60 Length: 3303
Score: 574.50 Matches: 138
Percent Similarity: 53.22% Conservative: 85
Best Local Similarity: 32.94% Mismatches: 137
Query Match: 25.94% Indels: 59
DB: 1 Gaps: 12

US-10-016-647-2 (1-425) x PCT-US04-03417-9 (1-3303)
Qy 11 ValValLeuAsnValGlyGlyAlaArgTyrSerLeuSerArgGluLeuLeuLysAspPhe 30
Db 540 GTGTGTCATCAATCTCCGGCTGCTTCGAGACGCGAGCTGAAGACCTTTGCCAGTTC 599
Qy 31 ProLeuArgValSerArgLeuHisGlyCysArgSerGluArgAspValLeuGluVal 50
Db 600 CCC- - - - -GAGACGCTGCTGGCGACCCCAAGCGCGCC- - - - - 632
Qy 51 CysAspAspTyrAspArgGluArgAsnGluTyrPhePheAspArgHisSerGluAlaPhe 70
Db 633 ATGAGGTACTTCGACCGCTCCGCAACAGTACTTCTTCGCGCAACCGCCAGCTTC 692
Qy 71 GlyPheIleLeuLeuTyrValArgGlyHisGlyLysLeuArgPheAlaProArgMetCys 90
Db 693 GACGCCATCTCTACTACTATCATCATCGCGGGGCGCATCCGC- - -CGGCGGTCAACGTG 749
Qy 91 GluLeuSerPheTyrAsnGluMetIleTyrTrpGlyLeuGluGlyAlaHisLeuGluTyr 110
Db 750 CCATCCACATTTCTCCGAGGATCCGCTTC- - - - - 782
Qy 111 CysCysGlnArgArgLeuAspAspArgMetSerAspThrTyrThrPheTyrSerAlaAsp 130
Db 783 - - - - -TACCAGCTGGCGAGGAGGCCATGGAGAAGTTC- - - - -CGCGAG 821
Qy 131 GluProGlyValLeuGlyArgAspGluAlaArgProGlyGlyAlaGluAlaAlaProSer 150
Db 822 GACGAGGCTTCCG- - -CGGAGGAGGAGCGGCC- - - - -TTGCCCGCG 863
Qy 151 ArgArgTrpLeuGluArgMetArgTyrPheGluGluProThrSerSerLeuAlaAla 170
Db 864 CGCGACTTCCAGCGCCAGGTGTGCTCTCTTCAGGTACCCCGAGAGCTCCGCGCGCGCC 923
Qy 171 GlnIleLeuAsnValSerValValPheValPheValSerMetValValLeuCysAla 190
Db 924 CGGGGATCCCATCGGTCCGTCCGTCTCATCTCATCTTCATCTTCATCTTCGCTG 983
Qy 191 SerThrLeuProAspTrpArg- - - - - 197
Db 984 GAGACGCTGCGGAGTTCCGCGAGAGAGACTACCCGCTCGAGTCGAGGACTCA 1043
Qy 198 - - - - -AsnAlaAlaAspAsnArg- - - - -SerLeuAspAsp 208
Db 1044 TTCGAGCAGCGCGCAACAGCAGCTCGGGTCCGCGAGGAGCCCTCCAGCTTCTCCGAT 1103
Qy 209 ArgSerArgIleIleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleValArg 228
Db 1104 CCCTTCTTCGTGGTGGAGCGCTGTCATCATCTGCTTCCTTCGACTGCTGGTGG 1163
Qy 229 PheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsnIleLeuAspLeu 248
```

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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 3303
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (381)...(1952)
US-10-772-636-9
Alignment Scores:
Pred. No.: 6,92e-60 Length: 3303
Score: 574.50 Matches: 138
Percent Similarity: 53.22% Conservative: 85
Best Local Similarity: 32.94% Mismatches: 137
Query Match: 25.94% Indels: 59
DB: 6 Gaps: 12

US-10-016-647-2 (1-425) x US-10-772-636-9 (1-3303)
QY 11 ValValLeuAsnValGlyAlaArgTy-SerLeuSerArgGluLeuLeuLysAspPhe 30
DB 540 GTGGTCATCAATCTCGGGCTCGCTTCGAGAGCGAGCTGAAGACCCITTCGCGAGTTC 599
QY 31 ProLeuArgArgValSerArgLeuHisGlyCysArgSerGluArgAspValLeuVal 50
DB 600 CCC-----GAGAGCTGCTGGGGAGCCCAAGCGCGC----- 632
QY 51 CysAspAspTyrAspArgGluArgAsnGluTyr-PhePheAspArgHisSerGluAlaPhe 70
DB 633 ATGAGGTACTTCGACCGCTCCGCAACAGAGTACTTCTTCGACCGCAACCGCGCGAGTTC 692
QY 71 GlyPheLeuLeuLeuTyrValArgGlyHisGlyLysLeuArgPheAlaProArgMetCys 90
DB 693 GACGCCATCTCTACTACTATCATGTCGGGGGCGCATCCGCGC---CGGCGCGTCAACGTG 749
QY 91 GluLeuSerPheTyrAsnGluMetIleTyrTrpGlyLeuGluGlyAlaHisLeuGluTyr 110
DB 750 CCCATCGACATTTCTCCGAGAGATCCGCTTC----- 782
QY 111 CysCysGlnArgLeuAspArgMetSerAspThrTyrThrPheTyrSerAlaAsp 130
DB 783 -----TACAGCTGGGGAGGAGCCATGGAAGTTC-----CGGAG 821
QY 131 GluProGlyValLeuGlyArgAspGluAlaArgProGlyGlyAlaGluAlaAspSer 150
DB 822 GACGAGGGCTTCCTG---CGGAGGAGGAGCGGCGC-----TTGCGCGCGC 863
QY 151 ArgArgTrpLeuGluArgMetArgArgThrPheGluGluProThrSerSerLeuAlaAla 170
DB 864 CGGACTTCCAGCGCGAGGTGTGCTCTTCGAGTACCCCGAGAGCTCGCGGCGCGC 923
QY 171 GlnLeuLeuAlaSerValValPheValLeuValSerMetValValLeuCysAla 190
DB 924 CGGGGATCGGCATCGTGTGCTGTCATCTCATCTCCATTCATCTTCGCTGCTGCTGCTG 983
QY 191 SerThrLeuProAspTrpArg----- 197
DB 984 GAGACGCTGCCGAGGTTCGCGAGAGAGAGACTACCCGCGCTCGAGCTCGACGACTCA 1043
QY 198 -----AsnAlaAlaAspAsnArg-----SerLeuAspAsp 208
DB 1044 TTCGAGGAGCGCGGCAACAGCACGCTCGGGGTCCCGCGAGGAGCTCCAGCTTCCTCCAT 1103
QY 209 ArgSerArgIleLeuGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleValArg 228
DB 1104 CCCTTCTTCGTGGTGGAGACGCTGTGCATCATCTGGTCTCTCCCTCGAACTCTGCTGCGG 1163
QY 229 PheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsnIleIleAspLeu 248
DB 1164 TTCCTCGCTTCTCTAGCAAGCCACCTTCTTCGGAACATCATGACCTGATCGACATT 1223

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RESULT 9

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US-10-772-636-9
; Sequence 9, Application US/10772636
; GENERAL INFORMATION:
; APPLICANT: Kelly, Louise M.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Farlow, Deborah
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 9118', 990, 17662, 81982, 630,
; TITLE OF INVENTION: 21472, 17692, 19290, 21620, 21689, 28899, 53659, 64549,
; TITLE OF INVENTION: 9465, 23544, 7366, 27417, 57259, 21844, 943, 2061, 5891,
; TITLE OF INVENTION: 9137, 13908, 14310, 17600, 25584, 27824, 28469, 38947,
; TITLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 12405 OR
; TITLE OF INVENTION: 5014
; FILE REFERENCE: MPI03-015PIRNOWNIM
; CURRENT APPLICATION NUMBER: US/10772,636
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US 60/445,241
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/448,389
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/456,320
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/460,279
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/465,924
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/470,052
; PRIOR FILING DATE: 2003-05-13
; PRIOR APPLICATION NUMBER: US 60/498,106
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/500,179
; PRIOR FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US 60/502,909
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/510,351
; PRIOR FILING DATE: 2003-10-10

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Db 1814 CAGCAGGAGCAGCAACAGCCAGTGGAGGAGCGGCCAGAAATGGCGAGCCCATGTCC 1873
Qy 274 GlyValThrLeuArgValLeuArgMetMetArgIlePheTrpValIleLysLeuAlaArg 293
Db 1874 CTGGCCATCCTCCGAGTCATCCGCTGGTCCGGGTTCGCGATCTTCAAGCTCTCCCGC 1933
Qy 294 HisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyArgGluMetVal 313
Db 1934 CACTCCAGGGGCTGCAGATCTCGGCAAGACCTTGCAGCGCTCCATGAGGAGCTGGG 1993
Qy 314 MetLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeu 333
Db 1994 CTGCTCATCTTCTCTCTCATCGGCTCACTCTCTCCAGCTCTCTCCAGCTCTCTCC 2053
Qy 334 GluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIleProAlaAlaCys 353
Db 2054 GAG-----GCTGACCATGACGATTCGCTTTTCCAGCATCCCGATGCCCTTC 2101
Qy 354 TrpTrpValIleSerMetThrThrValGlyTyrGlyAspMetTyProIleThrVal 373
Db 2102 TGGTGGCAGTGGTTACAAATGACCAACGCTAGGTACGGGGACATGTACCCCATGACTGTG 2161
Qy 374 ProGlyArgIleLeuGlyValCysValValSerGlyIleValLeuLeuAlaLeuPro 393
Db 2162 GGGGAAATCGTGGGCTCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2221
Qy 394 IleThrPheIleTyHisSerPheValGlnCysTyHis 406
Db 2222 GTGGCGGTATCGTCTCCAACCTCACTACTTCTACCAC 2260
RESULT 11
US-10-768-158-9
; Sequence 9, Application US/10768158
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Karichei, Venkateswarlu
; APPLICANT: Eliassof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 16386, 15402, 21165, 1423,
; TITLE OF INVENTION: 636, 12303, 21425, 27410, 38554, 38555, 55063, 57145, 59914,
; TITLE OF INVENTION: 94921, 16852, 33260, 58573, 30911, 85913, 14303, 16816,
; TITLE OF INVENTION: 17827 OR 32620
; FILE REFERENCE: MPI03-012PIRNOMIN
; CURRENT APPLICATION NUMBER: US/10768,158
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: US 60/444,781
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/452,291
; PRIOR FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: US 60/454,540
; PRIOR FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: US 60/478,805
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/491,048
; PRIOR FILING DATE: 2003-07-30
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 4234
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (863)...(2452)
US-10-768-158-9
Alignment Scores:
Pred. No.: 7e-56 Length: 4234
Score: 543.50 Matches: 144
Percent Similarity: 45.45% Conservative: 71
Best Local Similarity: 30.44% Mismatches: 149
Query Match: 24.54% Indels: 109
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DB: 6 Gaps: 12
US-10-016-647-2 (1-425) x US-10-768-158-9 (1-4234)
Qy 4 GlyArgSerGlyAlaAlaSer-----ValValLeuAsnValGlyGlyAlaArgTyr 20
Db 959 GGGGGGGGGGGCTGTGTAGTAGCGAGCGCTGTGATCAATATCTCCGGGCTGCGCTTT 1018
Qy 21 SerLeuSerArgGluLeuLysAspPheProLeuArgValSerArgLeuHisGly 40
Db 1019 GAGACACAATTGGCCACCTGTGCTGTTTCCG-----GACACGCTGCTCGGA 1066
Qy 41 CysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArgAsnGlu 60
Db 1067 GACCTCGCCGGCGA-----GTCCGCTTCTTCGACCCCTTGAGAGAGAG 1111
Qy 61 TyrPhePheAspArgHisGluAlaPheGlyPheIleLeuLeuTyrValArgGlyHis 80
Db 1112 TACTTCTTCGACCGCAACCGCCAGCTTCGACGCCATCTCTACTACTACCATCTGGG 1171
Qy 81 GlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyr 100
Db 1172 GCGCGCTGCGG---AGCGCGGTCAAGTGCCTCGACATTTTCTTGGAGAGATC-- 1225
Qy 101 TrpGlyLeuGluGlyAlaHisLeuGluTyrCysCysGlnArgArgLeuAspArgMet 120
Db 1226 -----CGCTTCTACCATCTGGG 1243
Qy 121 SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeu-----GlyArg 137
Db 1244 GACGAGGCCCTGGCGGCTTCGGGAGGAGCAG---GGCTGCTGCGCGAAGGTGGCGAG 1300
Qy 138 AspGluAlaArgProGlyGlyAlaGluAlaAlaProSerArgArgTrpLeuGluArgMet 157
Db 1301 GACGAG-----AAGCGCTGCCCTCCAGCCCTTCCAGCGCCAGGTG 1342
Qy 158 ArgArgThrPheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSer 177
Db 1343 TGGCTGCTCTTTAGTACCCAGAGAGCTCGGGCGCGCCAGGCGCATCGCATCTCC 1402
Qy 178 ValValPheValIleValSerMetValValLeuCysAlaSerThrLeuProAspTrpArg 197
Db 1403 GTGTTGTGTTCTTCATCTCATATGATCTCTTTTTCCTGGAGACCTTACCCAGTTCGT 1462
Qy 198 AsnAlaAlaAlaAspAsnArgSer----- 205
Db 1463 -----GTAGATGTCGAGGTGGAAACAATGGTGTGTGAGTCGAGTCTCCCGAGTT 1513
Qy 205 ----- 205
Db 1514 TCCAGGGGAGTCAGGAGAGAGAGGAGGATGAAGACGATTCTCTACACATTTTCATGGC 1573
Qy 205 ----- 205
Db 1574 ATCACCCTGGGAAATGGGAGCGGGGCTCTCTCCTACCTACCTACTCTTGGGGGCTCC 1633
Qy 206 ---LeuAspAspArgSerArgIleIleGluAlaIleCysIleGlyTyrPheThrAlaGlu 224
Db 1634 TTCATTACAGACCCCTTCTTCTGTTGAGAGCGGTGTGATTTGCTGTTTTCATCTTTCG 1693
Qy 225 CysIleValArgPheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsn 244
Db 1694 CTCCTGTGCTGCTTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1753
Qy 245 IleIleAspLeuLeuAlaIleThrProTyrTyrIleSerValLeuMetThrValPheThr 264
Db 1754 ATCATTTGCTGGTGGCTATCTTCTCCCTACTCTACCTCTGGGCGCATGAGCTGGTGCAG 1813
Qy 265 -----GlyGluAsnSerGlnLeuGluAlaArg 273
Db 1814 CAGCAGGAGCAGCAACAGCCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1873
Qy 274 GlyValThrLeuArgValLeuArgMetMetArgIlePheTrpValIleLysLeuAlaArg 293
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Db      1874  CTGGCCATCTCCGAGCATCCGCTGGTCCGGGTGTCCGCATCTTCAAGCTCTCCCGC 1933
Qy      294  HisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyrArgGluMetVal 313
Db      1934  CACTCCAAGGGGCTGCAGATCTCTGGGCAAGACCTTGCAGGCTCCATGAGGGAGCTGGG 1993
Qy      314  MetLeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeu 333
Db      1994  CTGCTCATCTTCTTCCTTCATCGGGGTTCATCTCTCCAGTCCGCTACTTCCGCA 2053
Qy      334  GluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIleProAlaAlaCys 353
Db      2054  GAG-----GCTGACGATGACGATTCGCTTTTCCAGCATCCCGGATGCTTC 2101
Qy      354  TrpTrpValIleIleSerMetThrThrValGlyTyrGlyAspMetTyrProIleThrVal 373
Db      2102  TGTGGGCAAGTGTACAAATGACCAAGTGTAGTTACGGGACATGTACCCCATGACTGTG 2161
Qy      374  ProGlyArgIleLeuGlyGlyValCysValValSerGlyIleValLeuLeuAlaLeuPro 393
Db      2162  GGGGGAAGATGTGGGCTCGCTGTGTGTCATCGTGGGTCTCTCACCATTGCCCTGCT 2221
Qy      394  IleThrPheIleTyrHisSerPheValGlnCysTyrHis 406
Db      2222  GTGCCCGTCATCGTCTCCAACTTCAACTACTTCTACCAC 2260

RESULT 12
US-10-796-280-12293/c
; Sequence 12293, Application US/10796280
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001510
; CURRENT APPLICATION NUMBER: US/10/796, 280
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 68533
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12293
; LENGTH: 64206
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-796-280-12293

Alignment Scores:
Pred. No.: 7,45e-53 Length: 64206
Score: 534.50 Matches: 105
Percent Similarity: 65.10% Conservative: 61
Best Local Similarity: 41.18% Mismatches: 84
Query Match: 24.13% Indels: 5
DB: 6 Gaps: 2

US-10-016-647-2 (1-425) x US-10-796-280-12293 (1-64206)
Qy      169  AlaAlaGlnIleLeuAlaSerValSerValPheValIleValSerMetValValLeu 188
Db      62556  TCTTCACAGATCTTGCATATATTTCCATCATGTTTCATCGTCTCTCCACCATGCGCTG 62497
Qy      189  CysAlaSerThrLeuProAspTyrArgAsnAlaAlaAspAsnArgSerLeuAspAsp 208
Db      62496  TCCTCAACAGCTGCTGAGCTACAGAGCTCGATGAGTTCGGCCAGTCCACAGACAAC 62437
Qy      209  ---ArgSerArgIleIleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleVal 227
Db      62436  CCCAGCTGCCGCACGTGAGCGCGTGTGCTGCTGATGCTGATGTTTCCATGAGTACCTGCTG 62377
Qy      228  ArgPheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsnIleIleAsp 247
Db      62376  AGTTTCTCTCTCGCCCAAGAGTGAAGTTCCTCAAGGGGCCCTCATGCTCCATTGAC 62317
Qy      248  LeuLeuAlaIleThrProTyrIleSerValLeuMetThrValPheThrGlyGluAsn 267

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Db      62316  TTGTTGGCCATCTCCCATATATGTACCATTTTCTCCACGAATCCACAGAGCGTG 62257
Qy      268  SerGlnLeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTrp 287
Db      62256  CTGCAATTCAGAAATGTCCGCGGTGTGTCCAGATCTTCCGCATCATCGCAATTCCTCGC 62197
Qy      288  ValIleLysLeuAlaAspHisPheIleGlyLeuGlnThrLeuLeuGlyLeuThrLeuLysArg 307
Db      62196  ATCTTAAGCTGTGACGCACTCCACTGGCTCCAGTCTCTGGGCTTCACATTTCCGGAGG 62137
Qy      308  CysTyrArgGluMetValMetLeuLeuValPheIleCysValAlaMetAlaIlePheSer 327
Db      62136  AGCTACATGATGTGGGTCTGCTCATCTCTCTTCCATGGCAATATGATCTTCTCC 62077
Qy      328  AlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThr 347
Db      62076  AGCCTTGTCTTCTTGTCTGAGAGGATGAGGAC-----GACACCAAGTTCAAA 62029
Qy      348  SerIleProAlaAlaCysTyrTrpValIleIleSerMetThrThrValGlyTyrGlyAsp 367
Db      62028  AGCATCCAGGCTCTTCTGTGTGGCCACCATCACCATGACTCTGTGGGTATGGAGAC 61969
Qy      368  MetTyrProIleThrValProGlyArgIleLeuGlyValCysValValSerGlyIle 387
Db      61968  ATCTACCCCAAGACTCTCTGGGGAATTTGTGGGGACTCTGCTGCATTCAGGAGTCTC 61909
Qy      388  ValLeuLeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCysTyrHisGlu 407
Db      61908  CTGTTGATGTCTTCCCATCCCATCTCATTAATCTCTGAGTCTCTATAAGGAG 61849
Qy      408  LeuLysPheArgSerAlaArgTyrSerArgSerLeuSerThrGlu 422
Db      61848  CAGAAGACAGAGAGAGAAAGCAATCAACGCGGAGAGCTCTGGAG 61804

RESULT 13
US-10-796-280-12305/c
; Sequence 12305, Application US/10796280
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001510
; CURRENT APPLICATION NUMBER: US/10/796, 280
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 68533
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12305
; LENGTH: 68305
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-796-280-12305

Alignment Scores:
Pred. No.: 8,24e-53 Length: 68305
Score: 534.50 Matches: 105
Percent Similarity: 65.10% Conservative: 61
Best Local Similarity: 41.18% Mismatches: 84
Query Match: 24.13% Indels: 5
DB: 6 Gaps: 2

US-10-016-647-2 (1-425) x US-10-796-280-12305 (1-68305)
Qy      169  AlaAlaGlnIleLeuAlaSerValSerValPheValIleValSerMetValValLeu 188
Db      62637  TCTTCACAGATCTTGCATATATTTCCATCATGTTTCATCGTCTCTCCACCATGCGCTG 62578
Qy      189  CysAlaSerThrLeuProAspTyrArgAsnAlaAlaAspAsnArgSerLeuAspAsp 208
Db      62577  TCCTCAACAGCTGCTGAGCTACAGAGCTCGATGAGTTCGGCCAGTCCACAGACAAC 62518
Qy      209  ---ArgSerArgIleIleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleVal 227
Db      62517  CCCAGCTGCCGCACGTGAGCGCGTGTGCTGCTGATGCTGATGTTTCCATGAGTACCTGCTG 62458

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QY 228 ArgPheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsnIleIleAsp 247
Db 62457 AGTTTCCTCTCTCCGCCAAGAGTGAAGTTCCTCAAGGCGCCCACTCAATGCCATTGAC 62398
QY 248 LeuLeuAlaIleThrProTyrTyrIleSerValLeuMetThrValPheThrGlyGluAsn 267
Db 62397 TTGTTGGCCATTCTGCCATPACTATGTACCACTTTTCCTCCCAAGATCCCAAGAGCGTG 62338
QY 268 SerGlnLeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTrp 287
Db 62337 CTGCAATTCAGAAATGTCGCGCGTGTGTCAGATCTTCGGCATCATGCGAATTCCTCCG 62278
QY 288 ValIleLeuLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArg 307
Db 62277 ATCCTTAAGCTTGCAGCCACTCCACTGGCCCTCCAGTCTCTGGGCTTCACITTTGGGAGG 62218
QY 308 CysTyrArgGluMetValMetLeuLeuValPheIleCysValAlaMetAlaIlePheSer 327
Db 62217 AGCTAATAGTGTGGCTTGTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 62158
QY 328 AlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThr 347
Db 62157 AGCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 62110
QY 348 SerIleProAlaAlaCysTrpTrpValIleIleSerMetThrThrValGlyTyrGlyAsp 367
Db 62109 AGCATCCAGCCTCTTCTGGTGGGCCACCATCATCATCATCATCATCATCATCATCATCAT 62050
QY 368 MetTyrProIleThrValProGlyArgIleLeuGlyValCysValValSerGlyIle 387
Db 62049 ATCTACCCCAAGACTCTCTGGGAAATTTGGGGACTCTGTCGATTCAGAGATC 61990
QY 388 ValLeuLeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCysTyrHisGlu 407
Db 61989 CTGGTGTGCTCTCTCCCATCCCATCATCATCATCATCATCATCATCATCATCATCATCAT 61930
QY 408 LeuLysPheArgSerAlaArgTyrSerArgSerLeuSerThrGlu 422
Db 61929 CAGAGAGACAGGAGAAAGCAATCAACCGCGAGGAGCTCTGGAG 61885

RESULT 14
US-10-796-280-12388
; Sequence 12388, Application US/10796280
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001510
; CURRENT APPLICATION NUMBER: US/10/796,280
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 68533
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12388
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-796-280-12388

Alignment Scores:
Pred. No.: 2,16e-52 Length: 123593
Score: 534.50 Matches: 105
Percent Similarity: 65.10% Conservative: 61
Best Local Similarity: 41.18% Mismatches: 84
Query Match: 24.13% Indels: 5
DB: 6 Gaps: 2
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US-10-016-647-2 (1-425) x US-10-796-280-12388 (1-123593)
QY 169 AlaAlaGlnIleLeuAlaSerValSerValPheValIleValSerMetValValLeu 188
Db 113659 TCCTCACAGATCTCTGCCATAATTTCCATCATGCTTCATCCCATTCGCCCTG 113718
```

```
QY 189 CysAlaSerThrLeuProAspTrpArgAsnAlaAlaIleAspIleArgSerLeuAspAsp 208
Db 113719 TCCTCAACACGCTGCTGAGCTACAGAGCTCGATGAGTTCGCCCATCCACAGACAAC 113778
QY 209 --ArgSerArgIleIleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleVal 227
Db 113779 CCCAGCTGCCACAGTGGAGGCGTGTGCATGCGATGGTTCACCATGGAGTACCTGCTG 113838
QY 228 ArgPheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsnIleIleAsp 247
Db 113839 AGGTTCTCTCTCTGCCCAAGAGTGAAGTCTTCAAGGCGCCCACTCAATGCCATTGAC 113898
QY 248 LeuLeuAlaIleThrProTyrTyrIleSerValLeuMetThrValPheThrGlyGluAsn 267
Db 113899 TTGTTGGCCATTCTGCCATATATGTACCATTTCTCCGATCCCAAGAGCGTG 113958
QY 268 SerGlnLeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTrp 287
Db 113959 CTGCAATTCAGAAATGTCGCGCGTGTGTCAGATCTTCCGATCATGCGAATTCCTCCG 114018
QY 288 ValIleLeuLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArg 307
Db 114019 ATCCTTAAGCTTGCAGCCACTCCACTGGCCTCCAGTCTCTGGGCTTCACITTTGGGAGG 114078
QY 308 CysTyrArgGluMetValMetLeuLeuValPheIleCysValAlaMetAlaIlePheSer 327
Db 114079 AGCTAATAGTGTGGCTTGTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 114138
QY 328 AlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThr 347
Db 114139 AGCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 114186
QY 348 SerIleProAlaAlaCysTrpTrpValIleIleSerMetThrThrValGlyTyrGlyAsp 367
Db 114187 AGCATCCAGCCTCTTCTGGTGGGCCACCATCATCATCATCATCATCATCATCATCATCAT 114246
QY 368 MetTyrProIleThrValProGlyArgIleLeuGlyValCysValValSerGlyIle 387
Db 114247 ATCTACCCCAAGACTCTCTGGGAAATTTGGGGACTCTGTCGATTCAGAGATC 114306
QY 388 ValLeuLeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCysTyrHisGlu 407
Db 114307 CTGGTGTGCTCTTCCCATCCCATCATCATCATCATCATCATCATCATCATCATCATCAT 114366
QY 408 LeuLysPheArgSerAlaArgTyrSerArgSerLeuSerThrGlu 422
Db 114367 CAGAGAGACAGGAGAAAGCAATCAACCGCGAGGAGCTCTGGAG 114411
```

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RESULT 15
US-60-545-213-3833
; Sequence 3833, Application US/60545213
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042099)
; CURRENT APPLICATION NUMBER: US/60/545,213
; CURRENT FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3833
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-545-213-3833

Alignment Scores:
Pred. No.: 9,65e-50 Length: 1400
Score: 487.50 Matches: 112
Percent Similarity: 56.48% Conservative: 58
Best Local Similarity: 37.21% Mismatches: 115
Query Match: 22.01% Indels: 16
```

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DB: 7 Gaps: 5
US-10-016-647-2 (1-425) x US-60-545-213-3833 (1-1400)
QY 129 AlaAspGluProGlyValLeuGlyValAspGluAlaAspProGlyGlyAlaGluAlaA 148
Db 31 GCAGCTCATCTGACACCTGGCGGTGGAGCGCGA---GGCGCGTGGCGCGCTG 87
QY 149 ProSerArgArg-TripLeuGluArgMetArgThrPheGluGluProThrSerSerLe 168
Db 88 CCAGAAGTGGCTCTGG-----AAGTCTCTGGAGAAGCCGAGTCGTCGTG 132
QY 168 uAlaAlaGluLeuAlaSerValSerValPheValPheValValSerMetValValle 188
Db 133 CCGCGCGCGGTGGTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 192
QY 188 uCysAlaSerThrLeuProAspTrpArgAsnAlaAlaAsp---AsnArgSerLeuAs 207
Db 193 GTGCATGGGCACCATCCCGAGCTGCAGGTGCTGGAGCGCGAGGCAACCGCGTGGAGCA 252
QY 207 pAspArgSerArgIleIleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleVa 227
Db 253 CCGGACCTGGAGAACCTGGAGACGGCTGCATTGGCTGCTTCACTGAGTACCTGCT 312
QY 227 LArgPheIleValSerLysAsnLysCysGluPheValLysArgProLeuAsnIleIleAs 247
Db 313 GCGCTCTCTCTGTCACCCACAGCTGCAGTGCCTTCGGCTGCTCTCTCATGAACATTGTGA 372
QY 247 pLeuLeuAlaIleThrProTyrTrpIleSerValLeuMetThrValPheThrGlyGluAs 267
Db 373 CGTGTGGCCATCTCTCCCTTCTACGTGAGCCTCAGCTCAGCCACCTGGGTGCCCGCAT 432
QY 267 nSerGlnLeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTr 287
Db 433 GATGGAGCTAACCACTGCAGAGCGCGGTGGAGCGCTGCGGATCATGCGCATCGCGG 492
QY 287 pValIleLysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysAr 307
Db 493 CATCTTCAAGCTGGCGCGCCACTCTCGGCGCTGCAGACCTCACCCTATGCCCTCAAGCG 552
QY 307 qCysTyrArgGluMetValMetLeuLeuValPheIleCysValAlaMetAlaIlePheSe 327
Db 553 CAGCTTCAAGAACTGGGTGCTGCTCATGTACCTGGCAGTGGGTATCTTCGTCTCTTC 612
QY 327 rAlaLeuSerGlnLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAsp----- 345
Db 613 TGGCTG-----GGCTACACCATGGAGAGAGCCATCCAGAGACCT 654
QY 346 -PheThrSerIleProAlaAlaCysTrpTrpValIleIleSerMetThrThrValGlyTy 365
Db 655 GTTTAAGAGCATCCCGCAGTCTCTCTGGTGGGCCATCATCACCATGACCACCGTGGGCTA 714
QY 365 rGlyAspMetTyrProIleThrValProGlyArgIleLeuGlyGlyValCysValValSe 385
Db 715 CGCGGACATCAACCAAGACCGCTGGCGAGCTCAACGGCGGCATCAGCTTCTTGTG 774
QY 385 rGlyIleValLeuLeuAlaLeuProIleThrPheIleTyrHisSerPheValGlnCysTy 405
Db 775 TGGTGTTCATCGCGCTGCGCCATCCACCCCATCATCAAACTTTGTGAGGTACTA 834
QY 405 rHisGluLeuLysPheArgSerAlaArgTyrSerArgSerLeuSerThrGluPheLeuAs 425
Db 835 CAACAAGCAGCGCTCTGGAGACCGCGGCCAAGCAGAGCTGGAGCTGATGGAACCTCAA 894
QY 425 n 425
Db 895 C 895
```

Search completed: April 19, 2004, 16:49:18
Job time : 321 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 19, 2004, 10:49:58 ; Search time 3475 Seconds
(without alignments)
3652.209 Million cell updates/sec

Title: US-10-016-647-2
Perfect score: 2215
Sequence: 1 MTFGSGAASVVLNVGGARY.....HELKFRSARYSRSLSTFLN 425

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -MODEL=frame; p2n model -DEV=xlh
-Q/cgn2_1/USPTO_spo01/US10016647/runat 19042004 104946 10083/app_query.fasta_1.583
-DB=EST -Qfmt=fastap -SUFFIX=first -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -ENDS=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10016647 @CGN 1.1 3437 @runat 19042004 104946 10083 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_est3:*
12: gb_est4:*
13: gb_est5:*
14: gb_est6:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pin:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_nam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gsl1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1189	53.7	971	29	CNS0206W
2	916	41.4	772	13	BU274588
3	887	40.0	523	9	AI043703
4	838	37.8	509	29	CG639652
5	779.5	35.2	2585	29	AY417318
6	777.5	35.1	2582	29	AY417320
7	757	34.2	484	29	CG662016
8	730	33.0	500	28	AQ402619
9	718.5	32.4	2757	11	AK012275
10	718.5	32.4	4390	11	AK034091
11	705	31.8	1857	11	AK076120
12	697	31.5	2936	11	AK046054
13	696	31.4	1476	29	AY415319
14	692.5	31.3	1503	29	AY398781
15	691	31.2	1406	29	AY398783
16	686	31.0	2360	11	AK087481
17	686	31.0	4111	11	AK048819
18	685	30.9	1476	29	AY415317
19	679.5	30.7	1503	29	AY398782
20	666.5	30.1	487	29	CG582101
21	649.5	29.3	652	12	BJ495239
22	625	28.2	5137	11	BC046490
23	620	28.0	1028	29	CNS04RK5
24	596	26.9	1488	29	AY412413
25	596	26.9	1488	29	AY412415
26	596	26.9	4030	11	AK039559
27	594.5	26.8	1758	29	AY398826
28	593.5	26.8	1758	29	AY398828
29	593.5	26.8	2146	11	BC023222
30	576.5	26.0	505	29	FR0020615
31	574.5	25.9	1572	29	AY400869
32	574.5	25.9	1587	29	AY400871
33	571.5	25.8	1965	29	AY412973
34	571.5	25.8	4780	11	AK036112
35	566	25.6	2946	11	AK045425
36	566	25.6	3458	11	AK044342
37	565.5	25.5	1956	29	AY408065
38	563.5	25.4	1284	29	AY412414
39	563.5	25.4	1944	29	AY408063
40	563.5	25.4	1962	29	AY412971
41	555	25.1	1893	29	AY406812
42	552	24.9	1893	29	AY406814
43	552	24.9	2997	11	AK032268
44	545	24.6	1911	29	AY419307
45	545	24.6	1911	29	AY419309

ALIGNMENTS

RESULT 1
CNS0206W
LOCUS
DEFINITION
221N08 of library G from Tetraodon nigroviridis, genomic survey
971 bp DNA linear GSS 01-SEP-2000
Tetraodon nigroviridis genome survey sequence T7 end of clone
sequence.
ACCESSION
AL175217
VERSION
AL175217.1
KEYWORDS
GSS: genome survey sequence.
SOURCE
Tetraodon nigroviridis
ORGANISM
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE

AUTHORS

Roest Crolius H., Jallou, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fzames, C., Wincker, P., Brotier, P., Quetier, F.,
Saurin, W., and Weissenbach, J.
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)

JOURNAL

MEDLINE

FUBMED

REFERENCE

AUTHORS

Roest Crolius H., Jallou, O., Dasilva, C., Ozouf-Costaz, C.,
Fzames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,
Saurin, W., Bernot, A., and Weissenbach, J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Genome Res. 10 (7), 939-949 (2000)

JOURNAL

MEDLINE

FUBMED

REFERENCE

AUTHORS

Genoscope.
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT

This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/tetraodon.

FEATURES

source

1..971
Location/Qualifiers
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="221N08"
/clone_lib="G"
/notes="Genoscope sequence ID : C0AG221D04LPI-end : T7"

ORIGIN

Alignment Scores:
Prad. No.: 5,78e-122 Length: 971
Score: 1189.00 Matches: 222
Percent Similarity: 79.76% Conservative: 32
Best Local Similarity: 70.09% Mismatches: 38
Query Match: 53.68% Indels: 30
DB: 29 Gaps: 4

US-10-016-647-2 (1-425) x CNS0205W (1-971)

82 LysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyrTrp 101
::: 222
8 AGCTCGCTTCTGCTGCTCAGATGTCGAGCTGCTCTTACACGAGATGCTACTG 67
::: 30
102 GlyLeuGluGluAlaHisLeuGluTyrCysGlnArgLeuAspArgMetSer 121
::: 30
68 GGTCTGAGAGCGCCAGCTCAGCGCTGCTCCACGCGCTGAGACCGCTGTC 127
::: 30
122 AspThrTyrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAlaArg 141
::: 30
128 GACTGCTTCTGCTCAGCTTCTCCGAGGAG- -GAG 160
::: 30
142 ProGlyGlyAlaGluAlaProSerArgArgTyrLeuGluArgMetArgThrPhe 161
::: 30
161 CCGCGGGTCCCGAG- -GAGCCAGAGCCGCTGAGAGCGCTTAGGCTGACCTT 217
::: 30
162 GluGluProThrSerSerLeuAlaGlnIleLeuAlaSerValSerValPheVal 181
::: 30
218 GAAGAACCCACCTCGTCACTGCGAGCGCAGATCTGGCTTCTGCTGCTGTTTGT 277
::: 30
182 IleValSerMetValValLeuCysAlaSerThrLeuProAspTyrArgAsnAla- - 199
::: 30
278 GTCTCTCCATGTGATGCTGTGTGCGACACCTTCCGCGAGCTGGAAGACCTCCGAGACC 337
::: 30

200 -----AlaAlaAspAsnArgSerLeuAsp----- 207
338 CTGGACCAGCACAGGTAGGTGGTGGGGGGGAGCTGTGTAGAGGTCTGGGGCTCT 397
208 -----AspArgSerArgIleGluAlaIleCysIleGlyTyrPheThr 222
398 CTCTGATTGGCGGCTCTCC-TCAGAAATCATCAGACTGTGTGATCAGCTGGTTCACC 456
223 AlaGluCysIleValArgPheIleValSerLysAsnLysCysGluPheValLysArgPro 242
457 GCCGAGTGTATGTTCCGGTTCCTGGTGGCGGGAGCAAGTGCAGATTGTCCCGCGCCT 516
243 LeuAsnIleIleAspLeuLeuAlaIleThrProTyrTyrIleSerValLeuMetThrVal 262
517 CTGAACATCATCGACCTGCTGGCCATCAGCCCTACTACGCTCCGTCACCGTCCACG 576
263 PheThrGlyGluAsnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLeuArgMet 282
577 CTGACGGGGGAAAACTCCAGCTGCAGCGGGCGGGGTGACCTCCGAGTGTCCGATC 636
283 MetArgIlePheTyrValIleLysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGly 302
637 ATGAGGATCTTCTGGGTATCAAGCTAGCGCGTCACTTCCTGGCGCTGCAGACGCTCGG 696
303 LeuThrLeuLysArgCysTyrArgGluMetValMetLeuValPheIleCysValAla 322
697 CTGACGCTTCGACGCTCTACCGGAAATGATGATGCTCTGCTGCTTCTCATCTCGTTGCC 756
323 MetAlaIlePheSerAlaLeuSerGlnLeuLeuGluHisGlyLeuAspLeuGluThrSer 342
757 ATGCGATCTTCAGTGCACCTGGCAGCTGCTGGACGCGCTCGACCTCGGAGCGGGA 816
343 AsnLysAspPheThrSerIleProAlaAlaCysTyrTrpValIleIleSerMetThrThr 362
817 AACGAGACTACGCCAGCTCCCGCAGCTGTTGGTGGTGCATCATCTCCATGACGACG 876
363 ValGlyTyrGlyAspMetTyrProIleThrValProGlyArgIleLeuGlyValCys 382
877 GTGGGCTACGCGGACATGTACCGGTGACGCGGCGCGGCTGCTGGCGGGCTGTGC 936
383 ValValSerGlyIleValLeuLeuAlaLeuPro 393
937 GTGTGAGCGGATCTGCTGCTGGCGCTGCC 969
RESULT 2
BU274588
LOCUS
DEFINITION 603533001F1 CS5QCHN53 Gallus gallus cdna clone ChEST490a2 5', mRNA
sequence.
ACCSSION
VERSION BU274588.1 GI:25545538
KEYWORDS EST.
SOURCE
ORGANISM Gallus gallus (chicken)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 772)
AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
22335534
MEDLINE
PUBMED 12443392
COMMENT
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

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source

Location/Qualifiers
1..772
/organism="Callus gallus"
/mol_type="mRNA"
/strain="Compton line 151"
/db_xref="taxon:9031"
/clone="ChSRT490a2"
/sex="Female"
/tissue_type="cerebrum"
/dev_stage="adult"
/lab_host="DHI08"
/clone_lib="CSEQCHNS3"
/note="Organ: brain; Vector: pbluescript II KS(+); Site_1:
EcoRI; Site 2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pbluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

ORIGIN

Alignment Scores:
Pred. No.: 1 54e-91 Length: 772
Score: 946.00 Matches: 210
Percent Similarity: 87.11% Conservative: 13
Best Local Similarity: 82.03% Mismatches: 13
Query Match: 41.35% Indels: 23
DB: 13 Gaps: 4

US-10-016-647-2 (1-425) x BU274588 (1-772)

Qy 178 ValValPheValLeuValSerMetValValLeuValCysAlaSerThrLeuProAspTrpArg 197
Db 5 ATCTCTTCGTCATCGTGC-ATGGTGTGTCTGTGGCCAGCAGCCCTGCCAGTGGCGG 63
Qy 198 AsnAlaAlaAspAsnArgSerLeuAspArgSerArg----- 211
Db 64 GC-GCCGGA-----AACCGCAGCTGGAGGAGCAGCAGGATACACACAGTCAGTG 116
Qy 212 -----IleIleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIle 226
Db 117 AGGAGCCCTCAGGGGATAATTGAAGCTATCTGCATAGGCTGTCTACTGCAGATGCATT 176
Qy 227 ValArgPheIleValSerIleAsnIleCysGluPheValIleValArgPheLeuAsnIleIle 246
Db 177 GTGAGTTTCATCGTTTCAAGAACAAAGTGTGAGTTTGTGAGAGACCTCTCACATTATT 236
Qy 247 AspLeuLeuAlaIleThrProTyrTrpIleSerValLeuMetThrValPheThrGlyGlu 266
Db 237 GATTTACTGGCAATTACTCTTACTACATCTCTGTTCTTAATGACAGTTTTACAGGGGAA 296
Qy 267 AsnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePhe 286
Db 297 AATTGCACTCCAGAGGGGTGGAGTCACTTTGAGGGTCTTAAGATGATGAGGA--TTT 354
Qy 287 TrpValIleLeuValLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLys 306
Db 355 TGGTGTGATTAATCGCTCTGCTCTTTCATTTGCGCTTCAACACTTGTCTGACTCTGAGAG 414
Qy 307 ArgCysTrpArgGluMetValMetLeuValPheIleCysValAlaMetAlaIlePhe 326
Db 415 CGTTGTACAGAGATGGTGTGCTCTTCTTATCTGTCTGCTATGCAATTTC 474
Qy 327 SerAlaLeuSerGlnLeuGluHisGlyLeuAspLeuGluThrSerAsnIleAspPhe 346
Db 475 AGTGCATTTTCCAGCTGTCTTGAATAATGGGCTGGACTTGGGAACAAAGATAGGATTAT 534

Qy 347 ThrSerIleProAlaAlaCysTrpTrpValIleIleSer-MetThrThrValGlyTyrGlu 366
Db 535 GCCAGCATCCCTGCTGCTGCTGGTGGTGGTATCATCTCTCATGCCACACAGTTGGTTACGG 594
Qy 366 YAspMetTrpProIleThrValProGlyArg----IleLeuGlyGlyValCysVal-Vals 385
Db 595 TGACATGTGTCCCATCACAGTACCGGAAAGGGATCTTGGAGGGGAATCTGCGTGGGTGA 654
Qy 385 erGlyIleValLeuLeuAlaLeuProIleThr---PheIleTyrHisSerPheValGlnC 404
Db 655 GTGGCATCGTTTACTAGCCCTTGCCTCAATCACCATTTCATTTATCATAGCTTTGTGCAGT 714
Qy 404 ysfYr-HisGlu-LeuLysPheArg-SerAlaArgTyr 415
Db 715 GTTACCATGAGGCTCAAGTTCCGGATCTGCTAGGTAT 752

RESULT 3
AI043703 523 bp mRNA linear EST 05-JUL-1999
LOCUS UI-R-CO-31-g-04-0-UI.s1 UI-R-CO Rattus norvegicus cDNA clone
DEFINITION UI-R-CO-31-g-04-0-UI 3', mRNA sequence.
ACCESSION AI043703
VERSION AI043703.1 GI:3290438
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 523)
AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu

Oligo-dT track not found. Not 1 site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.
Fatima Bonaldo, Ph.D. Clone distribution: clones will be available
through Research Genetics This clone is also available through the
I.M.A.G.E. Consortium at LNL (info@image.llnl.gov). IMAGE
ID=1783128
Seg primer: M13 Forward
POLYA-No. Location/Qualifiers
1..523
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CO-31-g-04-0-UI"
/dev_stage="adult"
/lab_host="DHI08 (Life Technologies)"
/clone_lib="UI-R-CO"
/note="Vector: p7T3b-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-CO
library is a subtracted library derived from the UI-R-A1
and UI-R-E1 libraries. The UI-R-A1 library consisted of a
mixture of individually tagged normalized libraries
constructed from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, and muscle. The UI-R-E1
library consisted of a mixture of individually tagged
normalized libraries constructed from 8, 12 and 18-day
embryo. The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dT track which

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allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-C0) was constructed as follows: PCR amplified cDNA inserts from a pool of UI-R-A1 and UI-R-E1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the pooled UI-R-A1 and UI-R-E1 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C0 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996)".

ORIGIN

Alignment Scores:
 Pred. No.: 1,4e-88 Length: 523
 Score: 887.00 Matches: 172
 Percent Similarity: 99.42% Conservative: 0
 Best Local Similarity: 99.42% Mismatches: 1
 Query Match: 40.05% Indels: 0
 DB: 9 Gaps: 0

US-10-016-647-2 (1-425) x AT043703 (1-523)

QY 200 AlaAlaAspAsnArgSerLeuAspArgSerArgIleGluAlaIleCysIleGly 219
 Db 3 GCGCCGACAAACCGAGTCGAGTATCCGAGGAGGAGGATTAATGAGCTATCTGATAGC 62
 QY 220 TrpPheThrAlaGluCysIleValArgPheIleValSerIlyAsnLysCysGluPheVal 239
 Db 63 TGGTTACCCGGAGTGCATCGTGGGTTTCATCGTCTCCAAAACAAGTGTGAGTTGTC 122
 QY 240 LysArgProLeuAsnIleIleAspLeuLeuAlaIleThrProTyrTyrIleSerValLeu 259
 Db 123 AAGAGACCCCTGACATCATCTAGCTTACTGGCAATCACCCCTATTACATCTCCGGCTG 182
 QY 260 MetThrValPheThrGlyGluAsnSerGlnLeuGluArgAlaGlyValThrLeuArgVal 279
 Db 183 ATGACAGTGTTCACGCGAGAACTCTCACTCCAGAGGGCTGGGTCACTGAGGTC 242
 QY 280 LeuArgMetMetArgIlePheThrValIleLysLeuAlaArgHisPheIleGlyLeuGln 299
 Db 243 CTCGGAATGATGGGATCTTCGGGTGATTAAAGCTTCCCGGCACCTCATCGGCTGCAG 302
 QY 300 ThrLeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeuValPheIle 319
 Db 303 ACCCTGGGCTTGACTCTCAAGCGATGCTACCGAGAGATGGTATGTGTCTGCTTCATC 362
 QY 320 CysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuGluHisGlyLeuAspLeu 339
 Db 363 TGTGTGCTATGGGATCTTCAGTGCACCTCTCAGCTCCTTGAGCAGGGTGGACTTG 422
 QY 340 GluThrSerAsnLysAspPheThrSerIleProAlaAlaCysTrpTrpValIleIleSer 359
 Db 423 GAGAGTCCAAAGACATTTGCCAGCATCCCGCTGCTGCTGGGTGATTATCTCT 482
 QY 360 MetThrThrValGlyTyrGlyAspMetTyrProIleThr 372
 Db 483 ATGACTACAGTGGGCTATGGAGACATGTATCTCATCA 521

RESULT 4

CG639652 509 bp DNA linear GSS 02-OCT-2003
 LOCUS OST371309 Mus musculus 129SV/EV Mus musculus genomic clone
 DEFINITION OST371309, genomic survey sequence.
 ACCESSION CG639652
 VERSION CG639652.1 GI:37463501
 KEYWORDS GSS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 509)
 Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
 Pigott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
 Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
 Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
 Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
 Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
 Zhu, Q., Person, C. and Sands, A.T.
 Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
 screen to identify potential targets for therapeutic intervention
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
 Contact: Zambrowicz BP
 OmniBank
 Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: materials@lexgen.com
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as
 described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
 Class: Gene Trap.
 Location/Qualifiers
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 /strain="129SV/EV"
 /db_xref="taxon:10090"
 /clone="OST371309"
 /cell_type="embryonic stem cell"
 /clone_lib="Mus musculus 129SV/EV"

TITLE

JOURNAL

COMMENT

FEATURES
source

ORIGIN

Alignment Scores:
 Pred. No.: 4.14e-83 Length: 509
 Score: 838.00 Matches: 164
 Percent Similarity: 98.20% Conservative: 0
 Best Local Similarity: 98.20% Mismatches: 2
 Query Match: 37.83% Indels: 1
 DB: 29 Gaps: 0

US-10-016-647-2 (1-425) x CG639652 (1-509)

QY 211 ArgIleIleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleValArgPheIle 230
 Db 5 AGGATAATTGAAGTATCTGCATAGGTGGTTCCCGCGAGTGCATCGCGGTTTCATC 64
 QY 231 ValSerIlyAsnLysCysGluPheValLysArgProLeuAsnIleIleAspLeuLeuAla 250
 Db 65 GTCTCCAAAACAAGTGTGAGTTGTCAAGAGACCCCTGACATCATTTACTTGGCA 124
 QY 251 IleThr-ProTyrTyrIleSerValLeuMetThrValPheThrGlyGluAsnSerGlnLe 270
 Db 125 ATCACAGCCCTATTACATCTCTGTGCTTAATGACAGTGTTCACAGGCGAGAACTCTCAACT 184
 QY 270 uGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTrpValIleLy 290
 Db 185 CCAGAGGGCTGGGTCACCTTGAGGGTCTCCGAGATGCGGATCTTCGGGTGATCAA 244
 QY 290 sLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLysArgCysTyrAr 310
 Db 245 GCTTGCCCGGCACCTTCATTGGTCTGCAGACACATGGGCTTGACTCTCAAGCGGTCTACCG 304
 QY 310 gGluMetValMetLeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeuSe 330
 Db 305 AGATGGTATGATGTATTCTGTCTTCATCTGTGTGCTGATGGCAATCTTTAGTGCATCTC 364
 QY 330 rGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIlePr 350
 Db 365 TCAGCTCTTGAACATGGGCTGGACCTGGAAACATCAACACAGGATTTGCCAGCATCCC 424
 QY 350 cAlaAlaCysTrpTrpValIleIleSerMetThrThrValGlyTyrGlyAspMetTyrPr 370
 Db 425 CGCTGCTCTGTTGGGTGATTATCTATGACTACAGTTGGCTGAGAGATATGATATCC 484

QY	370	oileThrValProGlyArg	376
Db	485	TATCAGCGCGCTCGAAGA	503
RESULT 5	AY417318	2565 bp	linear
LOCUS	AY417318	GSS	17-DEC-2003
DEFINITION	Homo sapiens KCNB1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.		
ACCESSION	AY417318	GI:39773278	
VERSION	AY417318.1		
KEYWORDS	GSS.		
SOURCE	Homo sapiens	(human)	
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 2565)		
AUTHORS	Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D., and Cargill, M.		
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios		
JOURNAL	Science	302 (5652)	1960-1963 (2003)
PUBMED	14671302		
REFERENCE	2 (bases 1 to 2565)		
AUTHORS	Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D., and Cargill, M.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-NOV-2003)	Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA	
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.		
FEATURES	Location/Qualifiers		
source	1..2565		
gene	/organism="Homo sapiens"		
	/mol_type="genomic DNA"		
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	/gene="KCNB1"		
	/locus_tag="HCM6184"		
ORIGIN			
Alignment Scores:			
Pred. No.:	2,46e-75	Length:	2565
Score:	779.50	Matches:	172
Percent Similarity:	59.76%	Conservative:	82
Best Local Similarity:	40.47%	Mismatches:	161
Query Match:	35.19%	Indels:	12
DB:	29	Gaps:	5
US-10-016-647-2 (1-425) x AY417318 (1-2565)			
QY	1	MetThrPheGlyArgSerGlyAlaAlaSer-----ValValLeuAsnValGlyValAla	18
Db	49	ATGGAGATCGTGGCGACGACGCGTCTCTCGCGCGGTCCGCTCAACGTCGGGGGCTG	108
QY	19	ArgTyrSerLeuSerArgGluLeuLeuLysAspPheProLeuArgArgValSerArgLeu	38
Db	109	GGCAGAGGTACTTGGCGTACCTCCCTGAGCCGCTGCGCGCGCGCGGCAAGCTC	168
QY	39	HisGlyCysArgSerGluArgAspValLeuGluValCysAspAspTyrAspArgGluArg	58
Db	169	CGGAGCTGCAACGACGACACGCTGCTGCTCGAGGTGTCGATGACTACAGCTCGACGAC	228
QY	59	AsnGluTyrPhePheAspArgHisSerGluAlaPheGlyPheLeuLeuTyrValArg	78
Db	229	AACGAGTACTTCTTTCACCGCCACCGCGCGCTTACCTCCATCTCTCAACTTCTACCGC	288
QY	79	GlyHisGlyLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMet	98

DEFINITION Mus musculus KCBN1 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY417320
VERSION AY417320.1 GI:39773280
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 2562)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source 1. 2562
location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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/gene="KCBN1"
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ORIGIN
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Pred. No.: 4,11e-75 Length: 2562
Score: 777.50 Matches: 175
Percent Similarity: 59.77% Conservative: 82
Best Local Similarity: 40.70% Mismatches: 153
Query Match: 35.10% Indels: 23
DB: 29 Gaps: 7
US-10-016-647-2 (1-425) x AY417320 (1-2562)
QY 1 MetThrPheGlyArgSerGlyAlaAlaSer-----ValValLeuAsnValGlyGlyAla 18
DB 49 ATGGAGATCGCGCAGCAAGCGGTGCTCGCGCGGTGGCGCTCAACGTCGGGGGCGCTG 108
QY 19 ArgTyrSerLeuSerArgGluLeuLeuLysAspPheProLeuArgArgValSerArgLeu 38
DB 109 GCGCAGAGGTGCTGTGGCGCATCTCGACCGCTCGCGCGGTGGCGCGGTGGCGCAAGCTC 168
QY 39 HisGlyCysArgSerGluArgAspValLeuGluValCysAspTyrAspArgGluArg 58
DB 169 CGGAGCTGCAACAGCGAGCATCTCTGCTCCAGGTGTGGCGAGCTACAGCTCGAGGAC 228
QY 59 AsnGluTyrPhePheAspArgHisSerGluAlaPheGlyPheLeuLeuTyrValArg 78
DB 229 AAGCAGTACTTCTTCAGCGCCACCTCGCGCGCTTCACCTCTATTCTCAATTCTTACCGC 288
QY 79 GlyHisGlyLysLeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMet 98
DB 289 ---ACCGCGCGGTGCACATGATGGAGAGATGTGGCGCTGAGCTTCAGCCAGAGCTG 345
QY 99 IleTyrTrpGlyLeuGluGlyAlaHisLeuGluTyrCysGlnArgArgLeuAspAsp 118
DB 346 GACTACTGGGGCATCGATGATGATCTACCTGGAGTCTCTGCTGCGAGCGCTACCAACAA 405
QY 119 ArgMetSerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeu-----Gly 136

Db 406 AAGAA-----GGAGCAGATGAACGAGGAGTGAAGCGGAGGC 443
QY 137 ArgAspGluAlaArgProGlyGlyAlaGluAlaProSerArgArgTrpLeuGluArg 156
Db 444 TGAGACGCTCGCGGAGCGGAGGCG-AGGAGTTCCGACACACACGTCGTCTGAGAAGA 502
QY 157 MetArgArgThrPhe-----GluGluProThrSerSerLeuAlaAlaGlnIleLeu 173
Db 503 GG-AGAAGACITGGGACCTGCTCGAGAGGCCAACTCATCGGTGGCGCCCAAGATCTG 561
QY 174 AlaSerValSerValPheValIleValSerMetValValLeuCysAlaSerThrLeu 193
Db 562 GCATCATCTCCATCATGTCCTCTCCACCATTCGCTCTCACTCAACACACTG 621
QY 194 ProAspTyrArgAsnAlaAlaAspAsnArgSerLeuLeuAspAsp---ArgSerArgIle 212
Db 622 CTTGAGCTACGAGGCTCGAGCAATTCGGCAGAGCAGCGACACCCGCACTGGCACAC 681
QY 213 IleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleValArgPheIleValSer 232
Db 682 GTGGAGGCTGTGTCATCGCTGGTTCACCATGAGTACTTGTGAGTTCTCTGCTCG 741
QY 233 LysAsnLysCysGluPheValLysArgProLeuAsnIleIleAspLeuLeuAlaIleThr 252
Db 742 CCCAAGAAATGGAAGTCTTTAAGGGCCCCCTCAACGCCATTGACTTACTGGCCATCTG 801
QY 253 ProTyrTyrIleSerValLeuMetThrValPheThrGlyGluAsnSerGlnLeuGlnArg 272
Db 802 CCTACTAGTCACCATCTCTCTCACAGAATCCAAAGACGCGTGTCTCAGTTCAGAT 861
QY 273 AlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTrpValIleLysLeuAla 292
Db 862 GTGCGCGCTGTGGTCCAGATCTTCGCGCATATGCGCATCTCGCGCATCTCTGAAGTTGGCC 921
QY 293 ArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysArgCysTyrArgGluMet 312
Db 922 CGCCACTCCACCGGTCTGAGTCTCTGGGCTTCACGCTGGCAGGAGTCAACAGAGCTG 981
QY 313 ValMetLeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeu 332
Db 982 GGCTTGCTCATCTCTCTCGCATGGCATCATGATCTTCTCCAGCTGGTCTCTTT 1041
QY 333 LeuGluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIleProAlaAla 352
Db 1042 GCGAGAGAGATGAGAT-----GACACCAAGTTCAAAAGCATCCCGCCCTCT 1089
QY 353 CysTrpTrpValIleIleSerMetThrThrValGlyTyrGlyAspMetTyrProIleThr 372
Db 1090 TTCTGGTGGGTACCATCACCATGACGCGTGGTTACGAGAGACATCTACCCCTAAGACT 1149
QY 373 ValProGlyArgIleLeuGlyGlyValCysValValSerGlyIleValLeuLeuAlaLeu 392
Db 1150 CTCTCGGGGAAAATCGTGGGGGCTCTGTGCAATTCGCGGTGCTGGTGGTATGGCCCTC 1209
QY 393 ProIleThrPheIleTyrHisSerPheValGlnCysTyrHisGluLeuLysPheArgSer 412
Db 1210 CCTTCATTAATTCGTAATAACTTCTCCGAGTTCTCAAGGAGGAGCAGAGCCGAGGAG 1269
QY 413 AlaArgTyrSerArgSerLeuSerThrGlu 422
Db 1270 AAGCCATCAAGCGGAGAGGCTCTGGAG 1299
RESULT 7
CG662016 484 bp DNA linear GSS 02-OCT-2003
LOCUS OST441129 Mus musculus 129Sv/Ev Mus musculus genomic clone
DEFINITION OST441129, genomic survey sequence.
ACCESSION CG662016
VERSION CG662016.1 GI:37485865
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 484)
Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP
Omnibank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
FEATURES             Location/Qualifiers
     source            1..484
     organism="Mus musculus"
     mol_type="genomic DNA"
     strain="129Sv/Ev"
     db_xref="taxon:10090"
     clone="OST444129"
     cell_type="embryonic stem cell"
     clone_lib="Mus musculus 129Sv/Ev"

ORIGIN
Alignment Scores:
Pred. No.:          4,55e-74      Length:          484
Score:              757.00        Matches:          152
Percent Similarity: 95.03%        Conservative:      1
Best Local Similarity: 94.41%      Mismatches:       6
Query Match:        34.18%         Indels:           2
DB:                  29            Gaps:             0

US-10-016-647-2 (1-425) x CG662016 (1-484)
QY 211 ArgilleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleValArgPheIle 230
Db 5 AGATTAATGAAGTATATCGATAGGTGGTTCCACGGAGTGCATCGTGGTTCATC 64
QY 231 ValSerIleAsnLysCysGluPheValLysArgProLeuAsnIleIleAspLeuAla 250
Db 65 GTCTCCAAAACAAGTGTGAGTTTGTCAAGAGACCCCTGAACATCATTCGCTACTGGCA 124
QY 251 IleThrProTyrIleSerValLeuMetThrValPheThrGlyGluAsnSerGlnLeu 270
Db 125 ATCAGCCCTATTACATCTCTGTGTAATGACAGTGTTCACAGCGAGACCTCAACTC 184
QY 271 GlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePheTrpValIleL 290
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QY 290 YsLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysAtqCysTyrA 310
Db 245 AGCTGCGCGGCATTCATTGGTCTGACAGACATGGGCTTGATCTCAACGGGTGTACC 304
QY 310 rgGluMetValMetLeuLeuValPheIleCysValAlaMetAlaIlePheSerAlaLeuS 330
Db 305 GAGAGATGGTCATGTTACTTCTTCTTCATCTGTGTGTCATGGCAATCTTTTGGCACTCT 364
QY 330 erGlnLeuLeuGluHisGlyLeuAspLeuGluThrSerAsnLysAspPheThrSerIleP 350
Db 365 CTCAGCTCCTTGAACATGGGTGACCTGGAAACATCCAAACAGGATTTCCGCCAGATCC 424
QY 350 roAlaAlaCysTrpTrpValIleIleSerMetThrThrValGlyTyrGlyAspMetTyr 369
Db 425 CCGCTGCTGCTGGTGGTGGTGAATATCTTATGACTACAGTTGGCTATGGAGATATGCAT 483

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RESULT 8 AQ402619/c

LOCUS
DEFINITION
HS 5066 A2_E01_T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=642 Col=2 Row=I, genomic survey sequence.

ACCESSION
AQ402619
VERSION
AQ402619.1 GI:4413531

KEYWORDS
GSS.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 500)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.

TITLE
Sequence-tagged connectors: A sequence approach to mapping and

scanning the human genome

JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

MEDLINE
9380589

PUBMED
1049764

COMMENT
Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)

or from Resear h Genetics (info@resgen.com). BAC end Web Server:

http://www.htsc.washington.edu

Plate: 642 row: 1 column: 2

Seq primer: T7

Class: BAC ends

High quality sequence stop: 500.

Location/Qualifiers

source

1..500

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/db_xref="taxon:9606"

/clone="Plate=642 Col=2 Row=I"

/sex="male"

/clone_lib="RPCI-11 Human Male BAC Library"

/note=Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;

Male blood DNA was isolated from one randomly chosen donor

and partially digested with a combination of EcoRI and

EcoRI Methylase. Size selected DNA was cloned into the

pBACe3.6 vector at EcoRI sites"

ORIGIN

Alignment Scores:
Pred. No.: 5,11e-71 Length: 500
Score: 730.00 Matches: 144
Percent Similarity: 93.63% Conservative: 3
Best Local Similarity: 91.72% Mismatches: 10
Query Match: 32.96% Indels: 0
DB: 28 Gaps: 0

US-10-016-647-2 (1-425) x AQ402619 (1-500)

QY 267 AsnSerGlnLeuGlnArgAlaGlyValThrLeuArgValLeuArgMetMetArgIlePhe 286

Db 498 AACTCTCAACTCCAGAGGGCTGAGTCCACCTTGAGGTACTTAGAATGATGAGGATATT 439

QY 287 TrpValIleLysLeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLys 306

Db 438 TGGGTGATTAAAGCTGCCAGTCACTTCATTTGCTTCAGACACTCGGTTTGACTCTCAA 379

QY 307 A-gCysTyrArgGluMetValMetLeuLeuValPheIleCysValAlaMetAlaIlePhe 326

Score:	718.50	Matches:	157
Percent Similarity:	57.47%	Conservative:	93
Best Local Similarity:	36.09%	Mismatches:	144
Query Match:	32.44%	Indels:	41
DB:	11	Gaps:	10

US-10-016-647-2 (1-425) x AK012275 (1-2757)

QY	13	LeuAsnValGlyValAlaArgTyrSerLeuSerArgGluLeuLeuLeuLysAspPheProLeu	32
DB	225	GTCAACGTGGGGGTAGCGCTTCGTCTCGCAGCAAGCTCTGCTCTCCGCGAC	284
QY	33	ArgArgValSer-----ArgLeuHisGlyCysArg	42
DB	285	ACGCGCTGGGAACTGGCGTAGTGGCTCTTACCCGCGCTGGTGGCTGGCT	344
QY	43	SerGluArgAspValLeuGluValCysAspTyrAspArgGluArgAsnGluTyrPhe	62
DB	345	CGCGCCCCGAGCCCTGGAGTCTTGGCATGATGCAATCGCGTGGCAACGAGTACTTC	404
QY	63	PheAspArgHisSerGluAlaPheGlyPheLeuLeuLeuTyrValArgGlyHisGlyLys	82
DB	405	TTTGATCGGAGCTCTCAGCGCTTCGTTATGTCCTGCACTACTATCGC---ACTGTCGC	461
QY	83	LeuArgPheAlaProArgMetCysGluLeuSerPheTyrAsnGluMetIleTyrTrpGly	102
DB	462	CTGCATGTCATGAGCAGCTGTGCGCTCTCTTCTTCAGGAGATCCAGTACTGGGC	521
QY	103	LeuGluGlyAlaHisLeuGluTyrCysGlnArgArgLeuAspArg-----Met	120
DB	522	ATAGATGAACCTCAGCATTGACCTCGCTGCGAGGACAGATCTTCAGAGAAGAGAGCTG	581
QY	121	SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla	140
DB	582	AGTGAACCTTCGACTTTAAGAGACACAGATGACCGAGGAAGTCAACATGAGCTGAA	641
QY	141	ArgProGlyGlyAlaGluAlaProSerArgArgTrpLeuGluArgMetArgArgThr	160
DB	642	CAGCAGCTTCTCAAAAGGACCTTGTCCACTGTCCGA-----CAAAAGCTCTGGATAT	695
QY	161	PheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValValPhe	180
DB	696	CTCGAAGACCTGGATCTTCCACAGAGCCCGATCTTTGGAGTAATCTCCATATTTT	755
QY	181	ValIleValSerMetVal-----ValLeuCysAlaSerThrLeuProAspTrpArgAsn	198
DB	756	GTGCGAGTGTCCATCGTCAACATGCCCTGATGTGAGCTGAGCTT---AGTGGCTCAAC	812
QY	199	AlaAlaAspAsnArgSerLeuAspAspSerArgIleLeuGluAlaIleCysIle	218
DB	813	CTA-----CAGCTGTGGAGATCTTGGAGTATGTGTGATC	848
QY	219	GlyTrpPheThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGluPhe	238
DB	849	AGCTGTTCACCGGGAGTTCGTCTGGCTTCCTATGTGTGAAAGACAGGTGCCACTTC	908
QY	239	ValLysArgProLeuAsnIleLeuAspLeuAlaIleThrProTyrTyrIleSerVal	258
DB	909	CTGAGGAGGTTCACAAACATCATAGACTCTCTGCGCTTGGCCCTCTTATATACCTCT	968
QY	259	LeuMetThrValPheThrGlyGluAsnSer-----GlnLeuGlnArgAlaGlyValThr	276
DB	969	CTGGTGAAGCTGTAGCGGACGACACACACAGAGCTGGAATGTGGAGCTGTG	1028
QY	277	LeuArgValLeuArgMetMetArgIlePheTrpValIleLysLeuAlaArgHisPheIle	296
DB	1029	GTCCAGGTCTTGAAGCTCTCAGAGCTCTGCGCATGCTGAACTGGGAAGCATCTTACA	1088
QY	297	GlyLeuGluThrLeuGlyLeuThrLeuLysArgCysTyrArgGluMetValMetLeuLeu	316
DB	1089	GGATTCGCTCACTTGGGATGACATCACTAGTGTCTATGAAGAGTGGCTACTGCTC	1148
QY	317	ValPheIleCysValAlaMetAlaIlePheSerAlaLeuSerGlnLeuLeuGluHisGly	336

Db	1149	CTGTTCTACTCTGGGGATTCTTATATTTTCAACAATAGATATACTTTCAGAGCAAGC	1208
QY	337	LeuAspLeuGluThrSerAsnLysAspPheThrSerIleProAlaAlaCysTrpTrpVal	356
DB	1209	ATTCTCTGATACAACC-----TTCAAGTGTTCCTTGTGTCATGGTGGGCC	1256
QY	357	IleIleSerMetThrThrValGlyTyrGlyAspMetTyrProIleThrValProGlyArg	376
DB	1257	ACAATATCCATGACTACAGTAGGATATGGGACATTAGACACACACACAGGCAAA	1316
QY	377	IleLeuGlyGlyValCysValValSerGlyIleValLeuLeuAlaLeuProIleThrPhe	396
DB	1317	ATCGTGGCTTCATGTGATTCGTGTCAGGAATCCTTCTTGGCTTGCCTATTGCCATT	1376
QY	397	IleTyrHisSerPheValGlnCysTyrHisGluLeuLysPheArgSerAla-----	413
DB	1377	ATTAAATGATCGATTCTCTGCTTCTACTTCACTTGAACCTCAAGAACGACCTGTGAG	1436
QY	414	-----ArgTyrSerArgSerLeuSerThrGlu	422
DB	1437	CAGCGTGAAGCTCTCAAGAACTTACCAAGATATAGCCACTGAC	1481
RESULT 10			
AK034091		4390 bp mRNA linear	HTC 18-SEP-2003
LOCUS		Mus musculus adult male diencephalon cDNA, RIKEN full-length	
DEFINITION		enriched library, clone:933015SW08 product:POTASSIUM CHANNEL KV8.1	
		homolog [Mesocricetus auratus], full insert sequence.	
ACCESSION	AK034091	GI:26329684	
VERSION	AK034091.1	GI:26329684	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE			
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,		
	Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to		
	prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,		
	Kono, H., Akiyama, J., Nishi, K., Kitasumi, T., Tashiro, H., Itoh, M.,		
	Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,		
	Yamamoto, R., Matsumoto, H		

JOURNAL

REFERENCE

AUTHORS

Nature 420, 563-573 (2002)
 6 (bases 1 to 4390)
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kojima, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, K., Sakai, C., Sakai, K., Sakazume, N., Sasaki, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sugabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaki-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
 Direct Submission
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.go.jp/
 URL: http://antom.gsc.riken.go.jp/

TITLE

JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.go.jp/
 URL: http://antom.gsc.riken.go.jp/

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.go.jp/
 URL: http://antom.gsc.riken.go.jp/

FEATURES

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Db	503	TTTGATCGCAGCTCTCAGCGCTTCGTATGTCCTGCACTACTATCGC-----	559
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Qy	121	SerAspThrTyrThrPheTyrSerAlaAspGluProGlyValLeuGlyArgAspGluAla	140
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Qy	161	PheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAlaSerValSerValPhe	180
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Qy	181	ValIleValSerMetVal-----ValLeuCysAlaSerThrLeuProAspTrpArgAsn	198
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Qy	199	AlaAlaAlaAspAsnArgSerLeuAspArgSerArgIleIleGluAlaIleCysIle	218
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Qy	219	GlyTrpPheThrAlaGluCysIleValArgPheIleValSerLysAsnLysCysGluPhe	238
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ORIGIN

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 Best Local Similarity: 36.09% Mismatches: 144
 Query Match: 32.44% Indels: 41
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US-10-016-647-2 (1-425) x AK034091 (1-4390)

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 AK046054
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 HTG; CAP trapper.
 Mus musculus (house mouse)
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 1
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 99279253
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 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 20499374
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 3
 Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
 11076861
 4
 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)
 5
 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6
 (bases 1 to 2936)
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akashira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

SOURCE Mus musculus (house mouse)
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 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
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 1 (bases 1 to 1476)
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D., and Cargill, M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 2 (bases 1 to 1476)
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D., and Cargill, M.
 Direct Submission
 TITLE Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 JOURNAL
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 QY 391 AlaLeuProIleThrPheIleTyrHisSerPheValGlnCysTyrHisGluLeuLys 409
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RESULT 14
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 VERSION AY398781.1 GI:39748569
 SOURCE GSS.
 ORGANISM Homo sapiens (human)
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1503)
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D., and Cargill, M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 1503)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
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 QY 39 -----HisGlyCysArgSerGluArgAspValLeuGluValCysAspAspTyr 54
 DB 223 TACCGCGCGCCCGGGCCCTCGCGCGCTGCCAGCCCTTCGAGCTTTGCCAGCATGCC 282
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 QY 75 LeuTyrValArgGlyHisGlyLysLeuArgPheAlaProArgMetCysGluLeuSerPhe 94
 DB 343 CACTACTACGCG---ACCGCGCCGCTGCATGTCTAGCAGCAGCTGTGCGGCTCTCTTC 399
 QY 95 TyrAsnGluMetIleTyrTrpGlyLeuGluGlyAlaHisLeuGluTyrCysCysGlnArg 114
 DB 400 CTCGAGGAGATCAGTACTCGGGCATCTGAGTACCTCAGCATCGCTCTGTCAGGGAC 459
 QY 115 ArgLeuAspAspArgMetSerAspThrTyrThrPheTyrSerAlaAspGluProGlyVal 134
 DB 460 AGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 519
 QY 135 LeuGlyArgAspGluAlaArgProGlyGlyAlaGluAlaAlaProSerArgArgTrpLeu 154
 DB 520 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 579
 QY 155 GluArgMetArgArgThrPheGluGluProThrSerSerLeuAlaAlaGlnIleLeuAla 174
 DB 580 CAGAGCTCTGGATATCTCTGGAGAACCTGGATCTTCACACTGCCGCTATCTTTGGC 639
 QY 175 SerValSerValValPheValIleValSerMetVal-----ValLeuCysAlaSerThr 192
 DB 640 GTCATCTCCATTATCTTCGTGGTGTGTCTCATCATTAAACATGCCCTGATCGAGCTAG 699
 QY 193 LeuProAspTrpArgAsnAlaAlaAlaAspAsnArgSerLeuAspArgSerArgGlie 212

DB 700 TTA---AGCTGG-----CTGGACCTGCAGCTGCTGGAA-----ATC 732
 QY 213 IleGluAlaIleCysIleGlyTrpPheThrAlaGluCysIleValArgPheIleValSer 232
 DB 733 CTGGAGTATGTGTGTCATTAGTGTTCACCGGGAGTTTGTCTCCCTTCTCTGTGTGTG 792
 QY 233 LysAsnLysCysGluPheValLysArgProLeuAsnIleIleAspLeuAlaIleThr 252
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 QY 291 LeuAlaArgHisPheIleGlyLeuGlnThrLeuGlyLeuThrLeuLysAspCysTyrArg 310
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 DEFINITION genomic survey sequence.
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 VERSION AY398783.1 Gi:39748571
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 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1406)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 1406)

AUTHORS

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.

TITLE

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
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Query Match:	31.20%	Indels:	71
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US-10-016-647-2 (1-425) x AY398783 (1-1406)

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